

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng) from *N. gonorrhoeae*:

m151/g151

m151.pep	10	20	30	40	50	60
	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMDSNDLEKERGITILAKNT					
g151	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMDSNDLEKERGITILAKNT					
	10	20	30	40	50	60
m151.pep	70	80	90	100	110	120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
g151	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
	70	80	90	100	110	120
m151.pep	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDES					
g151	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESS					
	130	140	150	160	170	180
m151.pep	190	200	210	220	230	240
	DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRIGIGRILNGRIKPGQTVAMN					
g151	DMRPLFDITILKYTPAPSGSADEPLQLQISQLDYDNYTGRIGIGRILNGRIKPGQTVAMN					
	190	200	210	220	230	240
m151.pep	250	260	270	280	290	300
	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
g151	HEQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
	250	260	270	280	290	300
m151.pep	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLOKELLTNVALRVEDTADADVFRVSGR					
g151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLOKELLTNVALRVEDTADADVFRVSGR					
	310	320	330	340	350	360
m151.pep	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR					
g151	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR					
	370	380	390	400	410	420
m151.pep	430	440	450	460	470	480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
g151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
	430	440	450	460	470	480
m151.pep	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
g151	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
	490	500	510	520	530	540
m151.pep	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELEERRHFK					
g151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELEERRHFK					
	550	560	570	580	590	600

433

m151.pep KLDX
 ||||
 g151 KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

a151.seq
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCACGTCG ACCACGGCAA
 51 AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
 101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
 151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
 251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
 301 CAGGAAGGCC CGATGCCGCA AACCCTTTTC GTGACCAAAA AAGCCTTGCC
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAATCGAC AAACCGTCCG
 401 CCCGTCCGAG CTGGGTCATC GACCAAACTT TCGAGCTGTT CGACAACCTG
 451 GGCGGCGACC ACGAGCAGTT GGATTTCCCG ATTGTTTATG CTTCCGGTCT
 501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
 551 CGCTGTTTGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
 601 GACGAAACGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
 651 CGGCCGCCTC GGTATCGGTC GTATCTTGAA CGGACGTATC AAGCCCGGTC
 701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGCATC
 751 AACCAGCTTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCGC TTGAAGAAGC
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATTGAAGAC ATCGGCATCG
 851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
 901 GTGGACGAAC CGACGCTGAC TATGGACTTT ATGGTCAACA CCAGCCCCTT
 951 GGCAGGTACG GAAGGCAAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
 1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGA AGATACCGCC
 1051 GATGCCGACG TGTTCCGCGT ATCCGGGCGC GGCGAGCTGC ACCTGACCAT
 1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
 1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
 1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAAGC GACGGCAACG
 1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGCTTC
 1351 CAAGCGGAAT TTATGACCCT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
 1401 GTTCGACGAT TACGCGCCCG TCAAACCGA TATGCCTGGC CGCCACAACG
 1451 GCGTCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTGG
 1501 AATCTGGAAG ACCGCGGCCG TATGTTGCTA TCGCCCAACG ACAAATCTA
 1551 CGAAGGTATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
 1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CCGTACCGAC
 1651 GAAGCCGTTT GCCTGACCAC GCCGATTAAG CTGACGCTGG AAGGTGCGGT
 1701 CGAGTTTATC GACGATGATG AGCTGGTAGA AATCACGCCG CAATCCATCC
 1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCATTTCAAA
 1801 AAGCTAGATT GA

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

a151.pep
 1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
 51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVVLLVDA
 101 QEGPMQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTPAPSGSA
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQAQGR
 251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGPLMLS
 301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
 351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
 401 NLTVDPVDDN QGAVMEELGR RRGELTNMES DGNGRTRLEY HIPARGLIGF
 451 QGEFMTLTRG VGLMSHVDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
 501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDDELVEITP QSIRLRKRYL SELERRRHFK
 601 KLD*

m151/a151 99.8% identity in 603 aa overlap

10 20 30 40 50 60

434

m151.pep	MKQIRNIAIIAHVDHGKTTLV	DQLLRQSGTFRANQQVDERV	MDSNDLEKERGITILAKNT
a151	MKQIRNIAIIAHVDHGKTTLV	DQLLRQSGTFRANQQVDERV	MDSNDLEKERGITILAKNT
	10 20 30 40 50 60		
m151.pep	AIDYEGYHINIVDTPGHADFG	GEVERVLGMVDCVLLVDAQ	EGPMPQTRFVTKKALALGL
a151	AIDYEGYHINIVDTPGHADFG	GEVERVLGMVDCVLLVDAQ	EGPMPQTRFVTKKALALGL
	70 80 90 100 110 120		
m151.pep	KPIVVINKIDKPSARPSWVIDQ	TFFELFDNLGATDEQLDFPI	VYASGLSGFAKLEETDESN
a151	KPIVVINKIDKPSARPSWVIDQ	TFFELFDNLGATDEQLDFPI	VYASGLSGFAKLEETDESN
	130 140 150 160 170 180		
m151.pep	DMRPLFDITILKYTPAPSGSA	DETLLQLQISQLDYDNYTG	RGLGIRILNGRIKPGQTVAVMN
a151	DMRPLFDITILKYTPAPSGSA	DETLLQLQISQLDYDNYTG	RGLGIRILNGRIKPGQTVAVMN
	190 200 210 220 230 240		
m151.pep	HDQQIAQGRINQLLGFKGLER	VPLEEAEAGDIVIISGIEDI	GIGVTITDKDNPKGLPMLS
a151	HDQQIAQGRINQLLGFKGLER	VPLEEAEAGDIVIISGIEDI	GIGVTITDKDNPKGLPMLS
	250 260 270 280 290 300		
m151.pep	VDEPTLTMDFMVNTSPLAGTE	GKFVTSRQIRDRLQKELLTN	VALRVEDTADADVFRVSGR
a151	VDEPTLTMDFMVNTSPLAGTE	GKFVTSRQIRDRLQKELLTN	VALRVEDTADADVFRVSGR
	310 320 330 340 350 360		
m151.pep	GELHLTILLENMRREGYELAV	GKPRVYRDI DGQKCEPYEN	LTVDVPDDNQAVMEELGR
a151	GELHLTILLENMRREGYELAV	GKPRVYRDI DGQKCEPYEN	LTVDVPDDNQAVMEELGR
	370 380 390 400 410 420		
m151.pep	RRGELTNMESDGNGRTRLEY	HIPARGLIGFQGEFMTLTR	GVGLMSHVFDYAPVKPDMPG
a151	RRGELTNMESDGNGRTRLEY	HIPARGLIGFQGEFMTLTR	GVGLMSHVFDYAPVKPDMPG
	430 440 450 460 470 480		
m151.pep	RHNGVLVSQEQGEAVAYALW	NLEDRGRMFVSPNDKIYEG	MIIGIHSRDNLDVNVPLKGKK
a151	RHNGVLVSQEQGEAVAYALW	NLEDRGRMFVSPNDKIYEG	MIIGIHSRDNLDVNVPLKGKK
	490 500 510 520 530 540		
m151.pep	LTNIRASGTDEAVRLTTPIK	LTEGAVEFIDDELVEITPQ	SIRLRKRYLSELERRRHFK
a151	LTNIRASGTDEAVRLTTPIK	LTEGAVEFIDDELVEITPQ	SIRLRKRYLSELERRRHFK
	550 560 570 580 590 600		
m151.pep	KLDX		
a151	KLDX		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

```

1  ATGAAAAaca aaACCaaagt ctgGGacttc cCaccocgcc ttTCCactG
51  GctgcttgCC gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGGCTCG GGCTGCTCGT CCTTTCCTG

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q152.ppt

The following partial DNA sequence was identified in *N.meningitidis* <SEO ID 621>:

```
m152.seq
```

1	ATGAAAAACA	AAACCAAAGT	CTGGGACCTC	CCCACCCGCC	TTTTCCACTG
51	GCTGCTTGCC	GCGTCCCTGC	CCTTTATGTG	GTATAGCGCG	AAAGCCGGCG
101	GCGATATGCT	GCAATGGCAC	ACGCGCGCTG	GGCTGTTCTG	CCTTTTCCTG
151	CTCGTATTTC	GCCTCTGCTG	GGGCATTTGG	GGCAGCGATA	CCGCGCCGTTT
201	TTCCCGTTTC	GTCCAAAGGT	GGGCAGGCAT	ACGCGCGTAT	CTGAAAAACG
251	GTATTTCCCGA	ACACATCCAG	CCCGGACACA	ACCCCTTGGG	CGCACTGATG
301	GTCGTTGCGC	TTTTGGCCGC	CGTGTCCTTC	CAAGTCGGGA	CCGGGCTTTT
351	TGCCGCCGAT	GAAAACACCT	TCAGCACCAA	CGGCTACCTC	AACCATTTGG
401	TTTCCGAACA	TACGGGCAGC	CTTATGCGGA	AAATCCACCT	CAACTTTTTC
451	AAGCTGCTCG	CCGTTTTTTT	TGCAATCCAC	ATCGCCGCCG	TCGCGCATA
501	CCGCGTATTC	AAAAAGAAAA	ACCTCATCCT	CCCGATGATA	ACCGGCTTCA
551	AATACATCGA	AGGCAAAACC	TCAATCCGCT	TTGCAGGCAA	AGCCGCGCTT
601	GCCGCGCGAT	TATCGGTTGC	CTCGCTTGCC	GCAGCCGCCA	TCCTGCTCCT
651	GTCCTGA				

m152.pep

1	MKNKTKVWDL	PTRLFHWLLA	ASLPFMWYSA	KAGGDMLQWH	TRVGLFVLFL
51	<u>LVFRLCWGIW</u>	GSDTARFSRF	VQGWAGIRGY	LKNGIPEHIQ	PGHNP <u>LGALM</u>
101	<u>VVALLAAVSF</u>	<u>QVGTGLFAAD</u>	ENTFSTNGYL	NHLVSEHTGS	LMRKTHLNFF
151	<u>KKLAVFSAIH</u>	<u>IAAAAYRVF</u>	KKKNLILPMI	TGFKYIEGKT	SIRFAGKAAL
201	<u>AAASVASLA</u>	<u>AAAILLS*</u>			

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng) from *N. gonorrhoeae*:

m152/q152

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFHWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVLFLLVFRLCWGIW					
	:					
g152	MKNKTKVWDFPTRLFWHLLAASLPFMWYSAKAGGDMQLQWHTRVGLLVFLFLLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFRVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	:					
g152	GSDTARFSRFRVRGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAN					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAHIAAVAAYRVFKKKNLILPMI					
	: : : :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFSAVHIAAVAAYRIFKKKNLVRPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVASLAAAAIILLSX			
	:			
g152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

```

a152.seq
1   ATGAAAAACA AAACCAAGT CTGGGACTTC CCCACCGGCC TTTTCCACTG
51  GCTGCTTGCC GCATCCCTAC CCTTTATGTG GTATAGCGCG AAAACCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTAT CCTTTTCCTG
151 CTCGTATTCC GCCTCTGCTG GGGCATTGCG GGCAGCGATA CCGCCCGTTT
201 CTCCCGTTTC GTCCGCGGAT GGTCCGGTAT CAGAGAGTAT ATGAAAAACG
251 GTATTCCCGA ACACGTCCAA CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGGCCGC CGTGTCGTTC CAAGTCGGCA CAGGGCTTTT
351 TGCCGCCGAT GTAAACACCT TCAGACCAAA CGGCTACCTC AACCATTGCG
401 TTTCCGAACA TACGGGCAGC CTATGCGGGA AAATCCATCT CAACTTTTTC
451 AAACGTGCTC CCGTTTTTTC CGCAGTCCAC ATCGCCGNCG TCGCCGCATA
501 CCGCGTGTTC AAAAAGAAAA ACCTCGTCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

```

a152.pep
1   MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KTGGDMLQWH TRVGLFILFL
51  LVFRLCWGIW GSDTARFSRF VRGWSGIREY MKNGIPEHVQ PGHNPLGALM
101 VVALLAAVSE QVGTGLFAAD VNTFSTNGYL NHLVSEHTGS LMRKIHLNEF
151 KLLAVFSAVH IAXVAAYRVF KKKNLVLPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAIILLS*

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m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVLLVFRLCWGIW					
	: : : :					
a152	MKNKTKVWDFPTRLFWLLAASLPFMWYSAKTGGDMLQWHTRVGLFILFLVFRLCWGIW					
	10	20	30	40	50	60

	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	: : : :					
a152	GSDTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	70	80	90	100	110	120

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAHIAAVAAYRVFKKKNLILPMI					
	: : : :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAVHIAAXVAAYRVFKKKNLILPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVASLAAAAIILLSX			
	:			
a152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

```
g153.seq
1  atgggggtttg  cttacAgat  gacgtatatc  gaggtCGGga  taccggaggc
51  ggcattccgtc  ctttcGctGC  CCGAGATgat  gcgcctgatG  GTGTTtCagg
101 attATGTTT  TttggcCGAA  GTGATGTTTG  TGctgaCTT  cGGCGcgcCG
151 GTTCTGTTtC  TGCTGCTGTG  CCTGTATGTC  TATGCCGCGC  TGATACGGAA
201 ACAGGCGTAT  CCTGCGCTGC  GTTGGCAAC  GCGTGTGATG  GTGCGCTTGA
251 GGCAGGCGAT  GATGGTGGAT  GTGTTTTTTG  TTTCCACTCT  GGTGGCGTAT
301 ATCAAGTCT  CGTCTGTGGC  AAAGGTTTCG  TTCGGGCCGG  CGTTTTATCT
351 GATGTTCCGG  CTGTCCGTTA  TGCTGATTCG  GACTTCGGTA  TCGGTTCCCC
401 AGCATTGGGT  GTATTTCCAA  ATCGGGCGGC  TGACGGGGAA  TAATGCGGTT
451 CAGACGGCAT  CGGAAGGCAA  AACCTGTTGC  AGCCGCTGCC  TGTATTTccg
501 cgacAGTgcc  gaatccCCT  GCGGGGTGtG  cgGCGcggaa  CTgtacggcg
551 gacggccgaa  aagtCTGAGt  atttCgtCGG  CGTTTCTgac  ggcggcggtT
601 GTTTTGTATT  TCCctgCcaa  TATCctgcgc  attatGAttt  cgtccAATCc
651 tgccgccacg  GAGGcCAACA  CCATCTTTAG  CGGCATCGCT  TATATGTGGG
701 ACgagggcga  CAGGCTGATT  GCGGCGGTTA  TTTTCAGCGC  GAGTATTTTG
751 GTGCCGGTGC  TGAAGATTGC  GGCAATGTCG  GTTTTGATTG  CGGCGGCACG
801 GTTCGCTTTG  CCGGCGGGCG  CAAAGAAATT  GTCGCACCTC  tacCGCATCA
851 CCGAAGCGGT  CGGCCGCTGG  TCGATGATTG  ATATTTTTGT  GATTATTATT
901 TTGATGTGTT  CGTTCacac  TTATGCCCGC  CGCGTCATTC  CGGGCAGTGC
951 GGCAGTCTAT  TTCTGCCTGG  TCGTGATTCT  GACGATGCTG  TCCGCTTATT
1001 ATTTGACCCC  GCGCCTGCTT  TGGGACAAAC  GCGCTTCAGA  CGGCATTGCT
1051 TTCAACGAAA  CGGAAAAATA  TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

```
g153.pep
1  MGFAYSMTYI  EVGIPEASV  LSLPEMMRLM  VFQDYGFLAE  VMFVLTFGAP
51  VLFLLLCLYV  YAALIRKQAY  PALRLATRV  VRLRQAMMVD  VFFVSTLVAY
101 IKLSSVAKVR  FGPAYLMFA  LSVMLIRTSV  SVPQHWVYFQ  IGRLTGNNAV
151 QTASEGKTCC  SRCLYFRDSA  ESPCGVCGAE  LYGGRPKSLs  ISSAFLTAAY
201 VLYFPANILP  IMISSNPAAT  EANTIFSGIA  YMWDEGDRLI  AAVIFSASIL
251 VPVLKIAAMS  VLIAAARFAL  PAGAKKLSHL  YRITEAVGRW  SMIDIFVII
301 LMCSFHTYAA  RVIPGSAAVY  FCLVVILTML  SAYYFDPRL  WDKRASDGIA
351 FNETEKYD*
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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

```
m153.seq
1  ATGGCGTTTG  CTTACGGTAT  GACGTATATC  GAGGTCGGGA  TACCGGGTGC
51  GGCATCCGTC  CTTTCGCTGC  CCGAGATGAT  GCGCCTGATG  GTGTTTCAGG
101 ATTATGTTT  TTTGGCCGAA  GTGATGTTTG  TGCTGACTTT  CGGCGCGCCG
151 GTTCTGTTT  TGCTGCTGTG  CCTGTATGTC  TATGCCGCGC  TGATACGGAA
201 ACAGGCGTAT  CTGCGCTGC  GTTGGCAAC  GCGTGTGATG  GTGCGCTTGA
251 GACAGGCGAT  GATGGTGGAT  GTGTTTTTTG  TTTCCACTTT  GGTGGCGTAT
301 ATCAAGTCT  CGTCTGTGGC  AGAGGTTTCG  TTCGGGCCGG  CGTTTTATCT
351 GATGTTCCGG  CTGTCACTTA  TGCTGATTCG  GACTTCGGTA  TCGGTTCCCC
401 AGCATTGGGT  GTATTTTCAA  ATCGGGCGGC  TGACGGGGGA  TAATGCGGTT
451 CAGACGGCAT  CGGAAGGTAA  AACCTGTTGC  AGCCGCTGCC  TGTATTTCCG
501 CGACAGTGCC  GAATCCCCCT  GCGGCGTGTG  CGGTGCGGAA  CTGTACCGCC
551 GACGGCCGAA  AAGTCTGAGT  ATTCGTCGG  CGTTTCTGAC  GGCggCGGTT
601 ATTTTGATT  TCCCTGCCAA  TATCCTGCCG  ATTATGATT  CGTCCAATCC
651 TGCCGCCACG  GAGGTCAATA  CCATCCTTAA  CGGCATCGCT  TATATGTGGG
701 ACGAGGGCGA  CAGGCTGATT  GCGGCGGTTA  TTTTCAGCGC  GAGTATTTTG
751 GTGCCGGTAC  TGAAGATTGC  GGCAATGTCG  GTTTTGATTG  CGTCCGCCCG
801 CTCGCTTTG  CCAACGGGTG  CAAAGAAATT  GTCGCACCTC  TACCGCATCA
851 CCGAAGCGGT  CGGCCGCTGG  TCGATGATTG  ATATTTTTGT  GATTATTATT
901 TTGATGTGTT  CGTTCACAC  TTATGCCCGC  CGCGTCATTC  CGGGCAGTGC
951 GGCAGTCTAT  TTCTGCCTGG  TCGTGATTCT  GACGATGCTG  TCCGCTTATT
1001 ATTTGACCCC  GCGCCTGCTT  TGGGACAAAC  GCGCTTCAGA  CGGCATTGCT
1051 TTCAATGAAA  CGGAAAAACA  TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

```
m153.pep
1  MAFAYGMTYI  EVGIPGAASV  LSLPEMMRLM  VFQDYGFLAE  VMFVLTFGAP
51  VLFLLLCLYV  YAALIRKQAY  PALRLATRV  VRLRQAMMVD  VFFVSTLVAY
```

101	<u>IKLSSVAEVR</u>	<u>FGPAFYLMFA</u>	<u>LSVMLIRTSV</u>	SVPQHWVYFQ	IGRLTGDNAV
151	QTASEGKTC	SRCLYFRD	ESVCTGCGAE	LYRRRPKSL	ISSAFLTAIV
201	<u>ILYFPANILP</u>	<u>MISSNPAA</u>	<u>EPNVTILNGA</u>	YMWDEGRLL	AAVIFSAAL
251	<u>VPVLKIAAMS</u>	<u>VLIASARFAL</u>	<u>PTGAKKLSHL</u>	YRITEAVGRW	<u>SMIDIFVII</u>
301	<u>LMCSFHTYAA</u>	<u>RVIPGSAAVY</u>	<u>FCLVVILTML</u>	SAYYFDPRL	WDKRASDGI
351	FNTEKH* -----				

m153 / q153 96.1% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPENMLVMFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
g153	MGFAYSMTYIEVGIPGAASVLSLPENMLVMFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMVRLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
g153	YAALIRKQAYPALRLATRVMVRLRQAMMVDVFFVSTLVAYIKLSSVAKVRFGPAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVPOHWVYFQIGRLTGDNNAVQTASEGKTCCSRCLYFRDSPAESPCGVCGAE					
g153	LSVMLIRTSVSVPOHWVYFQIGRLTGNNNAVQTASEGKTCCSRCLYFRDSPAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
g153	LYGGRPKSLSSISSAFLTAAVVLYFPANILPIMISSNPAATEANTIFSGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASITLVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVII					
g153	AAVIFSASITLVPVLKIAAMSVLIAARFALPAGAKKLSHLRYRITEAVGRWSMIDIFVII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHTYAAARVIPGSAAVYFCLVVIILTMSAYYFDPRLLLWDKRASDGIAFNETEKHDX					
g153	LMCSFHTYAAARVIPGSAAVYFCLVVIILTMSAYYFDPRLLLWDKRASDGIAFNETEKYDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 629>:

```

a153.seq
1  ATGGCGTTTG  CTTACGGTAT  GACGTATATC  GAGGTCGGGA  TACCGGGTGC
51  GGCATCCGTC  TTTTCGCTGC  CCGAGATGAT  GCGCCTGATT  GTGTTTCAGG
101 ATTATGGTTT  CTTTGGCGAA  GTGATGTTTG  TGCTGACCTT  CGGCGCGCCG
151 GTTCTGTTTC  TGCTGCTGTG  CCTGTATGTC  TATGCCGCGC  TGATACGGAA
201 ACAGGCGTAT  CCTGCGCTGC  GTTTGGCAAC  GCGTGTGATG  GTGCGCTTGA
251 GACAGGCGAT  GATGGTGGAT  GTGTTTTTTG  TTTCCACTTT  GGTGGCGTAT
301 ATCAAGCTCT  CGTCTGTGGC  AGAGGTTCCG  TTCGGATCGG  CGTTTTATCT
351 GATGTTCCGC  CTGTGCGTTA  TGCTGATTCG  GACTTCGGTA  TCGGTTCCCC
401 AGCATTGGGT  GTATTTTCAA  ATCGGGCGGC  TGACGGGGGA  TAATGCGGTT
451 CAGACGCGAT  CGGAAGGTAA  AACCTGTTGC  AGCCGCTGCC  TGTATTTCCG
501 CGACAGTGCC  GAATCCCCCT  GCGGCGGTG  CGGTGCGGAA  CTGTACCGCC
551 GACGGCCGAA  AAGTCTGAGT  ATTTCTGCGG  CGTTTCTGAC  GCGCGCGGTT
601 ATTTTGTATT  TCCCTGCCAA  TATCCTGCCG  ATTATGATTT  CGTCCAATCC
651 TGCCGCCACG  GAGGTCAATA  CCATCCTTAA  CGGCATCGCT  TATATGTGGG
701 ACGAGGCGCA  CAGGCTGATT  GCGGCGGTTA  TTTTTCAGCG  GAGTATTTTG
751 GTGCCGGTAC  TGAAGATTGC  GGCAATGTCG  GTTTTGATTG  CGTCCGCCCC
801 CTTTCGTTTG  CCAACGGGTG  CAAAGAAATT  GTCGCACCTC  TACCGCATCA

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851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CGTTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTCGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
  1 MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
 51 VLFLLCLYV YAALIRKQAY PALRLATRV MRLRQAMMVD VFFVSTLVAY
101 IKLSSVAEVR FGSAYFLMFA LSVMLIRTSV SVPQHWVYFQ IGRITGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSLS ISSAFLTAAY
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHXYAA RVIPGSAAYV FCLVVILTML SAYYFDPRL WDKRASDGIA
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
a153	LSVMLIRTSVSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
a153	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHXYAARVIPGSAAYVFCVLVILTMLSAYYFDPRLWDKRASDGIAFNETEKHDX					
a153	LMCSFHXYAARVIPGSAAYVFCVLVILTMLSAYYFDPRLWDKRASDGIAFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
  1 ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCTCAAG CACGCGTCCG
 51 CAAAAACAAC accttctctCT CGGCCGTCTG GCTGGTCCCG CTGATCGCGC
101 TGATTGCCG CGGCTGGCTT TGGGTAAAGG AAATCCGCAA CAGGGGCGCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATCGAAG TCAACAATAC
201 GGTCATTAAG GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTTA CTGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

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401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGcg GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTCGACccG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCCTCT GCCTGCCCTG
751 CTGTCAGGCG CGATTTCAAT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCTT GTcgaATACA AAGGGCtgaA
951 TGTcggCATG GTTTCCGATG TCCCTTATTT TGACCGCAAT gacagCCTGC
1001 ACctgtTTGA aaacggctgg aTTcccGtac gCATCCGCAT cgagccTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAAACAACA
1101 ATTCCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGCGCGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TGCGACCGCA TACCGTTTAT GCAGCGGATA CCGTCATCGC
1251 CACACGGGCG GCGGTTTGG ATGACTTGCA GGTCAAATTG GCGGATTTCG
1301 TGGACaaatT CAACAATCTG CCATTggata aAACCGTTGC CGAATTGAAC
1351 GGCTCGCTCG CCGAACTCAA GTCCGCACTC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCGgcaaTCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACCTG AAAGAGTTGC GCATAACCCT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGAgacgta caAAATAcgc tgCaaAGTTT
1551 GGACAAAACC TTTAAagacg TtcaACCGT CATTAACACT TTGAaAGAAa
1601 aacCCaaCgc actGATTTtc aacaACAGCA GCAAAGAccc tATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

```

g154.pep
1  MTDNSPPPNQ HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGLTL SGSYIAFTPG KSGEAKDVFQ
151 VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV GQIESAHFDP
201 LSDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL
251 LSGATSFDSF KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGK MIELNDQPSA
401 SPKLRPHTVY AGDVTIATRG GGLDDLQVKL ADLLDKFNNL PLDKTVAEIN
451 GSLAELKSAL KSANAALSSI DKLVGNPQTQ NIPNELNQLT KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSSKDPIPK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

```

m154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAACAAC ACCTTCCTCT CTGCCGTCTG GCTGGTTCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTAAAG AAATCCGCAA CAGGGGGCCT
151 GTGATTGACG TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTACATCAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCTG
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTCAAT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTGCGCC GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCCGACG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTTTCAGAC GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCA

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1201 TCACCTAAGC TGCACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GGCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTCG CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAATACGCG TGCAAAGTTT
1551 GGACAAAAC TTTAAAGACG TTCAACCCGT GATTAATACT TTGAAAGAAA
1601 AACCCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

```

m154.pep
1  MTDNSPPPNQ HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ
151 VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV GQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAELKSTL KSANAALSSI DKLVGKPTQ NIPNELNQT KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154 / g154 97.8% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPNQHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
g154	10	20	30	40	50	60
	MTDNSPPPNQHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
m154.pep	70	80	90	100	110	120
	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
g154	70	80	90	100	110	120
	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
m154.pep	130	140	150	160	170	180
	SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN					
g154	130	140	150	160	170	180
	SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN					
m154.pep	190	200	210	220	230	240
	SPVLYENFMV GQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
g154	190	200	210	220	230	240
	SPVLYENFMV GQIESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
m154.pep	250	260	270	280	290	300
	KLNSAPLPALL SGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ					
g154	250	260	270	280	290	300
	KLNSAPLPALL SGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFFKQ					
m154.pep	310	320	330	340	350	360
	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
g154	310	320	330	340	350	360
	SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
m154.pep	370	380	390	400	410	420
	KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATQG					
g154	KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATRG					

442

	370	380	390	400	410	420
	430	440	450	460	470	480
m154 . pep	GGLDDLQVKLADLLDKFDKPLDKTVAEIENGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
	: : : : : :					
g154	GGLDDLQVKLADLLDKFNNLPLDKTVAEIENGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154 . pep	NIPNELNQTLKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	: : : : : :					
g154	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154 . pep	NSSSKDPIPKGSRX					
	: :					
g154	NNSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCTG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCATCAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTA AAAACG ACCGCATCCT CAACGTC AAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCAATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTCTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTCAAT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CCGTTCGCCT GTCGAGTACA AAGGGCTGAA
951 TGTCGGCGTG GTTTCGATG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGGA AAATGCGCA CGAACAAGC AAAGAACATT GGAAACAACA
1101 ATTTTCAGAC GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTTGCA GGTCAAATTG GCGGATTTGC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAACCCCTG AAAGAGTTGC GCACAACCCT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAACC TTAAAAGACG TTCAACCCGT CATTAACTT TGAAAGAAA
1601 AACCACAACG GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154 . pep
1  MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFO

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151 VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV GQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAELKSTL KSANAALSSI DKLVGKPQTQ NIPNELNQTQ KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154/a154 100.0% identity in 553 aa overlap

	10	20	30	40	50	60
m154.pep	MTDNSPPPNGHAQARVRKNNFTLSAVWLVPALIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
a154	MTDNSPPPNGHAQARVRKNNFTLSAVWLVPALIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m154.pep	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGVETAQLNADVSGLIRSDTQFVWVKPRIDQ					
a154	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGVETAQLNADVSGLIRSDTQFVWVKPRIDQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m154.pep	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVFQVQDIPPVTAIGQSGRLRLNLIGKNDRIILNVN					
a154	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVFQVQDIPPVTAIGQSGRLRLNLIGKNDRIILNVN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m154.pep	SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTSGSI					
a154	SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTSGSI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m154.pep	KLNSAPLPALLSGAISFDSPKTKNSKNVKSSEDSTLYDSRSEVANLPDDRSLYYTAFFKQ					
a154	KLNSAPLPALLSGAISFDSPKTKNSKNVKSSEDSTLYDSRSEVANLPDDRSLYYTAFFKQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m154.pep	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
a154	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m154.pep	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
a154	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m154.pep	GGLDDLQVKLADLLDKFDKPLDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
a154	GGLDDLQVKLADLLDKFDKPLDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154.pep	NIPNELNQTQKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
a154	NIPNELNQTQKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540

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```

                    550
m154.pep      NSSSKDPIPKGSRX
              |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1   atGAAaatcg GtataCCACG CGAGTCAtta tcCGGCGAAA cccgcgtagc
51  ctgcAcgccc gCCACCGTTG CCctgtggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CGGTGCAggt TTGGCGGCAA GTTTggaCGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGCCTGCCC
201 TTTAATTTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGCTCA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CCTTGCGCGC CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCCCGC ATTTCCCGCG CTCAGGCCTT GGACGCTTTG TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCCTGCGCA
501 GGTTTTGGTG ATTGGCGCCG GTGTGGCGGG TTTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGTAAG TTcctGAAAC TCGACTTCCT
651 GCAAGAATCG GGCGGCAGCG GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAAATG AAGCTCTTTG CCGAACAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CTCCCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAAACCG GCAACGGCGT GAAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcgaAATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGcgacg gcgaaATCAC
1101 CTTCCCGCCT CCGccgaTtc aggtTTCcgc ccggccgCAG CAAAcgccgt
1151 ctgaAAAagc cgcGCCTGCC GCCAagcccg AgccGaaacc tggtCCcctg
1201 tggAAAAaac tcgCGCCCGC GCcatcgCC GCCGTATTGG tgctgtgGgt
1251 cggCgcggtc gcacccgcag CATTCTTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCCTGCGT CATCGGTAC CATGTCGTTT GgaacgTCAG CCACTCGCTG
1351 CACACACCGC TGatgtcggt aaccaaCgcc atctccGGCA tcatggtcgt
1401 cggCGCGCTG CTGCAAATCG GTCAGGGcaa cggcttcgtT TCgtGCTGT
1451 CGTTTGTGTC CATCTGATT GCCGGCATCA ATATCTTCG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTTAAG AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1   MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMVPR ISRAQALDAL SSMANISGYR AVIEAANAFA
151 RFFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDFLQES GSGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAaip GKPAKLITK EMVESMKSGS VIVDLAATGG NCELTRPGL
301 SVTNGVKII GYTDMANRLA QSSQLYATN LVNLTKLLSP NKDGEITLDF
351 EDVIIRNMTV TRDGEITFPF PPIQVSARPQ QTPSEKAAPA AKPEPKPVPL
401 WKKLAPAAIA AVLVLWVGAV APAFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMSVTNA ISGIMVVGAL LQIQGNGFV SLLSFVAILI AGNIFGGFA
501 VTRRMLNMFK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1   ATGAAATCG GTATCCCACG CGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTGCAAG CGGTGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGTCTGCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAACTG CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

```

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```

301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCGC ATTTGCGCGC CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACCGC GCCGTAATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCCGCGC
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GCGCGCAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCGG GGCAAACCCG CGCCCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGGACGGGC GGCAACTGCG AACTCACCCG CCCGGGCGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGTTGGAC
1051 TTCAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCGGA TTCAAGTTTC CGCCCAGCCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGGAAAA AACTCGCGCC CGCCGTCATC GCCCGCGTCT TGGTACTGTG
1251 GGTGCGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCGCGA TCAACATCTT CGGCGGCTTT
1501 GCGGTAACAC GCGGTATGCT GAATATGTTT AAGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
  1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
  51 QTAGATVADK AAVWVCLIIY KVNAPSEQEL PLLNEGQTIV SFLWPRQNEA
 101 LVEALRAKKV NALAMDMVPR ISRAQALDAL SSMANISGYR AVIEAANAFG
 151 RFFTQGITA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
 201 AEQIESMGGK FLKLDFFQES GSGDGYAKV MSDEFIAAEM KLFAEQAQEV
 251 DIIITTAaip GKPAKLITK EMVESMKSGS VIVDLAAATG GNCELTRPGE
 301 LSVTNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
 351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QQTPEKAVP AAKPEPKPVP
 401 LWKKLAPAVI AAVLVLWVGA VAPAAFLNHF IVFVLACVIG YYVWVNVSHS
 451 LHTPLMSVTN AISGIIVVGA LLQIGQNGF VSLLSFVAIL IAGINIFGGF
 501 AVTRRMLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
              10      20      30      40      50      60
m155.pep     MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              |||
g155          MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              10      20      30      40      50      60

              70      80      90     100     110     120
m155.pep     AAVWVCLIIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMVPR
              |||:|||||
g155          AAVWACPLIIYKVNAPSEGELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMVPR
              70      80      90     100     110     120

              130     140     150     160     170     180
m155.pep     ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPPAQVLVIGAGVAGLAA
              |||
g155          ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPPAQVLVIGAGVAGLAA

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	130	140	150	160	170	180
	190	200	210	220	230	240
m155.pep	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m155.pep	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
	250	260	270	280	290	
	310	320	330	340	350	360
m155.pep	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	300	310	320	330	340	350
	370	380	390	400	410	420
m155.pep	VTHDGEITFPPPIQVSAQPQOTPSEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLVWVGA					
g155	VTRDGEITFPPPIQVSARPPQOTPSEKAAPAKPEPKPVPLWKKLAPAAIAAVLVLVWVGA					
	360	370	380	390	400	410
	430	440	450	460	470	480
m155.pep	VAPAAFLNHFIVFVLACVIGYVWVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
g155	VAPAAFLNHFIVFVLACVIGYHVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIGQGNGF					
	420	430	440	450	460	470
	490	500	510			
m155.pep	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					
g155	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					
	480	490	500	510		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAATCG GTATCCCACG TGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTGGAACCG
101 TTGTCGAAAG CGGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGGCATACCC
201 TTTAATTTAT AAGGTTAACG CGCCGTCCGA AGACGAGCTG CCGCTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCCGC ATTTGCGCGC GCGAGGCTTT GGACGNTTTG TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCGG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCCG CCTG.AAGTG
601 GCGGAACAAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAATCG GGCGGCAGCG GCGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAGATG AAGCTTTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAACGN
801 NNTNANCAAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GGCGACGGGC GGCAACTGCG AACTCACCAA ACAGGGCGAA
901 TTGTTTCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCGCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGCTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCGCGC ACGCGAAAT
1101 CACCTTCCCC CCTCCGCCGA TTCAAGTTTC CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCAAGC CCGAACCAGG ACCCGTTCCC

```

```

1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTGCGGCGG GTCGCACCCG CAGCATTCTT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GGCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDXL SXMANISGYR AVIEAANAFG
151 RXFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDLPQES GSGDGYAKV MSDEFIAAEM KLF AEQAKEV
251 DIIITTAaip GKPAKXXXK EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LFVTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QOTPSEKAAP AAKPEPKPVP
401 LWKKLAPAXI AAVLVLWVGA VAPAAFLNHF IVFVLACVIG YYVWVNVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQGNF VSLLSFVAIL IASINIFGGF
501 FVTRRLNMF RKG*

```

m155/a155 95.3% identity in 513 aa overlap

m155.pep	10	20	30	40	50	60
	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK					
a155	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK					
	10	20	30	40	50	60
m155.pep	70	80	90	100	110	120
	AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
a155	AAVWAYPLIYKVNAPSEDELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
	70	80	90	100	110	120
m155.pep	130	140	150	160	170	180
	ISRAQALDALSSMANISGYRAVIEAANAFGRFFTGTQITAAGKVPPAQVLVIGAGVAGLAA					
a155	ISRAQALDXLSXMANISGYRAVIEAANAFGRXFTGTQITAAGKVPPAQVLVIGAGVAGLAA					
	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLVVAEQIESMGGKFLKLDLPQESGSGDGYAKVMSDEFIAAEM					
a155	IGTANSLGAVVRVFDTRLXVAEQLESMGGKFLKLDLPQESGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
m155.pep	250	260	270	280	290	300
	KLF AEQAKEVDIIITTAaipGKPAKPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
a155	KLF AEQAKEVDIIITTAaipGKPAKPKXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE					
	250	260	270	280	290	300
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
a155	LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	310	320	330	340	350	360
m155.pep	370	380	390	400	410	420
	VTHDGEITFPPIQVSAQPQOTPSEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLWVGA					
a155	VTRDGEITFPPIQVSAQPQOTPSEKAAPAAKPEPKPVPLWKKLAPAXIAAVLVLWVGA					
	370	380	390	400	410	420

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              430      440      450      460      470      480
m155.pep      VAPAAFLNHFIVFVLACVIGYYVWNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a155           VAPAAFLNHFIVFVLACVIGYYVWNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF
              430      440      450      460      470      480

              490      500      510
m155.pep      VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX
              |||||||||||:||||||| |||||||||:|||
a155           VSLLSFVAILIASINIFGGFFVTRMLNMFRRKGX
              490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

```

g156.seq
1  ATGACTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCTCG CGGTTTTCTG GCACATACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG ATTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT GCGCTCGCTG ATGTGGGCGG GCGGATTTCG
351 CTGCACCGTC GGA CTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

```

g156.pep
1  MTFAYWCILI ACLLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQQNGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LFRLAFIWCY
101 IADKAALRSL MWAGGFACTV GLFVAAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

```

m156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTGCCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCTCG CGGTTTTCTA GCGCACACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC GCGCAATCG ACCATCAACA
251 CGCTTGCTCG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAT
301 ATCGCCGACA AAGCCGCTAT GCGCTCACTG ATGTGGGCAG GCGGATTTCG
351 CTGCACCGTC GGGCTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 646; ORF 156>:

```

m156.pep
1  MTFAYWCILI ACLLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQQNGFEA FAPFAAAVLT AHATGNAAQS TINTLACLFI LFRLAFIWCY
101 IADKAAMRSL MWAGGFACTV GLFVAAA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m156 / g156 96.1% identity in 127 aa overlap

```

              10      20      30      40      50      60
m156.pep      MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
g156           MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
              10      20      30      40      50      60

              70      80      90      100     110     120
m156.pep      FAPFAAAVLT AHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFACTV
              |||||||||||:|:|:| |||||||||||||||:|||||||||

```

```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWAGGFACTV
              70      80      90      100      110      120

m156.pep  GLFVAAAX
           |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
  1  ATGACTTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
 51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101  ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151  CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201  CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251  CGCTTGCCGG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301  ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTTGT
351  CTGCACCGTC GGGCTGTTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
  1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAARA
 51  HAAQQNGFEA FAPFAAAVLTAHATGNAGQA TVNTLAGLFI LRLAFIWCY
101  IADKAALRSL MWVGGFVCTV GLFVVAAX*

m156/a156  90.6% identity in 127 aa overlap

              10      20      30      40      50      60
m156.pep    MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a156        MTFAYWCILIA YLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAARAHAAQQNGFEA
              10      20      30      40      50      60

              70      80      90      100      110      120
m156.pep    FAPFAAAVLTAHATGNAAQSTINTLACLFILRLAFIWCYIADKAAMRSLMWAGGFACTV
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a156        FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWVGGFVCTV
              70      80      90      100      110      120

m156.pep    GLFVAAAX
           ||||:|
a156        GLFVVAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
  1  atgaggaacg aggAAAAACg cgccctgcgc cgcggaattgC gCgGgcggcg
 51  ttgcgCAATg GGgcgagacg tGCGggCGGC GGCGgCgatA Aaaatcaacc
101  gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTg
151  cCGATGGGCA AGGAATTGcg TTTGGGCGGc tTgtcCGCG CGGCGCAAAA
201  ACGCGGCGCA AAactctatc tgccttATAT CGAACC GCAC AC GCGGCGGA
251  TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301  GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351  GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAAG
401  GCTACCGTTT GGGGCAGGCA GGCGGCTATT ACGATGCGAC GCTTTCGGCG
451  ATGAAATACC GTTTGCAGGC GAAAACCGTG GGCGTGGGCT TTGCCTGCCA
501  GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551  TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```


This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLLKRYI KRGRKIGVYW
  51 PMGKELRLGG FVRAAQKRG A KLYLPYIEPH TRRMWFTYPY ERGMERERKR
 101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
 151 MKYRLQAKTV GVGAFACQLVD RLPREAHDL LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
  1 ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCGAATTGC GCGGGCGGCG
  51 TTCGCAAATG GGGCGGGACG TGCGGGCGGC GGCAACGGTA AAAATCAACC
 101 ACCTGCTCAA ACGTTATATT AAAAAAGGGC GGAAATCGG CGTGTATTGG
 151 CCGATGGGCA AGGAATGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
 201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACC CGT TCGCGGCGGA
 251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAAACAAGA ACGCAAGCGC
 301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCGGA AAAAGCGTGT
 351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTCGGTATG GACAGGCTGG
 401 GCTACCGCTT GGGACAGGCA GCGGGCTATT ACGATGCGAC GCTTTTCAGCG
 451 ATGAAATACC GTTTCAGGC AAAAACCGTG GCGGTGGGCT TTGCCTGCCA
 501 GTTGGTGGAC AGGCTGCCGG TCGAGGCGCA CGACCGGTCT TTGGACGGTT
 551 TTGTGTCGGA GCGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAATV KINHLLKRYI KKGRKIGVYW
  51 PMGKELRLDG FVRAAQKRG A ELYLPYIEPR SRRMWFTYPY ADGVKQERKR
 101 GRAKLHVPQF AGRKKRVHDL NLLVPVVGMD RLG YRLGQA GGYDATLSA
 151 MKYRLQAKTV GVGAFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

m157.pep	10	20	30	40	50	60
	MRNEEKRALRRELGRRSQMGRDVRAAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG					
g157	MRNEEKRALRRELGRRSQMGRDVRAAAAIKINRLLKRYIKRGRKIGVYWPMGKELRLGG					
	10	20	30	40	50	60
m157.pep	70	80	90	100	110	120
	FVRAAQKRGAELYLPYIEPRSRMWFTYPYPADGVKQERKRGRAKLHVPQFAGRKKRVHDL					
g157	FVRAAQKRGAKLYLPYIEPHTRRMWFTYPYPERGMRERKRGRAKLHVPQFAGRKIRVHGL					
	70	80	90	100	110	120
m157.pep	130	140	150	160	170	180
	NLLVPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
g157	SVLLVPLVGIDREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP					
	130	140	150	160	170	180
m157.pep	190					
	LDGFVSEAGILCFX					
g157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
  1 ATGAGGAACG AGGAAAAACA CGCCTTGCGC CGAGAGTTGC GCCGCGCCCG
  51 CGCGCAGATG GGCATCAAG GCGGTTGGC GCGGGGCAA ACGATTAACC
```

451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACTTTATC TGCCTTATAT CGAACCCGCG TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGCTATT ACGATGCGAC GCTTGGCGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCGTG GGCGTGGGCT TTGCCTGCCA
501 GTTGTGGAC AGGCTGCCGC GCGAACCGCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

```

a157.pep
  1 MRNEEKHALR RELRRARAQM GHQGRLAAGQ TINRLLKRYI KRGRKIGVYW
 51 PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWFTYPY ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGFAQCFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

```

              10      20      30      40      50      60
m157.pep    MRNEEKRALRRELGRRSQMGRDVRAAATVKINHLKRYIKKGRKIGVYWPMGKELRLDG
              |||||:||||| |:|||: | ||  ||:|||||:|||||
a157        MRNEEKHALRRELRRARAQMGHQGRLAAGQTINRLLKRYIKRGRKIGVYWPMGKELRLDG
              10      20      30      40      50      60

              70      80      90      100     110     120
m157.pep    FVRAAQKRGAEKLYLPYIEPRSRMWFTYPYPADGVKQERKRGRAKLHVQFAGRKKRVHDL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a157        FVRAAQKRGAKLYLPYIEPRSRMWFTYPYPESGMERERIRGRAKLNVPQFAGRKIRVHGL
              70      80      90      100     110     120

              130     140     150     160     170     180
m157.pep    NLLLVVVGMMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS
              ::|||:|:| | |||||:|||||:|||||:|||||:|||||
a157        SVLLVPLVGI DREGYRLGQAGGYDATLAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL
              130     140     150     160     170     180

              190
m157.pep    LDGFVSEAGILCFX
              |||||:|||||
a157        LDGFVSEAGILCFX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

```

g158.seq
  1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
 51 CGGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAAcCTGctc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTGCGCGT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCcgac TTTGCTCGT TTCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCCT TACGGGCCGG AGAATTGGAC
451 GATTCCGGGC TGCGTGCACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGGAAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

452

```

801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
851 TATTTTGGGA TTTTGTAGTG AAGGAACTGG GAAAAAATAT GAATAGAACG
901 AATACCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

```

g158.pep
  1 MKTNSEELTV FVQVVESGSF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLNLT EEGAQYFRRR QRILQEMAAA ETEMLAVHEV PQGVLRVDSA
101 MPMVLHLLAP LAAKFNERYP HIRLSLVSSE GYINLIERKV DIALRAGELD
151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN
201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE
251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNLR LRVFLDFLV KELGKNMNRRT
301 NTK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

```

m158.seq
  1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
151 AACC GCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTTGAGCGT GGATTCCGCG
301 ATGCCGATGG TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCCGAC TTTCGCTCGT TTCTTCCGAA GGCTATATCA
401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGCG AGAATTGGAC
451 GATTCCGGGC TGCGTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT
501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG
551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGATGC GCAGGGAAAT CCCTATAAGA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT
701 GCGGTATTGT TTGCTTATCA GATTTTGGG TTGACAACGA CATCGTGAA
751 GGAAAGTTAA TTCCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC
801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG
851 TATTTTGGGA TTTTGTAGTG GAGGAACTGG GAAACAATCT CTGTGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

```

m158.pep
  1 MKTNSEELTV FVQVVESGSF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLSLT EEGAQYFRRR QRILQEMAAA ETEMLAVHEI PQGVLSVDSA
101 MPMVLHLLAP LAAKFNERYP HIRLSLVSSE GYINLIERKV DIALRAGELD
151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHQC LGFTEPGSLN
201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE
251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNLR LRVFLDFLV EELGNLGC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

```

          10      20      30      40      50      60
m158.pep  MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT
          |||
g158       MKTNSEELTVFVQVVESGSFSRAAEQLEMANSAVSRIVKRLEEKLGVNLLNRTTRQLNLT
          10      20      30      40      50      60

          70      80      90     100     110     120
m158.pep  EEGAQYFRRRQRILQEMAAAETEMLAHVHEIPQGVLSVDSAMPMLHLLAPLAAKFNERYP
          |||
g158       EEGAQYFRRRQRILQEMAAAETEMLAHVHEVPQGVLRVDSAMPMLHLLAPLAAKFNERYP
          70      80      90     100     110     120

```

453

	130	140	150	160	170	180
m158.pep	HIRLSLV	SEGYIN	LIERKVD	IARAGEL	DDSGLR	ARHLFDS
g158	HIRLSLV	SEGYIN	LIERKVD	IARAGEL	DDSGLR	ARHLFDS
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAG	HQCLGF	TEPGSL	NTWAVL	DAQGNPY	KISPHFTA
g158	SAEDLAN	HQCLGF	TEPGSL	NTWAVL	DAQGNPY	KISPHFTA
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDND	IAEGKLI	PLLAEQ	TSDKTH	PFNAVYY	SDKAVNL
g158	DFLVDND	ITEGKLI	PLFAEQ	TSNKTH	PFNAVYY	SDKAVNL
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAACCA	ATTCAGAAGA	ACTGACCGTA	TTTGTTCAAG	TGGTGGAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCGCGT	GGATTCGCGG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCCG	CTGGCAGCAA	AATTCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGCACG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCGG	CCACCAATGT	TTAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTTAGATGC	GCAGGGAAAT	CCCTATAAGA	TTTCAACGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCAGGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTTGGA	TTTTTTAGTG	GAGGAACCTG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRRA	QRILQEMAAA	ETEMLAHVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQC	LGFTTEPGSLN
201	TWAVLDAQGN	PKISPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYYSDKAVNL	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL	NRTTRQLSLT
a158	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL	NRTTRQLSLT
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRA	QRILQEMAAA	ETEMLAHVHEI	PQGVLSVDS	SAMPMVLHLL	APLAAKFNERYP
a158	EEGAQYFRRA	QRILQEMAAA	ETEMLAHVHEI	PQGVLRVDS	SAMPMVLHLL	APLAAKFNERYP
	70	80	90	100	110	120

	130	140	150	160	170	180
m158.pep	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
m158.pep	DFLVDNDIAEGKLIPLLAEQTSCLKTHPFAVYYSKAVNLRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSCLKTHPFAVYYSKAVNLRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGACattc  tgGACAAact  ggtcgatCTC  GCccaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATg  gcATTGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  CGGGTTATCT  CTCGATCGAG
151 GCGGAAACTT  CCCCgcGTCC  GGTGCGCACG  GGCGATATTG  TATTTTTCCC
201 GCGCGGCTTG  GGTcATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CATACGACAA  AACGGCACAT  TTATGGTCAA  ACAgTGCggG
301 AACGGGCTGG  ATATGAGcCT  GTTTTGCgCC  CGTTTCCGCT  ACgACACCCA
351 CGCGGATTTG  ATGAACGGGC  TGCCGGAaAC  CGTTTTTCTG  AACATTGCCc
401 ATCCAAGTTT  GCAGTATGTG  GTTTCAATGC  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGGTCAAC  GCATTACCGT  CCGTCTGCTc
501 GGTGCTTATC  CTGCGCGcCT  ATCTCGAACA  GGATAAGGAT  GTCGAACCTc
551 CGGGCGTATT  GAAAGGTTGG  CAGGACAAAc  GTTTGGGACA  TTTGATCCAA
601 AAGGTGATAG  ACAAACCGGA  AGACGAATGG  AATATTGACA  AAATGGTTGc
651 CGCCGCCAAT  ATGTcGCGCG  CGCAACTGAT  GCGCCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGCACGCC  TTTGTGAACC  ATATCCGCCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAaAC  CCCGgATTCC  GTTTTGGAGG  TCgCGCTGTc
801 GGTGGGCTTT  CAGTCGGAaA  CGCATTTCCG  CAAGCGCTTC  AAACGGCAAT
851 ATCACGTTTC  GCGGGGGCAA  TACCGGAaAG  AAGGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```
g160.pep
1 MDILDKLVDL AQLTGSADVQ CLLGGQWHEH LQREGLVHIV TAGSGYL CID
51 GETSPREPVGT GDIVFFPRGL GHVLSHDGKY GESLQPDIRQ NGTFMVKQCG
101 NGLDMSLFCA RFRYDTHADL MNGLPETVFL NIAHPSLQYV VSMLQLESEK
151 PLTGTVSVVN ALPSVLLVLI LRAYLEQDKD VESLGVGLKGW QDKRLGHLIQ
201 KVIDQPEDEW NIDKMQVAAN MSRAQLMRFF KSQVGLSPKA FVNHRILQKG
251 ALLLKKTPDS VLEVALSVGF QSETHFGKAF KRQYHVSPGQ FYRKEGGQK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```
m160.seq
1  ATGGACATTC  TGGACAAACT  GGTCGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGC AACGCGA  AGGATTGGTA  CACATTGTTA  CATCGGGCAG  CGGCTATCTC
151 TGC ATCGACG  GCGAAACTTC  CCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTCCCG  CGCGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTGCGGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCCC  GTTTCGCTA
351 CGACACCCAC  GCCGATTTGA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGAA
401 ACATTGCCCA  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTGTCGTG
```

455

```

501 CGTCTGCTG GTGCTTATCC TGCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTTCG TTTTGTGCGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAC GCACTTCGGC AAGCGGTTC
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AggCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||
g160      MDILDKLV DLAQLTGSADVQ CLLGGQW--- HETLQREGLV HIVTAGSGYL CIDGETSPRP
          10      20      30      40      50

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |:|
g160      VGTGDIVFFP RGLGHVLSHD GKKGESLQPD IRQNGTFMVK QCGNGLDMSL FCARFRYDTH
          60      70      80      90      100     110

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLESKKPLTGT VSMVNALSSVLLVLILRAYLEQ
          |||
g160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLESEKPLTGT VSVVNALPSVLLVLILRAYLEQ
          120     130     140     150     160     170

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS
          |||
g160      DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSQVGLS
          180     190     200     210     220     230

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||
g160      PHAFVNHIRL QKGALLLKKTPDSVLEVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          240     250     260     270     280     290

m160.pep KX
          ||
g160      KX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
  1 ATGGACATTC TGGACAAACT GGTGATTTC GCCCAATTGA CGGGCAGTGT
 51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```

```

101 TGCAACGCGA AGGATTGGTA CACATTGTGA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCGGCA ACGGACAGGA TATGAGCCTG TTTTGCGCCC GTTTCCTGTA
351 CGACACCCAC GCCGATTGTA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCCTGCTG GTGCTTATCC TGCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTTGTGGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGTCAT ACCGGAAGA AGGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||
a160      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          10      20      30      40      50      60

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||
a160      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          70      80      90      100     110     120

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTV SMNALSSVLL VLILRAYLEQ
          |||
a160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTV SMNALSSVLL VLILRAYLEQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||
a160      DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          190     200     210     220     230     240

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||
a160      PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          250     260     270     280     290     300

m160.pep KX
          ||
a160      KX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTtttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GCGGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTCAGGAA
451 CCGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAAGTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GCGGTGGCGA TGTGCTCggt ttgggacgacg
601 Ctgaccggct ggCACaccct GTCCTTTcca tcggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAcg cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCCCTCGC tttcctaTat gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTCTTg ggcaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAAA CAGCGGCTGC AAGCCCTCTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVTLGAAAVL RRDTRTPHW KNHLNRSMVG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTttTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GCGGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAAGTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTGTCGCGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCTGT
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCCTCGC TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTCTTg GGCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVALGAAAVL RRDTRTPHW KNHLNRSMVG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE

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458

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151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

```

          10      20      30      40      50      60
m161.pep  MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL
          |||:|||||
g161      MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMFLSTVTLGAAAVL
          10      20      30      40      50      60

          70      80      90     100     110     120
m161.pep  RRDXFERTPHWKNHLNRSMVGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE
          |||:|||||
g161      RRDTFERTPHWKNHLNRSMVGTGAMLLLFYAVTHLPLTTGVTLSYTSSIFLAVFSFLILKE
          70      80      90     100     110     120

          130     140     150     160     170     180
m161.pep  RISVYTQAVLLLGFAGVVLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG
          |||:|||||
g161      RISVYTQAVLLLGFAGVVLLNPSFRSGQEPAAALAGLAGGAMSGWAYLKVRELSLAGEPG
          130     140     150     160     170     180

          190     200     210     220     230     240
m161.pep  WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT
          |||:|||||
g161      WRVVFYLSATGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT
          190     200     210     220     230     240

          250     260     270     280     290     300
m161.pep  VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR
          |||:|||||
g161      VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR
          250     260     270     280     290     300

m161.pep  X
          |
g161      X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

```

a161.seq
1   ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGCG
51  GGCGGCCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATGGGTCT TTTGGCGCAT GCTGTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCACT TAAACCGCAG TATGGTCGGG ACGGGGCGA
251 TGCTGCTGCT GTTTACGCG GTAACGCATC TGCCTTGGC CACCGCGT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GCGGTGCTG CTCCTTGTT
401 TTGCCGCGCT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGCGGC GCGATGCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCATCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCTG
651 CATCGGCGTG TCCGCGCTGA TTGCCAACT GTCGATGACG CGCGCTACA
701 AAGTCGGCGA CAAATTCAG GTTGCTCGC TTTCTATAT GACCGTCGT
751 TTTCCGCTC TGTCTGCCG ATTTTCTCTG GCCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA

```

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMFLS
51 TVALGAAAVL RRDTFRTPHW KNHLNRSMSG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPSFRSGQE
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSCIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	10	20	30	40	50	60
m161.pep	RRDXFRTPHWKNHLNRSMSGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSMSGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
m161.pep	RISVYTQAVLLLGAFAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGAFAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSPSAVYLSCIGVSALIAQLSMTTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSPSAVYLSCIGVSALIAQLSMTTRAYKVGDKFT					
	190	200	210	220	230	240
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq
1 ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTTAACGTT TTCCATTTTt
151 ctgGGTTTt tgctGATACT CTCGGTCAGC GGTTTGGGAA ACATcagGCT
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGCC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGTCGGCG CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC

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451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG ACCCCACTGT
801 TTACCTGTTG TCGGCATTTCG GCGACAACAT AGGGAACCTAC CTCGGAATC
851 TGGTGCGCCT CAGTTTGAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTATTGG GCGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTGTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTGCGGGTT TTGCTCATCC CCGGCCGTGT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTCG
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCCTGTTTTT TGTAACCTCT GCCGACTCCG GGATTATATG
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCACTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCCG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

```

g163.pep
1  MVILTTLFFV  CVLVVLVLTV  PDQVQMWLDR  AKEVIFTEFS  WFFVLTFESIF
51  LGFLLILSVS  GLGNIRLGRD  EDVPEFGFLS  WLAMLF AAGM  GVGLMFFGVVA
101 EPLMHYFSDI  TVGAPEHRQQ  QALLHTVFHW  GVHAWSVYGT  IALALAYFGF
151 RYKLPLALRS  CFYPLLKEKI  SGRFGDAIDI  MALLATFFGI  ITTLGFGASQ
201 LGAGLQEMGW  IAENSFGVQV  LIIAAVMSLA  VVSAISGVGK  GVKVLSENLN
251 GLAFLLLFFV  LAADPTVYLL  SAFGDNIGNY  LGNLVRLSLK  TYAYEREHKP
301 WFESWTVLYW  AWWCSWAPFV  GLFIARISKG  RTIREFVFGV  LLIPGLFGVL
351 WFTVFGNTAI  WLNDGVAGGM  LEKMTSSPET  LLFKFFNYLP  LPELTSIVSL
401 LVISLFFVTS  ADSGIYVLNN  ITS RDKGLSA  PRWQAVMWGV  LMSAVAVLLM
451 RSGGLGNLQS  MTLIVSLPFA  LLMLIMCFSL  WKGLSADKKY  FETRVNPTS
501 FWTGKWKER  LVRIMSQTQE  QDILKFLKHT  ASPAMHELQR  ELSEEYGLSV
551 RVDKMFHQDE  PAIEFVIRKE  TMRDFMYGIK  SVGQDVSDQL  INDGKLPHIR
601 HQTTYKPYAY  FFDGRVGYDV  QYMNKDELIA  DILKNYERYL  MLLDDVQGEL
651 MAHEQVELAE  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

```

m163.seq
1  ATGGTTATTT  TGACGACTTT  GTTTTTTGTT  TGTGTTTTGG  TGGTATTGGT
51  TTTAACCGTG  CCGGATCAGG  TGCAGATGTG  GCTCGATCGG  GCAAAGAAG
101 TCATTTTAC  CGAGTTCAGC  TGGTTTTATG  TTTTAACGTT  TTCCATTTT
151 CTGGGTTTCC  TGCTGATACT  CTCGGTCAGC  AGTTTGGGAA  ACATCAGGCT
201 CGGACGGGAT  GAAGATGTGC  CGGAATTCGG  CTTCTGTCTG  TGGCTGGCGA
251 TGCTGTTTGC  GGCCGGGATG  GGCGTGGGTC  TGATGTTTTT  CGGCGTGGCA
301 GAGCCGTTGA  TGCATTATTT  TTCGGACATT  ACGGCCGGCA  CGCCGGAACA
351 CAGGCAGCAG  CAGGCATTGC  TGCACACGGT  GTTCCATTGG  GGCGTTCACG
401 CTTGGTCGGT  GTACGGTACG  ATTGCATTGG  CTTTGGCTTA  TTTCGGTTTC
451 CGCTACAAGC  TGCCGCTTGC  CCTGCGTTCT  TGTTTTTACC  CCCTGTTGAA
501 AGAAAAAATT  TCCGGAAGGT  TCGGCGATGC  CATTGATATT  ATGGCGTTGC
551 TTGCTACTTT  TTTTCGGCATC  ATCACCACAT  TGGGGTTCGG  GGCTTCGCAA
601 CTGGGCGCCG  GATTGCAGGA  AATGGGCTGG  ATTGCCGAAA  ACAGCTTCAG

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461

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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCGTGAAAG TGTTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTCG GCGACAACAT AGGGAACAC CTCGGAAATC
851 TGGTGCGCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTGTG GGTGTGTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTA
1501 TTTTGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAAGG CAGGATATTT TAAATTCCT CAAACAGACT GCATCGCCCC
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CCGGTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTG ATGTTGTTGG ATGATGTCGG TCAGGAAC TG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGV
101 EPLMHYFS DI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFSWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVQDQVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

	10	20	30	40	50	60
m163.pep	MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFESIF LGFLLILSVS					
g163	MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFESIF LGFLLILSVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m163.pep	SLGNIRLGRDE DVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ					
	:					
g163	GLGNIRLGRDE DVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITVGAPEHRQQ					
	70	80	90	100	110	120
	130	140	150	160	170	180

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m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFGVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
g163	GVKVLSELNLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSLKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQLKFLKQTASPAMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVIRIMSQTQEQLKFLKHTASPAMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGVDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGVDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGTTATTTT TGACGACTTT GTTTTTTG TGTTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

```

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201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGTCTTGCGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG GTCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACCTAC CTCGGAATC
851 TGGTGCGCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTTATG
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGAT
1451 TGAGTGCAGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGA
1501 TTTTGCACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTGAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

a163.pep

```

1  MVILTTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKQ RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITSROKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS
          |||||
a163       MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRDEDEVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ

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|||||
a163      SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
          70      80      90      100     110     120

          130     140     150     160     170     180
m163.pep  QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
          |||||
a163      QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
          130     140     150     160     170     180

          190     200     210     220     230     240
m163.pep  MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
          |||||
a163      MALLATFFGIITTLGFGASQLGAGLQEIWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
          190     200     210     220     230     240

          250     260     270     280     290     300
m163.pep  GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
          |||||
a163      GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
          250     260     270     280     290     300

          310     320     330     340     350     360
m163.pep  WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
          |||||
a163      WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
          310     320     330     340     350     360

          370     380     390     400     410     420
m163.pep  WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
          |||||
a163      WLNDGVAGGVLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
          370     380     390     400     410     420

          430     440     450     460     470     480
m163.pep  ITS RDKGLSAPRWQAVMWGVLM SAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
          |||||
a163      ITS RDKGLSAPRWQAVMWGVLM SAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
          430     440     450     460     470     480

          490     500     510     520     530     540
m163.pep  WKGLSADKKYFETRVNPTS VFWTGGKWKERLVQIM SQTQE QDILKFLKQTAS PAMHELQR
          |||||
a163      WKGLSADKKYFETRVNPTS VFWTGGKWKERLVQIM SQTQE QDILKFLKHTAS PAMHELQR
          490     500     510     520     530     540

          550     560     570     580     590     600
m163.pep  ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
          |||||
a163      ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
          550     560     570     580     590     600

          610     620     630     640     650     660
m163.pep  HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLM LDDVQGQELMAHEQVELAE
          |||||
a163      HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLM LDDVQGQELMAHEQVELAE
          610     620     630     640     650     660

m163.pep  X
          |
a163      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
  1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
 51  CAAGGCGCGC TTCCTGTTTC CCTCGGCCCG CCTGTCAAAA GAATTGGCGG
101  GCCTGAAGGC GCAAACGCCC GTCGAAAAAA TCATTGGGAC GGACAAAAGC
151  CGGCCGGCCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201  CCGCTTCCCC GAAAAACCCG ACTTGGGCGC CCAACCCCGG ATAAATGATT
251  TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301  CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351  CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTcctg ccgatgTTCC
401  ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451  TCGATTATTT TGGTCAAAtc cgttttCCcC ttttccaacg TTTTGAAACA
501  GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551  CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTCAGATG GTTCAACCGC
601  ATCCGCCTGT TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651  CGATTTTAAA GCCAAGTTCC CCGCGCCAA ATTGCTGGAA GGCTACGGAC
701  TGAGCGAAGC CTCGCCCCTC GTCGCCGTCA ATACGCCCGA ACGGCAAAAA
751  GCCCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801  TGAAGAATTG GTCGAAGTGC CGCGCGCGA AGTGGGCGAA CTGATCGTCA
851  GGGGCGGTTT GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901  GAAACCATCG TCAACGGCTG GTTGAAAACG GGCGATTTCG TTACCATAGA
951  CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCATC GCGGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTGCG
1151 GCGAGGACGA aatccgccc caccTGCGTA CCGTGCTGGC AAATTTCAAA
1201 ATCCCCAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
  1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
 51  RPAGETAEGD AFFENVRRFP EKPD LG RQPR INDLAHHIYT SGTTHGHPKA
101  LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151  SIILVKSVP FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201  IRLFISGGAP LAEQTILDFK AKFPRAKLLE GYGLSEASPV VAVNTPERQK
251  ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301  ETIVNGWLKT GDFVTIDEDG FIFIVDRKKD LIISKGQNVY PREIEEEIHK
351  LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRVTLANFK
401  IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
  1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
 51  CAAAAACGGA AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101  ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151  ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201  AGAATTTATT ACCGCCTATT TCGCCATCTC CGCCATCGGC GCGGTGCGCG
251  TACCGATGAA CACATTTTTG AAAACAGCG AATACGCGTA TATCCTGAAC
301  GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351  GCGGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAATCATT TGGACGGACA
401  AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451  GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501  TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551  GCGCGCTAAT CAGTTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601  CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651  GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701  CGTGTTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTC CAACGTTTTG
751  AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGCGC TACCCGCGAT
801  TTACACCGCG ATGAGCAAGG CGAAATCCC TTGGTATTTC AGATGGTTCA
851  ACCGCATTCT CCTGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901  ATCTTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA

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951 CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGCCAAAGCC
1051 GTCGATGAAG AATTGGTCGA AGTGCCGCGC GCGGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTGGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACCTGA TGCCGTCGAA GCCGCCGCGC TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTGAAG GAGCAGTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNQ NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIIIV KSVFPFSNVL
251 KQTLKRA TV FLGVP AIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVPR GEVGELIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFTV
401 IDEDFIFIV DRKKDLISK GQNVYPREIE EEIYKLDAVE AAIVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA
501 TGKVLKRVLK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

          60      70      80      90      100      110
m164.pep  GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
          |||||||||||||||||||||||||||||||||||||||||||
g164      MNTFLKNSEYAYILNDCKARFLFASAGLSK
          10      20      30

          120      130      140      150      160      170
m164.pep  ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
          |||||||||||||||:|||||||||:|||||||||:|||||||||
g164      ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT
          40      50      60      70      80      90

          180      190      200      210      220      230
m164.pep  SGTGHPKGALISYANL FANLNGIERIFKISKRDRFIVFLPMFHSFTLTAMVLLPIYMAC
          |||||||||||||||||||||||||||||||||||||||||||
g164      SGTGHPKGALISYANL FANLNGIERIFKISKRDRFIVFLPMFHSFTLTAMVLLPIYMAC
          100      110      120      130      140      150

          240      250      260      270      280      290
m164.pep  SIILVKSVPFSPNVLKQTLKRA TVFLGVP AIYTAMSKAKIPWYFRWFNRIRLFISGGAP
          |||||||||||||||:|||||||||:|||||||||:|||||||||
g164      SIILVKSVPFSPNVLKQALLKRA TVFLGVP AIYTAMSKAKIPWYFRWFNRIRLFISGGAP
          160      170      180      190      200      210

          300      310      320      330      340      350
m164.pep  LAEQTILDFKAKFPRAKLLLEGYGLSEASPVAVNTPERQKARSVGIPLPGLEAKAVDEEL
          |||||||||||||||:|||||||||:|||||||||:|||||||||
g164      LAEQTILDFKAKFPRAKLLLEGYGLSEASPVAVNTPERQKARSVGIPLPGLEAKAVDEEL
          220      230      240      250      260      270

          360      370      380      390      400      410

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467

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m164.pep  VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164      VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          280      290      300      310      320      330

          420      430      440      450      460      470
m164.pep  LIISKQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
          |||||||||||||||:|||||||||||||||||||||||||||||:|||||
g164      LIISKQNVYPREIEEEIHKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
          340      350      360      370      380      390

          480      490      500      510
m164.pep  HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
          |||||||||||||||||||||||||||||||||||:|||||
g164      HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
          400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTGT AAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAA CGCCGTCGA AAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCT CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCACAGC TTCACGTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TCCCCTTTTC CAACGTTTGT
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGCG ATCCCCCTGC CCGGTTTGGG AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTGA AGTGCCGCGC GGCGAAGTGG GCGAAGTATG
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAATCGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTT ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKNQ NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQALLKRATV FLGVPAIYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGEIVRGS GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDEGFIFV DRKKDLIISK QNVYPREIE EEIYKLDAVE AAIVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRTV LANFKIPKQI HFKDGLPRNA

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501 TGKVLKRVLK EQFDGNK*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKNGNGTAVFDGKEKTAYRALKQEAEEVAAYLQNIGVKFGDTVA					
a164	:					
	10	20	30	40	50	60
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
a164	LAVSNSTEFITAYFAVSAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
	70	80	90	100	110	120
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDLAGRQPRINDLAHIIYTSGETTG					
a164	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDLAGRQPRINDLAHIIYTSGETTG					
	130	140	150	160	170	180
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
a164	HPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
	190	200	210	220	230	240
m164.pep	250	260	270	280	290	300
	KSVFPFSNVLKQTLKRVATVFLGVPPIYATAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
a164	KSVFPFSNVLKQALLKRVATVFLGVPPIYATAMSKTKIPWYFRWFNRIRLFISGGAPLAEQT					
	250	260	270	280	290	300
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSVGIPPLGLEAKAVDEELVEVPR					
a164	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSVGIPPLGLEKAVDEELVEVPR					
	310	320	330	340	350	360
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLIISK					
a164	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLIISK					
	370	380	390	400	410	420
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHRLTV					
a164	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHRLTV					
	430	440	450	460	470	480
m164.pep	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
a164	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq

1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC

```

51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACGcCGgca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGC GGAAGGCAAG
301 TTGGAagaCA ATTCCTTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtccgCTGAT TATGCGCGGC CGGgacgaaA ACCAACCCGT
501 CGCCGCCAAC TATTCGCCCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAA AACCAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCCTCTT CCTCGGCGCG GGCGCGCGCG CACTGACCTT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGCGCGCGCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CcTGCTGGgc gAaTTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GLPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMVPHL
301 DTRNVDGKRH LMFPGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GGCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGTGCGAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCAAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GGCGGCGGCG CGCTGACCTT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGCGCGCGCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF

```

```

201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYGQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA
351 NMPLTK...

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

	10	20	30	40	50	60
m165.pep	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
g165	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAGTDVDF					
g165	HCRYLQKRYDVFKTQKLFENMEFSTDRNKISDWAPLIMRGRDENQPVAANYSAGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m165.pep	GRLTRQMVKYLGKGVKTEFNHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA					
g165	GRLTRQMVKYLGKGVKTEFNHVEDIKRESDGAWVLKTADTRNPDWQLTLRTRFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYGQASVGAPPMSPVPHL					
g165	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYGQASVGAPPMSPVPHL					
	250	260	270	280	290	300
	310	320	330	340	350	
m165.pep	DTRNVDGKRHLMFPGYAGFRSNFLKQGSMLDLPLSIHMDNLYPMLCAGWANMPLTK					
g165	DTRNVDGKRHLMFPGYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
g165	ELRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

```

a165.seq
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCAAAAACCT TTTTGGAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGAGGGGCA AGGGCGTAAA AACCGAGTTC

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601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCC GCCCTTACGC
951 AGGCTTCCGT TCCAATTCC TCAAGCAAGG CTCATTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACGCGA
1451 AAGTGTGGA TATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```

a165.pep
  1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSAWN
 51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQR FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAA N YSAEGTDVDF GRLTRQMKY LQGKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALLLQK
251 SGIPEGKGYG GFPVSGLFRR NSNPETAQH NAKVYGQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTEERF ASLLEYYPEA NPDDWELITA GQRVQIIKGD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165/a165 99.7% identity in 356 aa overlap

```

              10      20      30      40      50      60
m165.pep    MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSAWN NAGTGHSALC
              |||
a165         MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSAWN NAGTGHSALC
              10      20      30      40      50      60

              70      80      90     100     110     120
m165.pep    ELNYAPLGANGI IDPARALNIAEQFHVSQRFWATLVAEGKLEDNSFINAVPHMSLVMNED
              |||
a165         ELNYAPLGANGI IDPARALNIAEQFHVSQRFWATLVAEGKLEDNSFINAVPHMSLVMNED
              70      80      90     100     110     120

              130     140     150     160     170     180
m165.pep    HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAA N YSAEGTDVDF
              |||
a165         HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAA N YSAEGTDVDF
              130     140     150     160     170     180

              190     200     210     220     230     240
m165.pep    GRLTRQMKY LQGKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLT LRTRFLFLGA
              |||
a165         GRLTRQMKY LQGKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLT LRTRFLFLGA
              190     200     210     220     230     240

              250     260     270     280     290     300
m165.pep    GGGALLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSPVPHL
              |||
a165         GGGALLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSPVPHL
              250     260     270     280     290     300

```

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          310      320      330      340      350
m165.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTK
          |||
a165      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
          310      320      330      340      350      360

a165      ELRKTKEERFASLLEYYPEANPDDWELITAGQQRVQIIKKDSEKGGVLQFGTEIVAHADGS
          370      380      390      400      410      420

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGCGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCG cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctggTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAACGAAGAC CACTGCCGTT ACCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgcCTGAT TATGCGCGGC CGGGACGAAA ACCAACCCTG
501 CGCCGCCAAC TATTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCTCTTT CCTCGCGCGG GCGCGCGGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAACCTTC TCAAGCAAGG CTCGTTTATG GATTTGCCCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTtt gCCTCCCTGC TGgaatacta cccGaggcag acccGACGac
1151 tggtactcat cagcgaggn cCGCTcata tcattanata tgactCgaaa
1201 ctgcgcgctgc tgcagttgta cgagattgtg ccaCGCGacg ctcgctcgcg
1251 cattctggag cgctcgcgcg catcacgctn tgcgctgata tccgctgatg
1301 acactgctcc gaGCGcgccc gtcttggaat gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALE ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVNED HCRYLQKRYD VFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GLPVSGLFER NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFPGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPQ TRRLVLITQX TRHIIYDSK
401 LRVLQLYEIV PRDARSILE RRGASRXALI SADDTAPSAP VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

m165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGCGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTGC GGAAGGCAAG
301 TTGGAAGACA ATTCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC CGGTTTAAAA
401 CCAAAAACTT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCTG
501 CGCCGCCAAC TACTCCGCCG AAGGTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GTTCTCTCTT CCTCGCGCGG GCGCGCGGCG CGTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG

```

```
851 TGTACGGGCA GGCTTCCGTC GGCGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGGAATACTA CCCCAGAGGCA AACCCCGACG
1151 ACTGGGAACT CATCACCACA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGCG
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTTAA
```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

m165-1.pep

```
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFPGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA QQRVQIIKGD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLENE NPERADEIIA YTAKVLDI*
```

m165-1/g165-1 89.7% identity in 428 aa overlap

m165-1.pep	10	20	30	40	50	60
m165-1.pep	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
g165-1	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
m165-1.pep	70	80	90	100	110	120
m165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165-1	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
m165-1.pep	130	140	150	160	170	180
m165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGDRDNQPVAAANYSAGETDVDF					
g165-1	HCRYLQKRYDVFKTQKLFENMEFSTDRNKISDWAPLIMRGDRDNQPVAAANYSAGETDVDF					
m165-1.pep	190	200	210	220	230	240
m165-1.pep	GRLTRQMVKYLQKGKVKTEFNHVEDIKRESGAWVLKTADTRNPDGQLTLRTRFLFLGA					
g165-1	GRLTRQMVKYLQKGKVKTEFNHVEDIKRESGAWVLKTADTRNPDWQLTLRTRFLFLGA					
m165-1.pep	250	260	270	280	290	300
m165-1.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSPVPHL					
g165-1	GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSPVPHL					
m165-1.pep	310	320	330	340	350	360
m165-1.pep	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG					
g165-1	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
m165-1.pep	370	380	390	400	410	420
m165-1.pep	ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKGDSEKGGVLQFGTEIVAHADGS					
g165-1	ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKGDSEKGGVLQFGTEIVAHADGS					
	370	380	390	400	410	
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
 : |||
 g165-1 ILERRGASRXALISADDTAPSAPVLESVX
 420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq
 1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGGCGGCA TTATGAGCGC
 51 GACTTTGGGC GTTTTGCTCA AAGAAGCTCGA ACCGTCTTGG GAAATCACCC
 101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
 151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAAGT ATGCCCGGTT
 201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
 251 AGTTTCATGT GAGCGCCAG TTTTGGGCGA CGTTGGTGC GGAAGGCAAG
 301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
 351 GAATGAAGAC CATGTTCCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
 401 CCCAAAAAAT TTTTGAAGAT ATGGAATTTT CCACCGATCG GAACAAAATT
 451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCTG
 501 CGCCGCCAAC TACTCCGCGG AAGGCACGGA TGTCGATTTC GGACGGCTGA
 551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
 601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGCG CGTGGGTGCT
 651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
 701 GCTTCCTCTT CCTCGGCGCG GCGGCGCGCG CGCTGACCT GCTGCAAAAA
 751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCGGCCT
 801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAG
 851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
 901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTG GCCCTTACGC
 951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACTTATG GATTTGCCGC
 1001 TGTCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
 1051 AATATGCCGC TGACCAATAA CTGTCTGGGC GAATTGCGTA AAACCAAGA
 1101 AGAACGCTTC GCCTCCCTGC TGGAACTA CCGGAGGCA AACCCGACG
 1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
 1201 TCCGAAAAAG GCGCGTGT GCAGTTTGGT ACGGAGATTG TCGCACACGC
 1251 CGACGGCTCG CTCGCGCAT TGCTGGGCGC GTCGCGGGC GCATCGACCG
 1301 CCGTGCCCGT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
 1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
 1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACGCGA
 1451 AAGTGTGGA TATTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep
 1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
 51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWTALVAEGK
 101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFTDRNKI
 151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMKY LQKGKVFTEF
 201 NRHVEDIKRE SDGAVLTKTA DTRNPDGQLT LRTFLFLGA GGGALTLLQK
 251 SGIPEGKGYG GPFVSGLFFR NSNPETAQEH NAKVYQASV GAPPMSVPHL
 301 DTRNVDGKRH LMFPGYAGFR SNFLKQGLM DLPLSIHMDN LYPMLRAGWA
 351 NMPLTKYLLG ELRKTKEERF ASLEYYPEA NPDDWELITA GQRVQIIKID
 401 SEKGGLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
 451 PSWEGRLEKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWNNAGTGHSALC			
m165-1	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWNNAGTGHSALC			
	10	20	30	40	50	60
	70	80	90	100	110	120
a165-1.pep	ELNYAPLGANGIIDPARALN	IAEQFHVSQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
m165-1	ELNYAPLGANGIIDPARALN	IAEQFHVSQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
	70	80	90	100	110	120
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFTDRNKISDWAPLMMRG	RDNQPVAAANYSAEGTDVDF			
m165-1	HCSYLQKRYDAFKTQKLFEN	MEFTDRNKISDWAPLMMRG	RDNQPVAAANYSAEGTDVDF			
	130	140	150	160	170	180
	190	200	210	220	230	240

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a165-1.pep  GRLTRQMVKYLOGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
m165-1      GRLTRQMVKYLOGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYGOASVGAPPMSVPHL
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYGOASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
m165-1      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQVRQIIKKDSEKGGVLQFGTEIVAHADGS
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQVRQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
m165-1      LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
m165-1      YTAKVLDIX

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a165-1/p33940

sp|P33940|YOJH_ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION
>gi|1736851|gnl|PID|d1016718 (D90850) ORF ID: o372#5; similar to [SwissProt Accession Number
P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical
to 490 residues of YOJH_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct
identical to GB: ECOHU49_33
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548
Score = 458 bits (1167), Expect = e-128
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

```

Query: 3  EATDVVLVGGGIMSATLGVLKLEPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
Sbjct: 30  QETDVLLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

Query: 63  NYAPLGGANGIIDPARALNIAEQFHVSQFWATLVAEGKLED-NSFINAVPHMSLVMNEDH 121
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90  NYTPQNADGSISIEKAVAINAEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDN 149

Query: 122  CSYLQKRYDAFKTQKLFENMEFSTDNRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDFG 181
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150  VNFLRARYAALQQSSLFRGMYSEDHAQIKWAPLVMGRDPQKVAATRTEIGTDVNYG 209

Query: 182  RLTRQMVKYLOGKG-VKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
+TRQ++ LQ K + + V +KR D W + AD +N Q
Sbjct: 210  EITRQLIASLQKKSNSFLQSLSEVRALKRNDNTWTVTVADLKNGTAG-NIRAKFVFIGA 268

Query: 241  XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYGOASVGAPPMSVPHL 300
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269  GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVVNHHLAKVYGKASVGAPPMSVPHI 328

Query: 301  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329  DTRVLDGKRVLFGPFATFSTKFLKNGSLWDLMSTTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361  ELRKTKEERFASLLEYYPEANPDDWELITAGQVRQIIKKDSEKGGVLQFGTEIVXXXXXX 420
++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V
Sbjct: 389  QVMLSEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRDAEKGGVLRGLGTEVVSDDQGGT 448

Query: 421  XXXXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478

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P+M+ L+ + F +R +P W+ LK +VP YG KLN + +
 Sbjct: 449 IAALLGASPGASTAAPIMLNLLLEKVFGRVSSPQWQATLKAIVPSYGRKLNGDVAATERE 508
 Query: 479 IAYTAKVLDI 488
 + YT++VL +
 Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq
 1 atggcgggcg cggaaataaa acgccccctc gctgtcgatt tccagcacat
 51 agcgtccggt ctgcacggcg gcatagccgc ttttgccctgc ctgatagggt
 101 tgcagggcg aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc
 151 ggcgatattg cccaccagtt tggcaaaciaa ggtatggcac acgccgtttt
 201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg
 251 acgacggcct ccaagtcggt gggatgcttt ccggtcagcc ggacggcgtt
 301 ttgttccggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt
 351 tggtttttgc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta
 401 ttgtcgatgt atttgacttt gaaaaccggg ttcggcgcg tttgtgcgcg
 451 attttgcggc tgttccgcgc tattttcggg tttgccgcag gcggcaagca
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc
 551 tgatgggttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcgg
 601 aggttcggac ggcattgggt ttatttcaac gggcggatgc cgaccgcatc
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgct ttttgcgcgc
 701 ctgcctgcaa aatctcttcg atttgcgaag gattagaggt caatgcgttg
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF
 51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQVV GMLSGQPDGV
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDFD ENRFRRALCR
 151 ILRLFRRIFG FAAGGKQQA AOHGKRYFQH SALLMVSKCR LKCRLLKRRR
 201 RFRHWWYFN GRMPTASRTL SNNRASLRA FCAPACKISS ICEGLEVNAL
 251 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq
 1 ATGGCGGCGG CGGAAATAAA ACGCCCCTTC GCTGTTCGATT TCCAGCACAT
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCTGC CTGATAGGGT
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC
 151 GGCGATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT
 201 CTGCCCCAACC TGCCGGACTG TCCTTATCAT CGGTTTCCAT ACATTTGCCG
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTTGTTTT TTGCCGTCGT
 351 TGGTTTTGCC TTCGCTGCTT TGTCCCAAT CCAAACGGC AATCGCCGTA
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC
 451 GTTTTTCGGC TGTACCGCCG TATTTWCGGA TTTGCCGCaC GGCaaArGCAG
 501 CAGGCAGCCG CCCAATACGG CAAAArAwGT wTTCAGCATT CCACaYTCCT
 551 GATGGTTTCA AAATGCCGTC TGAAACGCGG CAGGCGGAGG TTCGGACGGC
 601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA
 651 ATAATTCGCG TGCTTCTTTA CGCGCTTTTC CCGCGCCTGC CTGCAAAATC
 701 TCTTCGATT GCGAAGGGTC GCGGTCAGC TCGTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep
 1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN *VIRQFAAVF
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRALYR
 151 VLRLYRRIXG FAATAQQQA AQYKXXXQH STXLMVSKCR LKGRRRRFRG
 201 HRVHFNGRMP TASGTLSNNS RASLRAFAAP ACKISSICEG SAVSSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 204 shows 82.0% identity over a 250 aa overlap with a predicted ORF (ORF 204.ng) from *N. gonorrhoeae*:

m204/g204

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIA SVLHGGIAAFAC LIGLQGGMRNXVIRQFAAVFGDIAHQFGKQ					
g204	MAAAEIKRPLAVDFQHIA SVLHGGIAAFAC LIGLQGGMRNQVISQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
g204	GMAHAVFRPARRRVLSVGFHTFADDGFQVVGMLSGQPDGVLFRQAFNRITDLFFAVVGFA					
	70	80	90	100	110	120
m204.pep	FAALSQIQTGNRRRVIDIYDFENRFRALYRVLRLYRRIXGFAATAXQQAAQYKXXXQH					
g204	FATLSQSQTGNRRRIVDVDFENRFRALCRILRLFRIFGFAAGGKQAAAQHGKRYFQH					
	130	140	150	160	170	180
m204.pep	STXLMVSKCRLK----RGRRRFGRHRVHFNGRMPTASGTLNNSRASLRAFAAPACKISS					
g204	SALLMVSKCRLKCRLKRGRRRFGRHWVYFNGRMPTASRTLSNNSRASLRAFCAPACKISS					
	190	200	210	220	230	
m204.pep	ICEGSAVSSLX					
g204	ICEGLEVNAL					
	240					
m204.pep	ICEGSAVSSLX					
g204	ICEGLEVNAL					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

a204.seq	1	ATGGCGGCGG	CGGAAATAAA	ACGCCCCCTC	GCTGTCGATT	TCCAGCACAT
	51	AGCGTCCGTT	CTGCACGGCG	GCATAGCCGC	TTTTGCCTGC	CTGATAGGGT
	101	TGCAGGCGG	AATGCGAAAT	CAGGTAATCC	GTCAGTTTGC	CGCCGTCTTC
	151	GGCGATATTG	CCCACCAAGT	TGGCAAACAA	GGTATGGCAC	ACGCCGTTTG
	201	CCGCCAGCC	CGAAGGCGCG	CCCTTTCCGT	CGGTTTCCAT	ACATTTGCCG
	251	ACGACGCTT	CCAAGTCGTT	GGGATGCTTG	CCGGTCAGCC	GGACGACGTT
	301	TTGTTCCGGC	AAGCCTTT..
	351
	401
	451
	501
	551AAGAG	GTTCCGACGG
	601	CATTGGGTTT	ATTTCAACGG	GCGGATACCG	ACCGCATCAC	GTACTTTGCC
	651	CAATAATTCG	CGTGCTTCTT	TACGCGCTTT	TTGCGCGCCT	GCCTGCAAAA
	701	TCTCTTCGAT	TTGCGAAGGG	TCGGCGGTCA	GCTCGTTGTA	G

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

a204.pep	1	MAAAEIKRPL	AVDFQHIA SV	LHGGIAAFAC	LIGLQGGMRN	QVIRQFAAVF
	51	GDIAHQFGKQ	GMAHAVCRPA	RRRALSFGFH	TFADDGFQVV	GMLAGQPDVV
	101	LFRQAF....
	151KRFR
	201	HWVYFNGRIP	TASRTLNNNS	RASLRAFCAP	ACKISSICEG	SAVSSL*

m204/a204 54.5% identity in 246 aa overlap

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIQLGGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLGGMRNQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
m204.pep	GMAHAVFCPTCRTLIIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSVMGFHTFADDGFQVVGMLAGQPDDVLFQRQAF-----					
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTLIIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSVMGFHTFADDGFQVVGMLAGQPDDVLFQRQAF-----					
	70	80	90	100		
m204.pep	FAALSQIQTGNNRIVDIYDFENRFRRLYRVLRLYRRIXGFAATAXQQAAAQYGKXXXQH					
a204	-----					
	130	140	150	160	170	180
m204.pep	FAALSQIQTGNNRIVDIYDFENRFRRLYRVLRLYRRIXGFAATAXQQAAAQYGKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKRGRRRFRGRVHFNRMPTASGTLNNRSLRAFAAPACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTLNNRSLRAFAAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

```

g205.seq
1  atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgcttgccgc
51  ctgcggaata tccgaaaata cggcggaaca gccgcaaat gcggcacaaa
101 gcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cggcaaatgt
301 atggaaaccg acggaagga cgcgccttcg ggctgggcgg aaaacggcgt
351 gtgccatacc ttgtttgcca aactggtggg caatatcgcc gaagacggcg
401 gcaaaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggctatgc cgcctgcag aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

```

g205.pep
1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51  AGLALGQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNIA EDGGKLT DYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

```

m205.seq
1  ATGCTGAAWA CwTyTTTTCG CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51  tGCGCAAAT CCGwAAATAC GGCGGTACAG CCGCAAACG CCGTACAAAG
101 CGCGCCGAAA CCGGTTTTC AAGTCATATA TATCGACAAT ACGCGGATTG
151 CCGGTTTGA TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGA AGCCGTCAGC GGCAAATGTA
301 TGGAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTCGCATGC CGCCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGCG CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

```
m205.pep
  1  MLXTXFAVLG GCLLXCRCGK SXNTAVQPQN AVQSAPKPVF KVIYIDNTAI
 51  AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101  METDDKDSPA GWAENGVCHT LFAKLVGNIA EDGGKLT DYLVSHAALQPYQ
151  AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

```
m205/g205

      10      20      30      40      50      60
m205.pep  MLXTXFAVLGGCLLXCRCGKSXNTAVQPQNAVQSAPKPVFKVIYIDNTAIAGLDLGQSSE
          ||||| ||||| ||||| ||||| ||||| |||||
g205       MLKIPFAVLGGCLLLAACGKSENTAEQPQNAASAPKPVFKVKYIDNTAIAGLALGQSSE
          ||||| ||||| ||||| ||||| ||||| |||||

      70      80      90     100     110     120
m205.pep  GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSPAGWAENGVCHT
          ||||| ||||| ||||| ||||| ||||| |||||
g205       GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT
          ||||| ||||| ||||| ||||| ||||| |||||

     130     140     150     160     170     180
m205.pep  LFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGA FYFRRRH
          ||||| ||||| ||||| ||||| ||||| |||||
g205       LFAKLVGNIAEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNGRYVLEIDSEGA FYFRRRH
          ||||| ||||| ||||| ||||| ||||| |||||

m205.pep  YX
          |
g205      Y
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

```
a205.seq (partial)
  1  TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG
 51  CAAGCATCCC AACGACTTGG AAGCCGTCGT CGGCAAATGT ATGGAAACCG
101  ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGGCGT GTGCCATACC
151  TTGTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAACGTAC
201  GGATTACCTG ATTCGCATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA
251  GCGGCTATGC CGCCGTGCAG AACGGACGCT ATGTGCTGGA AATCGACAGC
301  GAGGGGGCGT TTTATTTCCG CCGCCGCCAT TATTGA
```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

```
a205.pep (partial)
  1  SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVCHT
 51  LFAKLVGNIA EDGGKLT DYLVSHAALQPYQ AGKSGYAAVQ NGRYVLEIDS
101  EGAFYFRRRH Y*
```

m205/a205 88.3% identity in 111 aa overlap

```
      50      60      70      80      90     100
m205.pep  KVIYIDNTAIAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC
          | : ||||| ||||| ||||| ||||| |||||
a205       SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC
          ||||| ||||| ||||| ||||| |||||

      110     120     130     140     150     160
m205.pep  METDDKDSPAGWAENGVCHTLFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQ
```

g205-1.seq (partial)

g205-1.pep (partial).

m205-1.seq..

m205-1.pep

m205-1/g205-1 92.0% identity in 174 aa overlap

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAACGKSENTAEQPQNAASAPKPVFKVKYIDNTA	IAGLALGQSSE				
m205-1	MLKTSFAVLGGCLLLAACGKSENTAEQPQNAVQSAPKPVFKVKYIDNTA	IAGLDLGQSSE				
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENG	VCHT				
m205-1	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDS	PAGWAENG	VCHT			

481

```

              70      80      90      100      110      120
              130      140      150      160      170
g205-1.pep    LFAKLVGNI AEDGGKLT DYLVSHSAL QPYQAGK SGYAAVQNG RYVLEIDSE GAF
              |||||
m205-1        LFAKLVGNI AEDGGKLT DYLVSHSAL QPYQAGK SGYAAVQNG RYVLEIDSE GAFYFRRRH
              130      140      150      160      170      180
m205-1        YX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

```

a205-1.seq (partial)
1  CCTCTTAAAG GCTTGCCGGA ACAAACGTC GTCCGGCTGA CCGGCAAGCA
51  TCCCAACGAC TTGGAAGCCG TCGTCGGCAA ATGTATGGAA ACCGACGGAA
101 AGGGCGCGCC TTCGGGCTGG GCGGCAACG GCGTGTGCCA TACCTTGTTT
151 GCCAAACTGG TGGGCAATAT CGCCGAAGAC GCGGCAAAAC TGACGGATTA
201 CCTGATTTCG CATTCCGCCC TGCAACCCTA TCAGGCAGGC AAAAGCGGCT
251 ATGCCGCCGT GCAGAACGGA CGCTATGTGC TGGAAATCGA CAGCGAGGGG
301 GCGTTTATT TCCGCCGCCG CCATTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

```

a205-1.pep (partial)
1  PLKGLPEQNV VRLTGKHPND LEAVVGKCM ETDGKGAPSGW AANGVCHTLF
51  AKLVGNIAED GGLTDYLI S HSALQPYQAG KSGYAAVQNG RYVLEIDSEG
101 AFYFRRRHY*

```

m205-1/a205-1 89.0% identity in 109 aa overlap

```

              50      60      70      80      90      100
m205-1.pep    KYIDNTAIAGLDLGQSSEKGTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCM E
              |||||
a205-1        PLKGLPEQNVVRLTGKHPNDLEAVVGKCM E
              10      20      30
              110      120      130      140      150      160
m205-1.pep    TDDKDSPAGWAENGVCHTLFAKLVGNI AEDGGKLT DYLVSHSAL QPYQAGK SGYAAVQNG
              |||||
a205-1        TDGKGAPSGWAANGVCHTLFAKLVGNI AEDGGKLT DYLVSHSAL QPYQAGK SGYAAVQNG
              40      50      60      70      80      90
              170      180
m205-1.pep    RYVLEIDSEGAFYFRRRHYX
              |||||
a205-1        RYVLEIDSEGAFYFRRRHYX
              100      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 715>:

```

g206.seq
1  atgttttccc cgcacaaaac ccttttcctc tgtctcggcg cactgctcct
51  cgcctcatgc ggcacgacct ccggcaaaaca ccgccaaccg aaacccaaac
101 agacagtcgc gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctccgactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgcctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcattccatg ccccggcagc
451 ggcaaaaacca tcaaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttgga gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

```

g206.pep
1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

```


m206.seq

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

m206 . pep . .

Computer analysis of this amino acid sequence gave the following results:

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/q206

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

a206.seq

1	ATGTTTCCCC	CCGACAAAAC	CCTTTTCCTC	TGTCTCAGCG	CACTGCTCCT
51	CGCCTCATGC	GGCAGGACCT	CCGGCAAACA	CCGCCAACCG	AAACCCAAAC
101	AGACAGTCCG	GCAAATCCAA	GCCGTCCGCA	TCAGCCACAT	CGACCGCACA
151	CAAGGCTCGC	AGGAAGCTAC	GCTCCACAGC	CTCGGACTCA	TCGGCACGCC
201	CTACAAATGG	GGCGCGACGA	GCACCGCAAC	CGGTTTCGAT	TGCAGCGGCA
251	TGATTCAATT	CGTTTACAAA	AACGCCCTCA	ACGTCAAGCT	GCCGCGCACC
301	GCCCGCGACA	TGGCGGCGGC	AAGCCGCAAA	ATCCCCGACA	GCCGCGCTTAA
351	GGCCGGCGAC	CTCGTATTCT	TCACACCGGT	CGGCGCACAC	CGTACTCAC
401	ACGTCCGGAT	CTATATCGGC	AACGGCGAAT	TCATCCATGC	CCCCAGCAGC
451	GGCAAAACCA	TCAAAACCGA	AAACTCTCTC	ACACCGTTTT	ACGCCAAAAA
501	CTACCTCGGC	GCACATACTT	TCTTTACAGA	ATGA	

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIDRTQGSQELMLHS			
a206	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIDRTQGSQELMLHS			
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATG	FDCSGMIQFVYKNALNVKL	PRTARDMAAASRKIPDSRX	KAGD		
a206	LGLIGTPYKWGGSSTATG	FDCSGMIQFVYKNALNVKL	PRTARDMAAASRKIPDSRL	KAGD		
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYI	GNGEFIHAPSSGKTIKTEK	LSTPFYAKNYLGAHTFFTE	X		
a206	LVFFNTGGAHRYSHVGLYI	GNGEFIHAPSSGKTIKTEK	LSTPFYAKNYLGAHTFFTE	X		
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
1  atgctgcggc atttaggaaa cgacttcgcc ttgggcgcggt tgtttttcga
51  tgctgcggtt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcgggttcag ataggttttg gcgaacatcg ttgccgccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatcg
451 gtcgtcgccg tatttttctt tgatggtctg cagttcgggt gcggcgccac
501 gcattttcgc catcgaaagg taggagggcgt tgggtcaatg atacagtacg
551 gctttgacga tgatgggtcaa aacgacgatt gccagcccc agttgccgat
601 aatgttgtgc agttgggtta ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgctcgg gatgtttgcg
701 ataacggatg tggtttgccg accggcatac aggttgaccg ccattttcgg
751 ttttgcccc cggttgggga tagcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
1  MLRHLGNDFE LGALFFDAAV DVPLLGDGQE VVDHPVENQT GREEEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQOHRQTAA QRVDLFLFEK LHHRLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCFAPVAD
201 NVVQLVQEPE ERRCEPVYFT VFQCQLQVVG DVCDNGCGLR TGIQVDRHFR
251 FWPPGWDSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
1  ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGgGCGTT GTTTTTTCGAT
51  GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAGGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTTCGCC TGCATCGGGT CGGTGCGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTGCGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```

```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGGCGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTGCGCG ATGTTTGCGA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCGT TCGGCGGTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGGAGAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTCGGGG TTTTGCGGAT GTATTGCGCC
951 TCGGATTTGC CGGATTGGC ATCGTCGTCC AAGTCGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
  1 MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDGE
 51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDGDL DLQQRQAAA QRVDFLVCKV LHHRLLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQEP EERGEPVYFA VVFGQLQVVG DVCDDGCGLR AGVEVDGGFG
251 FAPFWMAAKG TLTLVLYSL LRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSKSE KLTFWKLPSP V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng) from *N. gonorrhoeae*:

```

m209/g209
      10      20      30      40      50      60
m209.pep MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR
g209      MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVENQTGREEEEHDGENQRHDFHHFR
      10      20      30      40      50      60

      70      80      90      100     110     120
m209.pep LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAAEVGNPTQPRCLAQFYGGEQCPIQSDG
g209      LHRVGRRRVQIGLGEHRCRHNDGQDVVGVGAAAEVGNPAQPRCLAQFYGGEQCPVQADEG
      70      80      90      100     110     120

      130     140     150     160     170     180
m209.pep DLQQRQAAAQRVDFLVCKV LHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
g209      DLQQRQTAAQRVDFLVFEKLHHRLLLRHTVVAVFFFDGLQFGCGGTHFRHRTVGGVGQW
      130     140     150     160     170     180

      190     200     210     220     230     240
m209.pep IQYGFDDDGXNDNRPAPVADDVVQLVQEP EERGEPVYFAVVFGQLQVVG DVCDDGCGLR
g209      IQYGFDDDGQNDDCPAPVADNVVQLVQEP EERRCEPVYFTVVFQQLQVVG DVCNDGCGLR
      190     200     210     220     230     240

      250     260     270     280     290     299
m209.pep AGVEVDGGFGF-APFWMAAKGTLTLVLYSL LRLMSMLHSPAAQTLCLPLGWRIQVDMK
g209      TGIQVDRHFRFWPPGWDG
      250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
  1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGCGT TGTTTTTCGA

```

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```

51  TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGTGATC
101 ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151 AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTGCGCG
201 GCGGGTTTCAG ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251 AGGATGTAGT AGGGGTTCGGC GCGGCTGAGG TCGGTAATCC A'CCAGCCA
301 AGGTGCCTGG CGCAATTCTA CGGAGGCGAA CAATGCCCAA TACAATCCGA
351 TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401 ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGTCT GCGCCATACG
451 GTCGTCGCCG TATTTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501 GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551 GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601 GATGTTGTGC AGTTGGTTCA AAAGCCAAAA GAGGGGGGAG GCGAACCAGT
651 GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTGCGC GATGTTTGC
701 ATAACGGATG TGGTCTGTGG GCCGGCGTAG AGGTTGATGG AGGCTTCGGT
751 TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGGTGCTGTA
801 CAGCTTGTCT TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851 AAACGCTTTG TCCGCCTTTG GGTGGAGGA TCCAGGTGGA CATGAAGTGG
901 TGTTCAATCA TGCCGAGCCA GCCGGTCGGG GTTTTGCGGA TGTATTCGGC
951 CTCGGATTTG CCGGATTTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```

a209.pep
1  MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDGDL DLQQRQAAA QRVDFLVCVK LHHGLLLRHT
151 VVAVFLFDGL QFGRGGTHFR HRTVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQKPK EGGGEPVYFA VVFGQLQVVG DVCNCGCLW AGVEVDGGFG
251 FAPFWIAAKG TLTLVLYSLS LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*

```

m209/a209 95.6% identity in 341 aa overlap

```

m209.pep      10      20      30      40      50      60
MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYVPVQYQTGREEEEHDGENQRHDFHHFR
|||||
a209          10      20      30      40      50      60
MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEEHDGENQRHDFHHFR

m209.pep      70      80      90     100     110     120
LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG
|||||
a209          70      80      90     100     110     120
LHRVGRRRVQIGLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG

m209.pep     130     140     150     160     170     180
DLQQRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
|||||
a209         130     140     150     160     170     180
DLQQRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGRGGTHFRHRTVRGVGQW

m209.pep     190     200     210     220     230     240
IQYGFDDDGXNDNRPAVADDVVQLVQEPPEERGGEVYFAVVFGQLQVVGDVCDGCGLR
|||||
a209         190     200     210     220     230     240
IQYGFDDDGXNDNRPAVADDVVQLVQKPKEGGGEVYFAVVFGQLQVVGDVCDNCGCLW

m209.pep     250     260     270     280     290     300
AGVEVDGGFGFAPFWMAAKGTLTLVLYSLSLRLMSMLHSPAAQTLCLPLGWRIQVDMKW
|||||
a209         250     260     270     280     290     300
AGVEVDGGFGFAPFWIAAKGTLTLVLYSLSLRLMSIRQSPAAQTLCPPLGWRIQVDMKW

m209.pep     310     320     330     340
CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX

```

```

a209      |||||
          CSIMPSQPVGVLRLMYASDLPDLASSKSEKLTFWKLP SGVX
          310      320      330      340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```

g211.seq
1  atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atggtgcggc
51  ggtgggaaac ggggtcgata agtttggcg tggtgctgat aatcaggttg
101 agtttttga aggaaacctg attgtagtcg gcgcgtccgg gcgtgccgct
151 gtaacggtag ccgtggcgca attcgagcgt gcgtttgttg tccttcagcg
201 agaagttacc ttctttggcg aagatgatgt tgtcgccgcc gtttttgtcc
251 tgttcgcgca ggaacaggtt ttcatgatg ccggaattcg tgtcaaaggt
301 ttcgacgaaa taaacctgc cgttgcgctt gcccaagtta ttgaactcgc
351 cggcttcac caaagacaat tcctgcttct gttcaaaat ttcggcatat
401 tcgcggtgc gcagctctgc ccacggtatc acccaaagct gcattgacggc
451 aatcaggatg gcaaacggca cggcaaactg catgacgggg cgtatccact
501 gtttcaacgc caatccgcag gatag

```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

```

g211.pep
1  MLRIAAANQL GGRNGAAVGN GVDKFGRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVLQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGVKG
101 FDEINPAVAL AQVIELAGFH QROFLLLLQN FGIFAAALC PRYHPKLHDG
151 NQDGKRHGKL HDGAYPLFQR QSAG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```

m211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTGA AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTTGTG TCGTTCAGCG
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTCGCCGCC GTTTTGTCC
251 TGTTCCGCGCA GGAACAGGTT TTTCATGATG CCGGATTCGG TATCGAAGGT
301 TTCGACAAAA TAAACCTGC CGTTGCGCTT GCCCAAAGT TTGAACCTGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAACG GCAAACGGCA CGGCAAAGT CATCACCGG CGTATCCATT
501 GTTCAATGC CAATCCGCA GATAG

```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

```

m211.pep
1  MLRVAAANQL GGRNGTAVGN GVDEFGRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVVQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGIEG
101 FDKINPAVAL AQTVELACLH QROFLLLLQD FSVFAAAXLC PRYHPKLHDG
151 NQNGKRHGKL HHRAYPLFQC QSAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

```

m211/g211
          10      20      30      40      50      60
m211.pep  MLRVAAANQLGGRNGTAVGNVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g211      MLRIAAANQLGGRNGAAVGNVVDKFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER
          10      20      30      40      50      60
          70      80      90     100     110     120
m211.pep  AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH

```

```
a211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GGCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTGGA AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGGTAG CCGTGCCGCA ATTCGAGCGT GCGTTTGTTG TCGTTCAGCG
201 AGAAGTTACT TTCTTTGGCG AAGATGATGT TGTGCGCGCC GTTTTTGTCC
251 TGTTGCGGCA GGAACAGGTT TTTCATGATG CCGGATTGCG TATCGAAGGT
301 TTCGACAAAA TAAACCCTGC CGTTGCGCTT GCCCAAAC TGGAACCCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAAAACGCA CCGCAAAC TG CATCACGGG CGTATCCATT
501 GTTTC AATGC CAATCCGCAG GATAG
```

a211.pep

1	MLRVAAANQL	GGRNGTAVGN	GVDEFGRGAD	NQVEFLEGNL	<u>IVVGASGRAA</u>
51	<u>VTVAVAQFER</u>	AFVTVVQREV	FFGEDDVVAA	VFVLFAQEQV	FHDAGFGIEG
101	FDKINPAVAL	AQTVEPACLH	QRQFLLLQLD	FSVFAAA*LC	PRYHPEKLHDG
151	NQNGKRHGKL	HHRAYPLFQC	QSAG*		

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
a211	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVAAVFLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH					
a211	AFVVVQREVTFFGEDDVAAVFLFAQEQVFHDAGFGIEGFDKINPAVALAQTVEPACLH					
	70	80	90	100	110	120
	130	140	150	160	170	
m211.pep	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLGHHRAYPLFQCQSAGX					
a211	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLGHHRAYPLFQCQSAGX					
	130	140	150	160	170	

```
g212.seq (partial)
  1  atggacaatc tcgatatggga cggcattccc gacatccgca cactcgacca
 51  aaccatccgc aaacacgcac acccgctcaa cctgattgtc tgccctcccc
101  ataatcagat tcccgatattt caaacccgac aagatgcttc ggactcgga
151  tgccgtctga agcaccggtt ggatcaggca acccagtgcc tccagttcga
201  cagcatcaac ctcatcgaac acatcctgcc cgatgtccgc ttctgggttc
251  ttcccccttc acgcaccgcg cgctgcacg aacacttcca ccacatttcc
301  ttgacagacc aagccatccc gcaaaccgaa agcaagtccg acaaaccctg
351  gtttgcactt ccacaaacat ccgaacggaa aaaaccggaa cacgtcctcg
```

```

401 tcatcggtgc aggcattgcc ggcgcacga ccgcccacgc cttagcatca
451 cacggcattt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctcggaacaca tcctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccg aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcacctctct cagccatccg ctgatcgaac tatatgaaaa cacaacgtta
901 accggcattt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcatctactg caccggcgcg cacagcccct
1001 gcctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaacgggcc tcacaccgtc caccgcgtt tccgaacaac tgcgttgcgc
1101 cgtttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgcactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacgcca agcattggca cacttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL PQTSEKPKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSAEA
251 EKIAGIPLNT PYAEPLCGLY WQHGVWLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 EEASNROALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCCTCAA CCTGATTATC TGCCTCCCCG
101 ATAAATCAGAT TCCCGATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAACCTTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GGCGCGGCAA CCGCCCACGC CTTAGCATCA
451 CACGGCATT TCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAACTTTTG CTTGCCGGCT ACGGCTACAC CAAACGCTTG
601 CTCGGACACA TCCTGCCCCG ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTCTGCC
851 GCACCCCTCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATTT CCCACGACGG GGAAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCGGA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCCTTGCCT
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCACG
1301 CCGCCATACG CTGCGACAGC CCGGACCACC TTCCCCTAGT CGGCGCACTC
1351 GGCGACATTG CCGCCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AAATACCGC ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CGGCACCCGC GGACTCGCCA CCGCCCCCAT CTGCGCCGCC

```

1501 GmCAwTGCAG CCCAAATCst AGGCyTGCCC CATCCCTTTT yAcAAcGCCT
 1551 gCGCCACGCC cTACACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE
 51 CRLKHLRDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS
 101 WQTEAIPQTE SKPDKPWFAL POTSERQKPE HILVIGAGIS GAATAHALAS
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LH CYGASFIP NSSHTGWNEA
 401 EEASNRQALA HLNPALESSE FAANPNPQKH QGHAAIRCDS PDHLPLVGAL
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
 501 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng) from *N. gonorrhoeae*:

m212/g212

m212.pep	10	20	30	40	50	60
	MDNLVWDGIPDIRTLDQAIRKHAPPLNLII	CLPDNQIPDFQTAQDASDAE	CRLKHLRDQA			
g212	MDNLVWDGIPDIRTLDQTIRKHAHPLNLIV	CLPDNQIPDFQTAQDASDSE	CRLKHLRDQA			
	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
	MQCLQFDSINLIEHILPDVRFWLVPPSRTH	HLHEHFHHISWQTEAIPQTESKPDKPWFAL				
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTR	RLHEHFHHISWQTEAIPQTESKSDKPWFAL				
	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
	PQTSEKPEHILVIGAGISGAATAHALASH	GISVTVLEARKAAQAASGNRQGLLYAKIS				
g212	PQTSEKPEHVLVIGAGIAGASTAHALASH	GISVTVLEARKAAQAASGNRQGLLYAKIS				
	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
	PHDTEQTELLLAGYGYTKRLLGHILPESET	WGGNGIIHLNYSRTEQQRNHELGLQKHHNH				
g212	PHDTGQTELLLAGYGYTKRLLGHILPDS	TWGGNGIIHLNYSRTEQQRNHELGLQKHHNH				
	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
	LYRSITSAEAEKIAGIPLSVPYDHPSCGLY	WQHGVLNPPAFVRTLLNHP LIGLHEDTPL				
g212	LYRSITSAEAEKIAGIPLNTPYAEP	LCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL				
	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
	TDISHDGEKWIASTPNGTFTATHIIYCTGA	NSPYLPETNL AALPLRQIRGQTGLTPSTPF				
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGA	HSPCLPETNL AALPLRQIRGQTGLTPSTPF				
	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
	SEQLRCAVSGESYISPSWHGLHCYGASFIP	NSSHTGWNEAEEASNRQALAHLPALSES				


```

a212.seq
1 ATGGACAATC TCGCATGGAA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AACCATCCGC AAACACGCAC ACCCGCTCAA CCTGATTGTC TGCCCTCCCG
101 ATAATCAGAT TCCCAATTTT CAAACCGCAC AAGATGCTTC GGACCGCGAA
151 TGCCGCTCTGA AGCACCGTTT GGATCAGGCA ACCCAGTGCC TCCAGTTCTGA
201 CAGCATCAAC CTGATTGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCAACCCG CGCCTGCACG AACACTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGTAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGAGC GGGCATATCC GGGCGGGCAA CCGCCACGC CTTAGCATCA
451 TACGGCATT TCCGTTACCG ATTGGAAGCC CGAAAAGCCG CCAAGCCGC
501 CAGCGCAAC CGCCAAAGGG TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAAAC CGAAGTCTG CTTGCCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACATA TCTCGCCGGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACGCA GGCAGAAGCC
751 GAAAAAATCG CCGGCATCCC TCTGAACACG CCCTACGCCG AACCATATG
801 CGGACTGTT TGGCAGTAGC GCGTATGGCT CAATCCTCCC ACATTCTGTC
851 GCGCCCTCCT CAGCCATCCG CTCATTGGAC TACACGAAGA CACACCGTTA
901 ACCGACATT CCCACGACGG GGAAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCCGA AACCAACCTC GCCACCTGCG CCCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACCCGTC CACCCCGTT TCCGAACAAC TCGTTTCGCG
1101 CGTTTCAGGC GAAAGTACA TCAGCCCGTC TGGGCAGGTA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTT TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCGGACCACC TCCCCTAGT CGGCGCACTC
1351 GGCGACATTG CCGCTATGCA ACAAACCTAC GTCAAACTCG CGCTGGACAA
1401 AAACATATCG ATCGATGCCC CCTGCCCGTA CCTGCCAAT GCCTACGCCA
1451 ACACCGCCCA CGGCACACGC GGGCTTGCCA CCGCCCCCAT CTGCGCGGCC
1501 GCCGTTGCG CCGAAATCCT AGGCTTGCCC CATCCCCTCT CAAAACGCCT
1551 GCGCCACGCC CTACACCCCA ACCGCGCCAT CATCCGCGCC ATCGTCAGAA
1601 GGAAGGATCT AACCCCTTAA

```

a212.pap

1	MDNLAWNGIP	DIRTLDQ TIR	KHAHPLNLIV	CLPDNQIPNF	QTAQDASDAE
51	CRLKHLRDQA	TQCLQFDSIN	LI EHILPDVR	FWLVPPSRTR	RLHEHFHHIS
101	WQTEAIPQTE	SKPKQPFAL	PQTSEKQPE	HILVIGAGIS	GAATAHALAS
151	YGISVTVLEA	RKAAQAASGN	RQGLLYAKIS	PHDTEQTELL	LAGYGYTKRL
201	LGHILPESET	WGGNGIHLN	YSRTEQQRNH	ELGLQKHNNH	LYRSITQAEA
251	EKIAGIPLNT	PYAEPLCGLF	WQYGVWLNPP	TFVRALLSHP	LIGLHEDTPL
301	TDISHDGEKW	IASTPNGTFT	ATHIIYCTGA	NSPYLPETNL	ATLPLRQIRG
351	QTGLTPSTPF	SEQLRCAVSG	ESYISPSWHG	LHCYGASFIP	NSSHGTWNEA
401	EEASNRLQAL	HLNPALSES	FAANPNPQKH	QGHAAIRCDR	PDHLPLVGAL
451	GDIAAMQQT	AKLALDKNYR	IDAPCPYQHN	AYANTAHGTS	<u>GLATAPICAA</u>
501	AVAAEILGLP	HPLSKRLRHA	LHPNRAIIRA	IVRRKDLTPT*	

m212.pép MDNLVWDGIPDIRTLDAQIRKHAPPLNLIICLPDNIQIPDFQTQAQDASDAECRLKHLRDLQA
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
a212 MDNLAWNGIPDIRTLDTQIRKHAPPLNLIVCLPDNOIENFOTAODASDAECRLKHLRDLQA

491

	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214.seq
1  atgatacaaa agatatgtaa gctattttgtt ttaattgttaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagcgtc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcaggc aaagggcgcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gtttcagcca aacggttgga gggggcaaag ggacggtgcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgctgttc
351 tgaccggcaa tgccaaaagt cagcgcgcg ggcagcgttc cgaaggtgcg
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep

```

1  MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQRTTFS
51  GNVIIIRQGT L NISASCVNVT RGRQRRRIRE GGRFARPLQP NVGRGQRDGA
101 RSGKQRYLFL RRKHCRSDRQ CQSAARRRRC RRCGHYLQHQ NRSLYHQRQH
151 EIGCEIRFQN RQGQRRHPAF KHTKNRITPM PSETETQFRR HLPTEMPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```

m214.seq (partial)
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...

```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```

m214.pep (partial)
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNVT RGRQRRRIRE GGRFASPLQP DIGRRQRHGA
101 RTGKQRC LFI CRQHRSLNR* CQSTARRRCR RRCGDYIQHQ NRSLYHQRQH
151 KI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

```

m214/g214
      10      20      30      40      50      60
m214.pep  MIQKICKLFVLIAFFSASPAFALQSDSRQPIQIEADQGS LDQANQSTTFSGNVVIRQGT L
          |||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
g214       MIQKICKLFVLIVIFATSPA FALQSDSRRP IQIEADQGS LDQANQRTTFSGNVIRQGT L
          10      20      30      40      50      60

      70      80      90      100     110     120
m214.pep  NISAARVNVT RGRQRRRIREGGRFASPLQPDIGRRQRHGARTGKQRC LFI CRQHRSLNRX
          |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
g214       NISASCVNVT RGRQRRRIREGGRFARPLQPNVGRGQRD GARS GKQRYLFLRRKHCRSDRQ
          70      80      90      100     110     120

      130     140     150
m214.pep  CQSTARRRCRRRCGDYIQHQNRSLYHQRQH KI
          |||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
g214       CQSAARRRRCRRCGHYLQHQNRSLYHQRQHEIGCEIRFQNRQGQRRHPAFKHTKNRITPM
          130     140     150     160     170     180

g214       PSETETQFRRHLPTMPRRDY
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```

a214.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGGC.GGC AAAGGCGGCG AATCCGTGAG GCGGGAAGGT
251 TCGCCAGTCC GCTTCAGCCA GACATTGGAC GGCGGCAAAG GCACGGTGCG
301 CGGACAGGCA AACAACGTTG CTTATTCATC TGCAGGCAGC ACCGTAGTCT

```

493

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGACGCG CATTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
  1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGSL DQANQSTTFS
 51 GNVVIRQGTI NISAA RVNVT RGXQRRRIRE GGRFASPLQP DIGRRQRHGA
101 RTGKQRCLFI CRQHRSLNR* CQSTARRRCR RRCGDYIQHQ NRSLYHQHQH
151 KIRRKIRFQI RQGQRRYP AF EYAKIRIIPM PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m214.pep	MIQKICKLFV	LIAFFSASPA	FALQSDSRQP	IQIEADQGSL	DQANQSTTFS	SGNVVIRQGTI
a214	MIQKICKLFV	LIAFFSASPA	FALQSDSRQP	IQIEADQGSL	DQANQSTTFS	SGNVVIRQGTI
	10	20	30	40	50	60
m214.pep	NISAA RVNVT	RGXQRRRIRE	GGRFASPLQP	DIGRRQRHGA	RTGKQRCLFI	CRQHRSLNRX
a214	NISAA RVNVT	RGXQRRRIRE	GGRFASPLQP	DIGRRQRHGA	RTGKQRCLFI	CRQHRSLNRX
	70	80	90	100	110	120
m214.pep	CQSTARRRCR	RRCGDYIQH	QNRSLYHQH	KIRRKIRFQI	RQGQRRYP	AF EYAKIRIIPM
a214	CQSTARRRCR	RRCGDYIQH	QNRSLYHQH	KIRRKIRFQI	RQGQRRYP	AF EYAKIRIIPM
	130	140	150	160	170	180
m214.pep	PSETXTWFG	RHLPTEILK	RYLX			
a214	PSETXTWFG	RHLPTEILK	RYLX			
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTTCGAAC
 51 TTCTCCCGCT TTTGCCCTTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGTAC CACATTTAGC
151 GGCAATGTCA TCATCAGACA GGTACGCTC AACATTTCCG CCTCGCGCGT
201 CAACGTCACA CGCGCGGCGA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCCGTCCG CTTAGCCCAA ACGTTGGACG GGGGCAAAGG GACGGTGCGC
301 GGTCAGGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAGTCT ATACCATCAA CCGCAGCACG
451 AAATCGGGTG CGAAATCCGC TTCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
  1 MIQKICKLFV LIVIFATSPA FALQSDSRQP IQIEADQGSL DQANQSTTFS
 51 GNVVIRQGTI NISAS RVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR
101 GQANNVTYSS AGSTVVL TN AKVQRGGDVA EGAVITYNTK TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
 51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCCGCGT

```

m214-1.pgp

m214-1/g214-1 93.8% identity in 176 aa overlap

Q214-1/p38685

```

Query: 19  PAFALQSDSRQPIQIEADQGSGLDQANQSTTFSGNVVIRQGTNLNISAARVNVTR--GGKGG 76
          PAFA+  D+ QPI IE+DQ SLD          TF+GNV++ QGT+ I+A +V VTR  G +G
Sbjct: 24  PAFAVTGDTDQPIHIESDQQSLDMQGNVVFTTGNVIVTQGTIKINADKVVVTRPGEQGG 83

Query: 77  ESVRAEGSPVRFSQTLDDGGKGTVRGQANNVAYSSAGSTVVLTGNAKVQRGGDVAEGAVIT 136
          E +   G P  F Q  D GK  V G A+ + Y  A  VVLTGNA +Q+      +G IT
Sbjct: 84  EVIDGYGKPFATFYQMDDNGK-PVEGHASQMHYELAKDFVVLTGNAYLQQVDSNIKGDKIT 142

Query: 137 YNTKTE 142
          Y  K +
Sbjct: 143 YLVKEQ 148

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pgp

1 MIKICKLFLV LIAFFSASPA FALQSDSROP IOIEADOGSL DOANOSTTFS

51 GNVVIRQGTI NISAARVNVT RGGKGGESVR AEGSPVRFSSQ TLDGGKGTVR
 101 GQANNVAYSS AGSTVVLGTN AKVQRGGDVA EGAVITYNTK TEVYTISGST
 151 KSGAKSASKS GRVSVVIQPS STQKSE*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQICKLFLVLI	AFFSASP	FALQSDSR	QPIQIEAD	QGSLDQAN	QSTTFSGNVVIRQGTI
m214-1	MIQICKLFLVLI	AFFSASP	FALQSDSR	QPIQIEAD	QGSLDQAN	QSTTFSGNVVIRQGTI
	70	80	90	100	110	120
a214-1.pep	NISAARVNVT	RGGKGGES	VRAEGSP	VRFSSQTL	DGGKGTVR	GQANNVAYSSAGSTVVLGTN
m214-1	NISAARVNVT	RGGKGGES	VRAEGSP	VRFSSQTL	DGGKGTVR	GQANNVAYSSAGSTVVLGTN
	130	140	150	160	170	
a214-1.pep	AKVQRGGDVA	EGAVITYN	TKTEVYTI	SGSTKSGA	KSASKSGR	VSQPSSTQKSEX
m214-1	AKVQRGGDVA	EGAVITYN	TKTEVYTI	SGSTKSGA	KSASKSGR	VSQPSSTQKSEX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq
 1 atgaaagtaa gatggcggta cggaattgcg ttccattga tattggcggg
 51 tgccctgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
 101 tcgaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc
 151 ttggacggaa ggcggtttga cgaacagggg tacttgaaaag aacatttgag
 201 cgcgaaaagg gcgaaacagt ttcccgaaaa cagcgacatc cattttgatt
 251 cgccgcattc cgtgttcttc caagaaggca ggctgttgta cgaagtcggc
 301 agcgatgaag ccgtttacca taccgaaaac aaacagggttc tttttaaaaa
 351 caacgtttgt ctgacaaaaa ccgccgacgg caggcggcag gcgggtaaa
 401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaacc
 451 gatacgctg tcagtttcca atatggcgcg tcgcacgggc aggcgggcgg
 501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
 551 aagccgcgat ttatgataca aaagatatgt aa

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep
 1 MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS
 51 LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPLVFF QEGRLLYEVG
 101 SDEAVYHTEN KQVLFKNNVV LTKTADGRRQ AGKVETEKHL VDTESQYAQT
 151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAAYDT KDM*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)
 1 ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
 51 CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA
 101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG CGCGAAGGGC
 151 GCGAAACAGT TTCCGAAAG CAGCGACATC CATTTTGATT CGCCGCATCT
 201 CGTGTCTTTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC AGCGACGAAG
 251 CCGTTTACCA TACCGAAAAC AAACAGGTTT TTTTAAAAA CAACGTTGTG
 301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
 351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCCTG
 401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG CATGACTTAC
 451 GACCACAwwA CAGGCATGTT GAACCTCTCA TCTAAAGTGA AAGCCACGAT
 501 TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)
 1 ..SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG
 51 AKQFPENSDI HFDSPLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNNVV
 101 LTKTADGKRQ AGKVEAEKHL VDTESQYAQT DTPVSFQYGA SHGQAGGMTY

151 DHXTGMLNFS SKVKATIIYDT KDM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
		:			
g215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTMDGLDGRRFDEQG			
	10	20	30	40	50
	50	60	70	80	90
m215.pep	YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV				
	:				
g215	YLKEHLSAKGAKQFPENSIDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV				
	70	80	90	100	110
	110	120	130	140	150
m215.pep	LTKTADGKRQAGKVEAEKLVHVDTSQYAQTDTVPVSFQYGASHGQAGGMTYDHXTGMLNFS				
	: :				
g215	LTKTADGRRQAGKVETEKLVHVDTSQYAQTDTVPVSFQYGASHGQAGGMTYNHKTGMLNFS				
	130	140	150	160	170
	170				
m215.pep	SKVKATIIYDTKDMX				
	:				
g215	SKVKAIIYDTKDM				
	190				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq

1	ATGAAAGTAA	GATGGCGGTA	CGGAATTGCG	TTCCCATTGA	TATTGGCGGT
51	TGCCTTGGGC	AGCCTGTCGG	CATGGTTGGG	ACGCATCAGC	GAAGTCGAGA
101	TTGAAGAAGT	CAGGCTCAAT	CCCGACGAAC	CGCAATACAC	AATGGACGGA
151	TTGGATGGCA	GGCGGTTTGA	CGAACAGGGA	TACTTGAAAG	AACATTTGAG
201	TTCGAAGGGC	GCGAAACAGT	TTCCCGAAAAG	CAGCGACATT	CATTTCTGACT
251	CACCGCATCT	CGTGTCTTTC	CAAGAAGGCA	GGTTGTTGTA	CGAAGTCGGC
301	AGCGATGAAG	CCGTTTACCA	TACCGAAAAC	AAACAGGTTT	TTTTTAAAAA
351	CAACGTTGTG	CTGACCAAAA	CCGCCGACGG	CAAACGGCAG	GCGGGTAAAG
401	TTGAAGCCGA	AAAGCTGCAC	GTCGATACCG	AATCTCAATA	TGCCCCAACC
451	GATACGCCTG	TCAGTTTCCA	ATATGGTGCA	TCGCACGGTC	AGGCGGGCGG
501	CATGACTTAC	GACCACAAAA	CAGGCATGTT	GAACCTCTCA	TCTAAAGTGA
551	AAGCCACGAT	TTATGATACA	AAAGATATGT	AA	

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pep

1	MKVRWRYGIA	FPLILAVALG	SLSAWLGRIS	EVEIEEVRLN	PDEPQYTMDG
51	LDGRRFDEQG	YLKEHLSSKG	AKQFPESDI	HFDSPHLVFF	QEGRLLYEVG
101	SDEAVYHTEN	KQVLFKNNVV	LTKTADGKRQ	AGKVEAEKLV	VDTSQYAQT
151	DTPVSFQYGA	SHGQAGGMTY	DHKTGMLNFS	SKVKATIIYDT	KDM*

m215/a215 98.3% identity in 173 aa overlap

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
		:			
a215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTMDGLDGRRFDEQG			
	10	20	30	40	50
	50	60	70	80	90
m215.pep	YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV				

```

a215      |||||:|||||
          YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
          70      80      90      100      110      120

m215.pep  110      120      130      140      150      160
          LTKTADGKRQAGKVEAEKLVHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHXTGMLNFS
a215      |||||:|||||
          LTKTADGKRQAGKVEAEKLVHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHKTGMLNFS
          130      140      150      160      170      180

m215.pep  170
          SKVKATIIYDTKDMX
          |||||:|||||
a215      SKVKATIIYDTKDMX
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga ttctcgagctc ggtaccacgc gacgaaatca ccgccatcat
51  ccccgccactc aaacgcaaaag acattaccct cgtctgcac accgcccgc
101 ccgattcaac catggcgcgc catgccgata tccacatcac cgcacgggt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttgccggt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgccgg cagcctcggc
301 aaacgcctgc ttttgccgct tgcgcacatt atgcacaaag gcggcgccct
351 gcccgcgctc cgactcggca cgccttgaa aggagccatc gtcagcatga
401 gcgagaaaag tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSVPS DEITAIIPAL KRKDITLVC I TARPDSTMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVVLL RARAFTPDDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGA I VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT *
51  GCACGCCGAA GCGGAAGGCT TGC GCGAAAT TGCAGCGGAA TTGsACAAAA
101 ACTTCGTCCT TCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGCGACGC CTGCGTTTTT CGTCCACCCCT GCGGAAGCGG
251 CACACGgCGA TTTGGGTATG ATTGTGGACA rCGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTCG TCctGCTGCG CgcACGCGCG TTCACGCCCC
551 ACGATTTTCG CTGAGCCAT CCTGCCGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCTGCG CTGCCGTCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GGCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAAD ALLHCKGRVV

```


498

```

51  ITGMVKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLMG IVDXDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPPTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGRLLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHHPKT ISAERLATEA LKVMQANHVN
301 GLLVTDADGV LIGALNMHDL LAARIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng) from *N. gonorrhoeae*:

m216/g216

```

              70      80      90      100      110      120
m216.pep      TMASTGTPAFFVHPAEAAHGDLMGIVDXDVVVAISNSGESDEIAAIIPALKRKDITLVC
g216                                     :::|||:| ||||:|||||||
              10      20      30
              130     140     150     160     170     180
m216.pep      TARPDMSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
g216           |||||||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||
              40      50      60      70      80      90
              190     200     210     220     230     240
m216.pep      ALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQGR
g216           |||||||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||
              100     110     120     130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

```

a216.seq
1  ATGGCGATGG CAGGAAACGA AAAATATCTT GATTGGGCAC GCGAAGTGT
51 GCACACCGAA GCGGAAGGCT TGCGCGAAAT TGCGGCGGAT TTGGACGAAA
101 ACTTCGCCCT TGCGGCGGAC GCGTTGTTGC ACTGCAAAGG CAGGGTCGTT
151 ATCACGGGCA TGGGCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 CATGGCCTCG ACCGGCACGC CCGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGGCGA TTTGGGCATG ATTGTGGACA ACGACGTGGT CGTCGCGATT
301 TCCAATTCCG GTGAAAGCGA CGAAATCGCC GCCATCATCC CCGCGCTCAA
351 ACGCAAAGAT ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGCG TTATGGCTTT
501 GGGCGATGCG TTGGCGGTTG TCCTGCTGCG CGCCCGCGCG TTCACGCCCC
551 ACGACTTCGC CTTGAGCCAC CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GGCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTACCGG
801 TCTTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTT TTGGCGGCGC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

```

a216.pep
1  MAMAGNEKYL DWAREVLHTE AEGLEIAAD LDENFALAAD ALLHCKGRVV
51 ITGMGKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLMG IVDNDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPPTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGRLLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHHPKT ISAERLATEA LKVMQANHVN

```

301 GLLVTDADGV LIGALNMHDL LAARIV*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENGKYLDWAREVLHAEAEGLREIAAEELXKNFVLAADALLHCKGRVVITGMVKSGHI					
a216	MAMAGNEKYLDWAREVLHTEAEGLREIAADLDENFALAADALLHCKGRVVITGMGKSGHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIIPALKRKD					
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDNDVVVAISNSGESDEIAAIIIPALKRKD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
a216	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRCLKGVFTDGDRLRRLFQECNFTGLSIDEVMHHPKTISAERLATEALKVMQANHVN					
a216	DGQGRCLKGVFTDGDRLRRLFQECNFTGLSIDEVMHHPKTISAERLATEALKVMQANHVN					
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADGVLIGALNMHDLAARIVX					
a216	GLLVTDADGVLIGALNMHDLAARIVX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggatg acggtttgtt gcggcaactg tccgaaaaac ccagccaaag
51  tgcctctctt ctgccatttg acccattcgt tttcgagggt ttggactgcc
101 ttttggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga ccgtcgagg ttgccgccat atccgggcaa
201 tatccgacag ggtttcgagg aaggcggcaa aacgtccgaa catggcgggt
251 tgattcacgt cggcatacca cgcgctgaca tcctgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgcgcgcga tttctccgtc caatccccaa
401 tggacgttca aatcggcaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcag aaacggcgca acacgggcgc ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttccagca agtcggacac gcaactccaa
551 gcataaaaaa acgggttgccg gcggctgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgataa gggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPPYPGNIRQ GFEEGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAFAQQVGH ALQRIKKRLP AADFHVRNGI

```

500

201 RQCLRAGLRL SEHGFKRRI GFDIRG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

m217.seq

```

1  ATGGCGGATG  ACGGTGTGCG  GCGGCAACTG  TCCGGAAAAT  TGCGCCAATT
51  CGGTTTCCGC  CTCCATTG  ACCCATTCGT  TTTCAAGGTT  TTGGACTGAC
101 TTTTGGTCAT  CGGCTTCAGC  TTGGAACAAT  GTTTCAGCA  AATCCCGGCA
151 ACGCGCCACC  CATTGCGCGA  CCGTTGCGGG  CTGCCGCCAT  ATCCGTACAA
201 TATCCGTGAG  GGTTCGAGG  AAGGCGGCAA  AACGTCCGAA  CATGGCGGTT
251 TGATTACAGT  CGGCATACCA  CGCGCTGACA  TCCTGCCACA  TCGGATTGCC
301 GCCTTTGGGC  AGCATCCAGC  CCAATATCAT  GCGTTCTACC  GCCTGCTTCC
351 AGGTGAACAG  CTGATCCGTG  CCGCCGCGCA  TTTCTCCGTC  CAAACCCAG
401 TGGACGTTCA  AATCGGCAAC  CATGTCGTGC  AAAAGCGGTA  AATCGTCCTC
451 AGTCAGTCCG  AAACGGCGCA  ACACGGGCGC  GGTTCCTAAA  AGCACAAGCA
501 CTTTATCGAC  TTCAAATCGG  CTTTCCAACA  AGTCGAACAG  GCATGACAAA
551 GCATGAAACA  GCGGTGGCG  GCGGCTGATT  TTCACGTCTG  ACACGGAATA
601 CGGCAATGCC  TGCGCACCgG  GctGCGCCTG  TCCGAACACG  GCTTCGATAA
651 AAGGCGTATA  GGATTGATA  TTCGGGGTTA  A

```

This corresponds to the amino acid sequence <SEQ ID 766; ORF 217>:

m217.pep

```

1  MADDGVRRL  SGKLRQFGFR  LPFPDPFVKV  LDXLLVIGFS  LEQCFKQIPA
51  TRHPFADRCG  LPPYPYNIRQ  GFEEGGKTSE  HGGLIHVGIP  RADILPHRIA
101 AFGQHPAQYH  AFYRLLPGEQ  LIRAAAHFSV  QTPVDVQIGN  HVVQKRXIVL
151 SQSETAQHGR  GFXKHKHFID  FKSAFQVEQ  AXQSMKQRLA  AADFHVXHGI
201 RQCLRTGLRL  SEHGFDKRR  GFDIRG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

m217/g217

	10	20	30	40	50	60
m217.pep	MADDGVRRLSGKLRQFGFRLPFPDPFVKVLDXLLVIGFSLEQCFKQIPATRHPPFADRCG					
	: :: : : :					
g217	MADDGLLRQLSEKPSQSALFLPFPDPFVFEVLDCLLVIGPGLKQCFKQIPATRHPPFADRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pep	LPPYPYNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
	: : :					
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRVA AFGQHPAQYHTVCRLLPGKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVVQKRXIVLSQSETAQHGRGFXKHKHFIDFKSAFQQVEQ					
	: : : : :					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKRQIVPGQSETAQHGRGFQKREHFADFKTAFQQVGH					
	130	140	150	160	170	180
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGI RQCLRTGLRLSEHGFDKRRIGFDIRGX					
	: : : :					
g217	ALQRIKKRLPAADFHVVRNGIRQCLRAGLRLSEHGFKRRI GFDIRG					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 767>:

a217.seq

```

1  GTGGCGGATG  ACGGTGTGCA  GCGGCAACTG  TCCGGAAAAT  TGCGCCAATT
51  CGGTTTCCGC  CTGCCATTG  ACCCATTCGT  TTTCGAGGCT  TTGGACTGCC
101 TTTTGGTCAT  CGCCTTCGAC  TTGGAACAAT  GTTTCAGCA  AATCCCGGCA
151 ACGCGCCACC  CATTCGTCAA  CCGTCGCAGG  TTGCCGCCAT  ATCCGTACAA

```

501

```

201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CAGGGCGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTTCTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCAG
401 CGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGCA AATCGTCTCT
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGTCT GCGGCTGATT TTCACATCCG AAACGGAATA
601 CGGCAATGCC TGC GCGCCG GCTGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 768; ORF 217.a>:

```

a217.pep
1 VADDGVQRQL SGKLRQFGFR LPFDPFVFEEA LDCLLVIAFD LEQCQFKQIPA
51 TRHPFVNRRR LPPYPYNIRO GFEEGKTSE QGGLVHVIGIP RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KHKHFID FKSFAQQVEQ A*QSMKQRLS AADFHIRNGI
201 RQCLRAGLRL SEHGFDKRRRI GFDIRG*

```

m217/a217 90.3% identity in 226 aa overlap

```

          10      20      30      40      50      60
m217.pep  MADDGVRRQLSGKLRQFGFRLPFDPFVKVLDXLLVIGFSLEQCQFKQIPATRHFPADRCG
          :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a217       VADDGVQRQLSGKLRQFGFRLPFDPFVFEEALDCLLVIAFDLEQCQFKQIPATRHFPVNRRR
          10      20      30      40      50      60

          70      80      90     100     110     120
m217.pep  LPPYPYNIROGFEEGKTSSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a217       LPPYPYNIROGFEEGKTSSEHGGLVHVIGIPRADPLPHRIA AFGQHPAQYHAFYRLLPGEQ
          70      80      90     100     110     120

          130     140     150     160     170     180
m217.pep  LIRAAAHFSVQTPVDVQIGNHVQKRKXIVLSQSETAQHGRGFXKHKHFIDFKSAFQQVEQ
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a217       LIRAAAHFSVQTPADVQIGNHVQKRQIVLSQSEMAQHGRGFXKHKHFIDFKSAFQQVEQ
          130     140     150     160     170     180

          190     200     210     220
m217.pep  AXQSMKQRLAAADFHVXHGIRQCLRTGLRLSEHGFDKRRIGFDIRGX
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a217       AXQSMKQRLSADFHIRNGIRQCLRAGLRLSEHGFDKRRIGFDIRGX
          190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 769>:

```

g218.seq
1 atggttgccg tggatcctta tacggcaaaa gtggtcaaca ccatgccgcg
51 caatcagggt tggatcacca ctatggatga aatcccacggc gatatgatgc
101 tcggtgcggc aggcgattat cttttggaaa cggcagcttc actgaccatt
151 attatggttg tcagcggcctt gtacctttgg tgggcgaaac agcgcggcat
201 taaagcgatg ctgctgccgc caaaaagcag ggcgcgttct tgggtggcgg
251 atctgcacgg cgcgtttgga acttggtgtg cgttgatttt actggtgttc
301 tgccgtgctg gtattgcttg ggcaggatatt tggggcggca aattcgtgca
351 ggcttggaat cagttcccgg ccggcaaatg ggtgtgcgaa ccgaacccc
401 tttcaatcgt gccgaccac gccgaggtat tgaatgacgg caagggttaag
451 gaagtgccgt ggattttgga gcttatgcct atgcctgtct cagggacgac
501 tgtgggtgaa aacggcatta accccaccga gcccaataac attggaaacc
551 gtcgaccgtt tcgcgcggga aatcggtttc aaagggcggt atcagttgaa
601 tttgccccaa ggcgaggacg gggataggac tttgtcgag gattctatga
651 gttatga

```

This corresponds to the amino acid sequence <SEQ ID 770; ORF 218.ng>:

```

g218.pep
1 MVAVDPYTAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

```

m218.seq

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/q218

		10	20	30	40	50	60
m218.pep		MVAVDPYTAKVVSTMPRNLQGWYYTMDEIHSDMMLGAAGDYLL	ETAASLTIIIMVVSGLYLVW				
		: : :					
g218		MVAVDPYTAKVVNTMPRNQGWYHTMDEIHDMMMLGAAGDYLL	ETAASLTIIIMVVSGLYLVW				
		10	20	30	40	50	60
<hr/>							
	70	80	90	100	110	120	
m218.pep		WVKRRGIKAMLLPSKGXARSWWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
		: : : : : :					
g218		WAKQRGIKAMLLPPKSRRSWSWRNLHGAFTGTWVSLILLLFCLSGIAWAGIWGGKFVQAWN					
		70	80	90	100	110	120
<hr/>							
		130	140	150	160	170	180
m218.pep		QFPAGKWGVEPNPVSVPVTHGEVLNDGKVKEVPWVLELTPMPVSGTTVGKDGINPD	EPMPT				
		: : : :					
g218		QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKEVPWILELMPMPVSGTTVGENGINPT	EPNN				
		130	140	150	160	170	180
<hr/>							
		190	200	210			
m218.pep		LETVDRFARXNRFQRLSV	EFAQRRGRMDVFAGFYEL				
		> :					
g218		IGNRRPF	RAGNRFRQRLSV	EFAQRRGRGMDFVAGFYEL			
		190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq

```

1   ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51  CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GGCGCGTTCT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGGG ACTTGGGTGT CGTTGATTTT ACTGTTGTTT
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGCAA CCGAACCTTG
401 TTTCACTCGT GCCGACCCAC GGCGAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTTGGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAAACCG
551 TCGACCGTTT TGCGCGG.GA AATCGGTTTC AAAGGGCGTT ATCAGCTGAA
601 TTTGCCCAAA GGCGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep

```

1   MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51  IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVFPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRLSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMDEIHS	DMMLGAAGDYLLETAASLTIIMVVSGLYLW				
a218	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHS	DMMLGSTGDYLLETAASLTIIMIISGLYLW				
	10	20	30	40	50	60
	70	80	90	100	110	120
m218.pep	WVKRRGIKAMLLPSKGXARSWWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
a218	WVKRRGIKAMLLPPKGRARSWWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
a218	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFQRLSVEFAQRRGRMDFVAGFYEL					
a218	LETVDRFARXNRFQRLSAEFAQRRGRMDFVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

```
g219.seq
1   atgacggcaa ggtaaggaa gtgccgtgga ttttggagct tatgcctatg
51  cctgtctcag ggacgactgt gggtgaaaac ggcattaacc ccaccgagcc
101 caataacatt ggaaccgctc gaccgtttcg cgcgggaaat cggtttcaaa
151 gggcggtatc agttgaattt gcccaaaggc gaggacgggg tatggacttt
201 gtcgcaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251 cggtagatat cgaccagtac agcggcgaga ttcttgccga catccgtttt
301 gacgattaca acccggttcg caaatttatg gcggcaagca ttgcgctgca
351 tatggggact ttgggctggg ggagcgtggt ggcgaaacgtc gtgttctgcc
401 ttgcccgtgat ttttatcggc atcagcggct gcgtgatgtg gtggaaacgc
451 cgtccgtccg gcgtggcggg cattgttcct ccggcgcaaa aaatcaaact
501 gcccgctctg tgggcgatgg cattgccgct gctgttgatt gcactgcttt
551 tcccgaccgc gctgcttgcc attgccgtga tttggctggt ggataccttg
601 ctgctgtcgc ggattcctgt gttgaggaaa tggtttaaat ga
```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

```
g219.pep
1   MTARLRKCRG FWSLCLCLSQ GRLWVKALT PPSPITLETV DRFAREIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGEILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV VFCLAVIFIG ISGCVMWWR
151 RPSGVAGIVP PAQIKLPVW WAMALPLLLI ALLFPTALLA IAVIWLDDTL
201 LLSRIPVLRK WFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

```
m219.seq
1   ATGACGGCAA GGTAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGaCyGt gGGCAAAGAC GGCATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGCTTTGC GCGGnGAAAT CGGTTTCAAA
151 GGGCGTTATC AGTTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCCTTT GCCGACCGCA
251 CGGTACATAT CGACCAGTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTT
301 GACGATTACA ACCCGTTTCG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT CTGGGCTGGT GGAGCGTGTT GGCGAACGTC TTGTTCTGCC
401 TTGCCGTCAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGACCG GAGCGGTGGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501 GCCGGTTTGG TGGATGATGG CATTGCCGCT ATTGGCAATC GCACTGCTCT
551 TCCCGACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 TCGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```
m219.pep
1   MTARLRKCRG FWSLRLCLFQ GRXWAKTALT LTSRXHWKPS TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMWWR
151 RPTGAVGIVP PAQVKLPVW WMMALPLAI ALLFPTSLA IAVIWLDDTL
201 LLSRIPVLRK WFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

```
m219/g219
10      20      30      40      50      60
m219.pep MTARLRKCRGFWSLRLCLFQGRXWAKTALTLSRXHWKPS TALRGEIGFKGRYQLNLPKG
|||||
g219      MTARLRKCRGFWSLCLCLSQGRLWVKALTTPSPITLETVD RFAREIGFKGRYQLNLPKG
10      20      30      40      50      60

70      80      90      100     110     120
m219.pep EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG T
|||||
g219      EDGVWTLSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMG T
```

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKKRRPTGAVGIVPPAQKVKLPVWMMALPLLAI					
	: : : : :					
g219	LGWWSVLANVVFCLAVIFIGISGCVMMWKKRRPSGVAGIVPPAQKIKLPVWAMALPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : : :					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWFK					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
1   ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTCG GCGG.GAAAT CGGTTCACAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CGGTGCATAT CGACCACTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTT GGCGAACGTT TTGTTC TGCC
401 TTGCCGTGAT TTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAACGC
451 CGTCCGTCCG GCGCGGTGGG CATGGTTCCG CCGGCGCAAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
1   MTARLRKCRG FWSLRCLFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSDQ SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMMWKR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*

```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	: : : :					
a219	MTARLRKCRGFWSLRCLFQGRWLWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	: : : :					
a219	EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKKRRPTGAVGIVPPAQKVKLPVWMMALPLLAI					
	: : : :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMMWKKRRPSGAVGMVPPAQKIKLPVWAMAVPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
  1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
 51  gatgcggcga gccgtaaatac adatcgacgc tgacggattt gaaccctgcc
101  tcacggggcg catcgatgac ttctttgggt tcttcgtagc tttggatgcg
151  gttgactgcc gcctgcactt tggggtcgaa atcctgaatg ccgacgctca
201  tgcggttgaa gccgagtcctg ccgagcatga ggacggtgtc gcggctgact
251  ttgcgcgggt cgatttcgat ggaatattcg ccggacggtg tcagttcgaa
301  atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351  aggtcggcgt gccgcccgcg aagtgcagtt gggcaagctg gtgccgtccg
401  ttcagatgtg gagcgagcag ttccatttct ttttcaagat attcgatgta
451  ggtatcggcg cggcttttgt ctttggatgat gattttgttg cagccgcagt
501  agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaaagcggg
551  ttgttttaa
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
  1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FFGFFVALDA
 51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101  MFADHAEDTF DLFVAQKGRR AAAEVQLGKL VPSVQMWSEQ FHFFFKIFDV
151  GIGAAVFVGD DFVAAAVVAD GVAERNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
  1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
 51  CGACGCTGAC GGATTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101  TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151  GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201  GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251  TATTGCGCCG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGCGGAAGAC
301  ACGTTCGATC TGTTCGTCGC TCAAAAAGGt GCGTGCCcCCG CCGAAGTGCA
351  GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCCATT
401  TCTTTTCAA GATATTGAT GTAGGCATCG GCGCGGCTTT TGTCTTTGGT
451  GATGATTTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501  TGTGAATGTA AAGGGAAAGC GGTTTGTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
  1  MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DDFGFFVTL DAVDRRLHFG
 51  VEILNADAH VEAESAHEH GVAADFARVD FDGVFAGGDx LEMFAYHAED
101  TFDLFVAQKG ACPAEVQLGK LVPSVQMWSE QFHFFFKIFD VGIGAAVFVGD
151  DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

```
m221/g221
      10      20      30      40      50
m221.pep      MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVE
      ||::||| ||||| ||: |||||::||| |||||
g221      MHDHGAMDRRLPAFGSLMRRAVNXIDADGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE
      10      20      30      40      50      60

      60      70      80      90      100      110
m221.pep      ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDxLEMFAHYHAEDTFDLFVAQKGA-
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g221      ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKGRR
      70      80      90      100      110      120

      120      130      140      150      160      170
```

507

```

m221.pep    CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFFVGDDFVAAAVVADGVAERNVNVK
            |||||||
g221        AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFFVGDDFVAAAVVADGVAERNVNVK
            130      140      150      160      170      180

m221.pep    GKRFVX
            |||||
g221        GKRFVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 785>:

```

a221.seq
1  ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51 CGACGCTGAC GGATTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTGCGCG CTGACTTTCG GCGGGTCGAT TTCGATGGAG
251 TATTCGCCCG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGCGGAAGAC
301 ACGTTCGATT TGGTCGTCGC TCAAAAAGGT CGGCGTGCCG CCGCCGAAGT
351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC
401 ATTTCTTTTT CAAGAAATTC GATGTAGGCA TCGGCGCGGC TTTTGTCTTT
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACG
501 GAATGTGAAT GTAAAGGGAA AGCGGTTTGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

```

a221.pep
1  MVVLMRLSLV RQAVNQIDAD GFEPFRFARRI DDFFGFFVTL DAVDRRLHFG
51 VEILNADAH AVEAESAEHED GVAADFARVD FDGVFAGGD* LEMFAYHAED
101 TFDLVVAQKG RRAAAEVQLG KLVPSVQWMS EQFHFFFKKF DVGIGAAFEV
151 GDDEFVAAAV ADGVAERNVN VKGKRFV*

```

m221/a221 95.5% identity in 177 aa overlap

```

              10      20      30      40      50      60
m221.pep    MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDDFFGFFVTLDAVDRRLHFGVEILNADAH
            |||||
a221        MVVLMRLSLVRQAVNQIDADGFEPFRFARRIDDDFFGFFVTLDAVDRRLHFGVEILNADAH
              10      20      30      40      50      60

              70      80      90      100     110     119
m221.pep    VEAESAHEHDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLFVAQKGA-CPAEVQLG
            |||||||
a221        VEAESAHEHDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLVVAQKGRRAAEVQLG
              70      80      90      100     110     120

120      130      140      150      160      170
m221.pep    KLVPSVQMWSEQFHFFFKIFDVGIGAAFFVGDDFVAAAVVADGVAERNVNVKGKRFVX
            |||||||
a221        KLVPSVQMWSEQFHFFFKIFDVGIGAAFFVGDDFVAAAVVADGVAERNVNVKGKRFVX
              130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 787>:

```

g223.seq
1  atggaattca ggcaccaggt agtggttagtt ggtgtcgaac catttggtca
51 tttcgatggc gaattggtct ttgttgccgc gcgccagttg gaagaattgt
101 tccaaaggca ggttttggct atcgaagccg aaacgggcg gaatcgcgcc
151 cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta
201 cagcaacgta atcagcgtta ggagcagctt ggtgtttcca gtttttctcg
251 cgcaggtctt tggcaacgtc gagcagctct tgttctactga tctctttgcg
301 ccagtatttt tcttgggcga atttcaattc acggaaggcg ccgacacgcg
351 ggaagcctga

```

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pep..

```
m223.seq
1   GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTGGTCA
51  TTTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT
101 TCCAAAGACA GGTTTTGGCT TCGAAGCCG AAGCGGGCGG GAATCGCGCC
151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCtCTAC
201 GGCAACGAAA TCGGCGTTGG CAGCGACCTG GTGTTTCCAG TTTTCTCGC
251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGCTGAT TTCTTTGCGC
301 CAGTATTTTT CTTGTGCGAA TTTCAATTCT CGGAAGCGCG CGACACGCGG
351 GAAGCCTGA
```

```
m223.pep
  1  VEFRHQVVVV  GVEPFGHFDS  ELVFVTARQL  EELFQRQVLA  VEA EAGGNRA
 51  GGD LQVEDVV  VESEIXY GNE  IGVGSDLVFP  VFLAQVFSNS  QQFL LADFFA
101  PVFF LCEFQF  AEGADTREA*
```

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

```

m223/g223
      10      20      30      40      50      60
m223.pep  VEFRHQVVVVGVPEFGHFDSELVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDV
:|||||:|||||:|||||:|||||:|||||:|||||:
g223      MEFRHQVVVVGVPEFGHFDGELVFVAARQLEELFQRQVLAIEAETGGNRARGYLQVEDVM
      10      20      30      40      50      60
      70      80      90     100     110     120
m223.pep  VESEIXYGNEIGVGS DLVFPVFLAQVFSNSQQFLLADFFAPVFFLCEFQFAEGADTREAX
:|||||:|:|:|:|||||:|:|:|:|||||:|:|:|:|||||:|:|:|:|||||:|:|:|:
g223      VESEITYSNVISVRSSLVFPVFLAQVFGNVEQLLFTDLFAPVFFLGEFQFTEGADTREAX
      70      80      90     100     110

```

a223.seq

1	GTGGAATTCA	GGCACCAAGT	AGTGGTAGTT	GGTGTGCAAC	CATTTGGTCA
51	TTTCGATAGC	GAATTGGTCT	TTGTTACCGC	CGCCAGTTTG	GAAGAATTGT
101	TCCAAAGATA	GGTTTTGGCT	GTCGAAGCCG	AAGCGGGCGG	GAATCGCGCC
151	GGTGGCGACT	TGCAGGTCGA	GGATGTGGTC	GTAGAAAGTG	AAATCGCCTA
201	CGGCAACGTA	ATCGGCGTTG	GCAGCGGCCT	GGTGTTTCCA	GTTTTTCTCG
251	CGCAAGTCTT	TAGCAACAGC	CAGCAATTCT	TGCTCGCTGA	TTTCTTTGCG
301	CCAGTATTTT	TCTTGTGCGA	ATTTCAATTC	GCGGAAGGCA	CCGACACGCG
351	GGGAAGCTGA				

a223.pep

1	VEFRHQVVVV	GVEPFGHFDS	ELVFVTARQL	EELFQR*VLA	VEAEAGGNRA
51	GGDLQVEDVV	VESEIAYGNV	IGVGSGLVFP	<u>VFLAQVFSNS</u>	QQFLLADFFA
101	PVFFLCFOF	AEGTDTREA*			

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGV	EPFGHFDSEL	VFVTARQLEEL	FQRQVLAVEAE	AGGNRAGGDL	QVEDVV
a223	VEFRHQVVVVGV	EPFGHFDSEL	VFVTARQLEEL	FQRXVLAVEAE	AGGNRAGGDL	QVEDVV
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYGNIEG	VGSGLVFPVFL	QAQVFSNSQQF	LLADFFAPVFF	LCEFFQAEAGD	TREAX
a223	VESEIAYGNIVG	VGSGLVFPVFL	QAQVFSNSQQF	LLADFFAPVFF	LCEFFQAEAGT	DTREAX

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1   atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcgcgtccg cccgcccctt cgcacgagtt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag ttgtccgaag acgaacagcc cgttttaccc
151 gtcaaccgag ccccgccccg gcgggcgggc aatgccgacg aactcatcgg
201 cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251 ccgcccggcg ggcgggcaat gccgacaaac tcacgcgcag cgcgatgcgg
301 cttttgggta ttgcctaccg ctacggcggc acatcgggtg ctaccggttt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgccgcg cacgtcggcg gaacaggcgc ggatgggcgc acccgttgcc
451 cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501 cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551 acgcgcgcgc cacggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcg gcaaatatgc gttcgcccgc cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1   MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FFRTLGGSRV SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKKNDSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1   ..TTTTCAAACC CGGCAGTTTG GCGGTTTTTG TGGCTGAwGT TTGCCGTCGG
51  CCCC GCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101 TTCTCAGACA GTTTGCCGAA GACGAACAGC CCGTTTTACC CATCAACCGA
151 GCCCCCGCCC GCGGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201 GGGGCTTAAC GAACAGCCCG TTTTACCCGT CAACCGAGTC CCCGCCCGGC
251 GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301 CAGCCCGTTT TACCCGTCAA CCGAGCCCCC GCCCGCGGG CGGGCAATGC
351 CGACGAACTC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401 ACGCGGGCAC ATCGGTTTCT ACCGGTTTTG ACTGCAGCGG CTTTCATGCAG
451 CACATCTTCA AACGCGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501 ACAGGCACGG ATGGGTACGC CGGTTGCCCG AAGCGAATG CAGCCCGGAG
551 ATATGGTGTT TTTCCGACG CTCGGCGGCA GCCGCATTTC CCATGTCGGA
601 CTTTATATCG GCAACAACCG CTTTCATCCAC GCGCCGCGCA CGGGGAAAAA
651 TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701 TCGCCGCGG GGTCAAGAAA AACGACCCGT CCCGCTTCT GAACCTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1   ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQPVLPINR
51  APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101 QPVLVNRAP ARRAGNADEL IGNAMGLLGI AYRYGGTSVS TGFDCSGFMQ
151 HIFKRAMGIN LPRTSAEQAR MGTPVARSEL QPGDMVFFRT LGGSRIHVG
201 LYIGNNRFIH APRTGKNIEI TSLSHKYWSG KYAFARRVKK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

m225/g225

```

              10      20      30      40      50
m225.pep      FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
               | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g225           MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
```

510

	10	20	30	40	50	60
m225 . pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
	: :					
g225	NADELIG-----GAMGLNEQPVVRVNRAXARRAGNA					
		70	80	90		
m225 . pep	120	130	140	150	160	170
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
	: :					
g225	DKLIGSAMRL LGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225 . pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225 . pep	240	249				
	VKKNDPSRFLNX					
g225	VKKNDPSRFLN					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225 . seq
  1  ATGGATTCTT  TTTTCAAACC  GGCAGTTTGG  GCGGTTTTGT  GGCTGATGTT
 51  TGCCGTCCGC  CCCGCCCTTG  CCGACGAGTT  GACCAACCTG  CTCAGCAGCC
101  GCGAGCAGAT  TCTCAGACAG  TTTGCCGAAG  ACGAACAGCC  CGTTTTACCC
151  ATCAACCGAN  CCCCCGCCG  GCGGGCGGGC  AATGCCGACG  AACTCATCGG
201  CAGCGCGATG  GGGCTTAACG  AACAGCCCGT  TTTACCCGTC  AACCGANTCC
251  CCGCCCGGCG  GGCGGGCAAT  GCCGACNAAC  TCATCGGCAA  CGCGATGGGG
301  CTTAACGAAC  AGCCCGTTTT  ACCCGTCAAC  CGAGTCCCG  CCCGGCGGGC
351  GGGCAATGCC  GACGAACTCA  TCGGCAACGC  GATGGGGCTT  AACGAACAGC
401  CCGTTTTACC  CGTCAACCGA  GCGCCCGCCC  GGCGGGCGGG  CAATGCCGAC
451  GAACTCATCG  GCAACGCGAT  GGGACTTTTG  GGTATTGCCT  ACCGCTACGG
501  CGGCACATCG  ATTTCTACCG  GTTTTGACTG  CAGCGGCTTC  ATGCAGCACA
551  TCTTCAAACG  CGCCATGGGC  ATCAACCTGC  CGCGCACGTC  GGCAGAACAG
601  GCGCGGATGG  GTACGCCGGT  TGCCCCAAGC  GAATTGCAGC  CCGGGGATAT
651  GGTGTNTTTC  CGCACGCTCG  GCGGCAGCCG  CATTTCCTTC  GTCGGACTTT
701  ATATCGGCAA  CAACCGCTTC  ATCCACGCGC  CGCGCACGGG  GAAAAATATC
751  GAAATACCA  GCCTGAGCCA  CAAATATTGG  AGCGGCAAAT  ACGCGTTCGC
801  CCGCCGGGTC  AAGAAAAACG  ACCCGTCCCG  CTTTCTGAAC  TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225 . pep
  1  MDSFFKPAVW  AVLWLMFAVR  PALADELTNL  LSSREQILRQ  FAEDEQPVLP
 51  INRXPARRAG  NADELIGSAM  GLNEQPVLPV  NRXPARRAGN  ADXLIGNAMG
101  LNEQPVLPVN  RVPARRAGNA  DELIGNAMGL  NEQPVLPVNR  APARRAGNAD
151  ELIGNAMGLL  GIAYRYGGTS  ISTGFDCSGF  MQHIFKRAMG  INLPRTSAEQ
201  ARMGTPVARS  ELQPGDMVXF  RTLGGSRISH  VGLYIGNNRF  IHAPRTGKNI
251  EITSLSHKYW  SGKYAFARRV  KKNDDPSRFLN  *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225 . pep	FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG				
	:				
a225	MDSFFKPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG				
	10	20	30	40	50
	60	70	79		80
m225 . pep	NADELIGSAMGLNEQPVLPVNR-----VPARRAGNA				

```

      |||
a225  NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
      70      80      90      100     110     120

      90      100     110     120     130     140
m225.pep DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
      |||
a225  DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
      130     140     150     160     170     180

      150     160     170     180     190     200
m225.pep MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
      |||
a225  MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
      190     200     210     220     230     240

      210     220     230     240     249
m225.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLNX
      |||
a225  IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLNX
      250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

g225-1.seq

```

1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttacct
151  gtcaaccgag ccccgcccg gcgggcgggc aatgccgacg aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccgt tgtaecgctc aaccgagccn
251  ccgcccggcg ggcgggcaat gccgacaaac tcatcggcag cgcgatgcgg
301  cttttgggta ttgectaccg ctacggcgcc acatcggtgt ctaccggttt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgccgcg cagctcggcg gaacaggcgc ggatggcgcc acccgttgcc
451  cgaagcgaat tgcagcccg ggatatgggt tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551  acgcgcgcgg cgcggggaat aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gttcgcccg gcgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDQPVLP
51  VNRPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101  LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNDFSRF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151  ATCAACCGAG CCCCCGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCGGTC AACCGAGTCC
251  CCGCCCGGCG GCGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301  CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGCCCGG CCGGGCGGGC
351  GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGACTT TTGGGTATTG
401  CCTACCGCTA CGCGGCACA TCGGTTTCTA CCGGTTTGA CTGCAGCGGC
451  TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCCGCGCAC
501  GTCCGCAGAA CAGGCACGGA TGGGTACGCC GGTGCGCCGA AGCGAATTGC
551  AGCCCGGAGA TATGGTGT TTCCGCACGC TCGGCGGCAG CCGCATTTCC
601  CATGTCGGAC TTTATATCGG CAACAACCGC TTCATCCAG CGCCGCGCAC
651  GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGGAGCGGCA
701  AATACGCGTT CGCCCGCCG GTCAAGAAAA ACGACCCGTC CCGCTTTCTG
751  AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQPVLPV NRVPARRAGN ADELIGNAMG
101 LNEQPVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKKNDPSRFL
251 N*

```

m225-1/g225-1 84.9% identity in 251 aa overlap

```

              10      20      30      40      50      60
m225-1.pep  MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
              |||||
g225-1      MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
              10      20      30      40      50      60

              70      80      90      100     110     120
m225-1.pep  NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
              |||||
g225-1      NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA
                      70      80      90

              130     140     150     160     170     180
m225-1.pep  DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
              |||||
g225-1      DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR
              100     110     120     130     140     150

              190     200     210     220     230     240
m225-1.pep  SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPARTGKNIEITSLSHKYWSGKYAFARR
              |||||
g225-1      SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPARTGKNIEITSLSHKYWSGKYAFARR
              160     170     180     190     200     210

              250
m225-1.pep  VKKNDPSRFLNX
              |||||
g225-1      VKKNDPSRFLNX
              220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCGCG CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCCGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCGC CCCGGCGGGC
351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCGCCCC GCGGGCGGGC CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAIYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNNDPSRFLN *

```

a225-1/m225-1 88.6% identity in 280 aa overlap

```

      10      20      30      40      50      60
a225-1.pep MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRXPARRAG
|||||
m225-1     MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
      10      20      30      40      50      60

      70      80      90     100     110     120
a225-1.pep NADELIGSAMGLNEQVLPVNRXPARRAGNADXLIGNAMGLNEQVLPVNRVPARRAGNA
|||||
m225-1     NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA
      70      80      90

      130     140     150     160     170     180
a225-1.pep DELIGNAMGLNEQVLPVNRAPARRAGNADELIGNAMGLLGIARYGGTISTGFDSCSGF
|||||
m225-1     DELIGNAMGLNEQVLPVNRAPARRAGNADELIGNAMGLLGIARYGGTSVSTGFDSCSGF
      100     110     120     130     140     150

      190     200     210     220     230     240
a225-1.pep MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
|||||
m225-1     MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
      160     170     180     190     200     210

      250     260     270     280
a225-1.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLNX
|||||
m225-1     IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLNX
      220     230     240     250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGcgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccggatacc caattctcct tcccgcctcg tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcca
451 tttctgttgc ctccgcctct cctgccgcgc ctcgggccgc atacattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggt cctttctcct Ccgggcctcg cccctccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

g226.pep

```

1  MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
101 GSVTGIVTGM YFAAWLGPDT QSFPPRLQY LLFTPSGIPI HTLYARVLPP
151 FLLPPPLLPR LGPHTLRRFT ILPKKL RPFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```


514

501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTGGGT ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGTATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TCATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226 . pep
 1 MNEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

	10	20	30	40	50	60
m226 . pep	MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	:					
g226	MSEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m226 . pep	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGM YFAKWLGAER					
	:					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGM YFAAWLGPDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m226 . pep	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSSVG					
	:					
g226	QFSFPRLQYLLFTPSGIPHTLYARVLPPFLLPPPLPRLGPHTLRRFTILPKKL RPFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226 . seq
 1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC
 51 CGTGTCACGC CTTGCGATTA TCGTGCGCAC GCGCACGGGT AATATCTTCT
 101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
 151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATTT
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
 251 GCCGTAAAT CTTCAACCAA TGGCTGCCCG TCATCGTTTC GCAGCTTGGC
 301 GGCAGCGTTA CGGGCATGTG TACGGGGATG TATTTTGCCA AATGGCTGGG
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAATC
 401 CTATCGCCAT CGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
 451 GCCGCCACCG TCATCATTGC CGGCCTGGTC GGACAGATTG CCGGTTACAA
 501 AATGTTGAAA AACACGGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGCATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TTATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226 . pep
 1 MNEILRQPSI LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

515

```

m226.pep      MNEILRQPSVLLFLT LAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a226          MNEILRQPSILFLT LAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
              10      20      30      40      50      60

              70      80      90      100     110     120
m226.pep      AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a226          AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
              70      80      90      100     110     120

              130     140     150     160     170     180
m226.pep      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVVG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a226          EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVVG
              130     140     150     160     170     180

              190     200     210     220     230
m226.pep      MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a226          MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1   atgaacatca tccgcgcgct cctcatcatc ctcggctgcc tcgcccgcgg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccggc agcatcgtcg
101 gcatgggcgt gctgtttgcg cttttgcagg cgggttggtc caaaacgtct
151 tggctgcaac agcttacga cgcgctgatg gcaaacctga cgctgttcct
201 cgtgccgcc tgcgtggcgg tcatcagcta tttgatttg attgccgacg
251 attggtttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1   MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLFA LLQAGWLKTS
51  WLQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVRHWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1   ..ACGTCTTtGC TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTtG GATTtGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCCG CCTCCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1   ..TSXLQQLTDA LMSNLTLFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227
              10      20      30
m227.pep      TSXLQQLTDALMSNLTLFLVPPCVAVISYL
              || |||||:|||||:|||||:|||||:|||||:|||||
g227          TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTLFLVPPCVAVISYL
              20      30      40      50      60      70

              40      50      60

```

516

```

m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
                |||||||||||||||||||||||||||||||||||
g227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
                80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
  1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
 51  CGAAACCGCC GTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101  GCATGGGCGT ACTGTTTGGC CTTTTCAGG CGGGTTGGGT CAAAACGTCT
151  TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201  CGTGCCGCCC TGGCTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251  ATTGGTTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301  CTGGTTACAG GCAAGGTTCA CCGCTGGATA CGGAGCATTA TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
  1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLFA LLQAGWVKTS
 51  WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101  LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

                                10      20      30
m227.pep                      TSXLQQLTDALMSNLTFLVPPCVAVISYL
                                || |||||||||:|||||||||||||
a227          TAVFLAGIKLPGSIVGMGVLFA LLQAGWVKTSWLQQLTDALMANLTFLVPPCVAVISYL
                20      30      40      50      60      70

                                40      50      60
m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
                |||||||||||||||||||||||||||||||||||
a227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
                80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
  1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
 51  TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101  CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151  GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201  AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251  CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301  AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
  1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
 51  VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101  KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
  1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
 51  TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101  CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151  GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201  AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251  CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301  AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

```

a228.pep
  1 MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
 51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

m228/a228 100.0% identity in 107 aa overlap

```

m228.pep      10      20      30      40      50      60
MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD
|||||
a228          10      20      30      40      50      60
MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD

m228.pep      70      80      90     100
AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX
|||||
a228          70      80      90     100
AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

```

g229.seq
  1 atggctgccg tatcgggcgg cggtgcggtc ttctgataa tgcttcacac
 51 tattgccgc gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag
101 aaatcgcat tgaagccgcc ggcgaaattg tatcggtgc cgcccaagag
151 gttttgccg acaaacggca cggtgccgaa cgagcgcgtt accgaacggg
201 ttgatggcc gaacgacagg cgcaggttct gttcgtgaa atctttgtta
251 tcccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgccc
301 gcccgcattg atttcgcgcg acacgcccac gccgtagcgc aaaccgtgtg
351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat
401 tcaatcgttt ttctggacga agcgttggtt atagcggatt aacaaaaatc
451 aggacaaggc ggcgggccgc aggcagtacg gatggtacgg aaccggttcg
501 cccggtgctt ggacgcctta gggaaccggt ccctttgagc cggggcgggg
551 caacccgtag cggtttttgt tcatccgcca tattgtgttg a

```

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

```

g229.pep
  1 MAAVSGGGAV FLIMLPHIAR VOROPPAFAQ ASGEIGIEAA GEIVSAAAE
 51 VLPDKRHGAE RARYRTVLMR ERQAQVLF AE IFVIPIMHAA ADAAVEEMMP
101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFFGR SVVYSGLTKI
151 RTRRRAGST DGTEPVRPVL GRLREPFLS RGGATRTGFC SSAILC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

```

m229.seq (partial)
  1 ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
 51 GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC
201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCGCGCGA CACGCCTAAG
251 CCCTAGCGCA AACCCTGTGC CTTTTCGGC AGGCTGTCGG CGGTTTTCTG
301 CCAGCTTCTG CCCGCAAATT CAATCGTTTT TTCGGACGAA GCGTTGTTTA
351 TAGCGGATTA ACAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
401 AATAGTACGG AACCATTCA CTTGGTGCTT CAGCACCTTA GAGAATCGTT
451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

```

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

```

m229.pep (partial)
  1 ..AALGEIGIE AAEIVSAAA XEVLLDKRHD AERARYRTVF IAERQAQALF
 51 AEIFVIPIMH AAAADA AVEE MMPARIDFAR HAXALAQTVC LLRQAVGGFR
101 PASARKFNRF FGRSVVYSL TKIRTRQSA DSTNSTEPIH LVLQHLRESR
151 SLFCSSAILC *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 229 shows 80.5% identity over a 169 aa overlap with a predicted ORF (ORF 229.ng) from *N. gonorrhoeae*:

m229/g209

```

                                10      20      30
m229.pep                      A QALGEIGIEAADEIVSAAAXEVL LDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      MAAVSGGGAVFLIMLP HIARVQRQPPAFAQASGEIGIEAAAGEIVSAAAEVL PDKRHGAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAE I FVIPIMHAAAADA AVEEMMPARIDFARHAXALAQTVC LL
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RARYRTV LMAERQAQV LFAE I FVIPIMHAAA -DA AVEEMMPARIDFARHAQAVAQTVC LL
                                70      80      90      100     110

                                100     110     120     130     140
m229.pep      RQAVGGFRPASARKFN RFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRE ---
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RQAVGGFRPASARKFN RFFGRSVVYSGLTKIRTRRRRAAGSTDGTEPV RVPVLGR LREPFP L
                                120     130     140     150     160     170

                                150     160
m229.pep      -----SRSLFCSSAILCX
                                :|: ||| ||| |||
g229      SRGGATRTGFCSSAILC
                                180     190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

a229.seq (partial)

```

1  ATGGCTGTCG TATCGGGCGG CGGTGCGGTC TTCCTGATAA CGCTTCCACA
51 TATTGCCAC  GTTCAGCGTC AGCCGCCA.. GTTCGCTCAA GCGTCGGGAG
101 AAATCGGCAT TGAAGCCGCC GACGAAATG TATCGGCTGC CGCCTAAGAG
151 GTTTTGCTCG ATAAACGGCA CGATGCCGAA TGAGCGCGTT ACTGAACGGT
201 TTTTATAGCC GAGCGACAGG CGCAGGCTCT GTTCGCTGAA ATCTTTGTTA
251 TCCTAATAGT GCACGCCGCC GCGCGTGATG TCTCCGTAGA GGAAATGATG
301 CCCGCCCGCA TTGATTTGCG GCGACACGCC CAAGCCGTAG CGCAAACCGT
351 GTGCCTTTTG CGGCAGGCTG TCGGCGGTTT TCGTCCAGCT TCTGCCTGCA
401 AATTCAATCG TTTTTTCGGA CGAAGCGTTG TTTATAGCGG ATTAACAAAA
451 ATCAGGACAA GGCGACGAAG CGCAGACAGT ACAGATAGTA CGGAACCGAT
501 TCACTTGGTG CTTCAGCACC TTAGAGAATC GTCTCTTTGA GCTAAGGCCA
551 GGCAACGCCG TACTGGTTTT TGTTTCATCCA CTATA

```

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

a229.pep (partial)

```

1  MAVVSGGGAV FLITLPHIAH VQRQPPXFAQ ASGEIGIEAA DEIVSAAA*E
51 VLLDKRHDAE *ARY*TVFIA ERQAQALFAE IFVILIVHAA AADVSV EEMM
101 PARIDFARHA QAVAQTVCLL RQAVGGFRPA SACKFN RFFG RSVVYSGLTK
151 ITRRRSADS TDSTEP IHLV LQHLRESSL* AKARQRRTGF CSSTI

```

m229/a229 85.6% identity in 167 aa overlap

```

                                10      20      30
m229.pep                      A QALGEIGIEAADEIVSAAAXEVL LDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      MAVVSGGGAVFLITLPHIAHVQRQPPXFAQASGEIGIEAADEIVSAAAXEVL LDKRHDAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAE I FVIPIMHAAAADA AVEEMMPARIDFARHAXALAQTVC LL
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      XARYXTVFIAERQAQALFAE I FVILIVHAAAADVSV EEMMPARIDFARHAQAVAQTVCLL
                                70      80      90      100     110     120

```

519

	100	110	120	130	140	149
m229.pep	RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---					
	: : : :					
a229	RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pep	-----RSLFCSSAILCX					
	: :					
a229	AKARQRRTGFCSTI					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

g230.seq

```

1  atgtttccatt ccacgaaaa atacagaaca cccgcccaag tcttattagg
51  cctgattgca ttaacttttg tcggcttcgg cgtcagcacg gtttcccatc
101 cgggcgccga ctacatcgtc caagtgggcg acgaaaaaat cagcgagcac
151 tcaatcaaca acgccatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaaacagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtcacgc
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtgtg
401 tcgaagaaat ccgcgacgag ttgccttgc agaatttggg aagcctcgtc
451 caaacggcg tattggtcgg cgacgcgcag gcggaacagc tgatcaggct
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcacgcccc agtcaaagcg tctgaagccg atttgcagaa attttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaaat tggaatatgt
651 cgcccttgaat ctgaaggatt ttgcagacaa gcagaccgtc agtgaaacgg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaag gcggttgccg acttcaacaa ggcaaaagaa aagctgggcg
851 acgattgcgt caatcatccc tcctcgcttg ccgaagccgc caaaaacagc
901 ggtttgaaag tggaaaccca agaaaacttg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaat acctaataa tgccgtattc agcgacgacg
1001 tattgaagaa aaaacacaat tccgaagtgc tgaccatcaa cagcgaaacc
1051 gcgtgggtcg tccgcgccaa agaagtccgc gaagaaaaaa acctactgtt
1101 tgaagaagcc aaagatgcgg tgcgtcaggc ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

g230.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQAKLMGI SVSSEIQKM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMSE DQFVEEIRDQ FALQNLVSLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAUF SDDVLKKKHN SEVLINSET
351 AWWVRAKEVR EEKNLLFEEA KDAVRQAYIR TEAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

m230.seq (partial)

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCc .GACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC

```

520

```

451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGC.GT cAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT.. ...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
  1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
 51 SINNAIQNEQ ADGGGPPSDA VFQSLQRAY LKQGAQLMGI SVSSEIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFPY
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELMKKK AVADFNKAKE KLGDDAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINA VF SDDVLKKKHN SEVL TINSET
351 AWVVRakeVR EEKTLPFaea KDAVRQAYIR TEAAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

```

m230/g230
      10      20      30      40      50      60
m230.pep MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ
g230      MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ
      10      20      30      40      50      60

      70      80      90     100     110     120
m230.pep ADGGGPPSDAVFQSLQRAYLKQGAQLMGISVSSEIKQIIVDDPNFHDANGKFDHALLN
g230      ADGGSPWRDAVFQSLQRAYLKQGAQLMGISVSSEIKQMIVDDPNFHDANGKFSHALLS
      70      80      90     100     110     120

      130     140     150     160     170     180
m230.pep RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
g230      QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
      130     140     150     160     170     180

      190     200     210     220     230     240
m230.pep PDEFIAQVKVSEADLQKFPYNANKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
g230      PDEFIAQVKASEADLQKFPYNANKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
      190     200     210     220     230     240

      250     260     270     280     290     300
m230.pep ERVARLPANEAKPSFEQEKA AVENELMKKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS
g230      ERVARLPAHEAKPSFEQEKA AVENELMKKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
      250     260     270     280     290     300

```

521

	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRakeVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRakeVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPF AEAKDAVRQAYIRTEAAKL					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGTCA TATGTCGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTCGCA CACTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAAA AAGACTACCT GCTTCCAAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCCCA
951 AATGTCCGGT ATGCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT

```

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51  SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGAQLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRakeVR EEKTLPF AEAKDAVRQAYIR TEAAKL

```

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGSPDAVFQSLQRAYLKQGAQLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
a230	ADGGGSPDAVFQSLQRAYLKQGAQLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

522

```

m230.pep  RYLSQRHMSSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAAEQILRLTQVNRTIRSHTFN
a230      RYLSQRHMSSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAAEQILRLTQVNRTIRSHTFN
           130      140      150      160      170      180

           190      200      210      220      230      240
m230.pep  PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE
a230      PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE
           190      200      210      220      230      240

           250      260      270      280      290      300
m230.pep  ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGD DAVNHPSSLAEAAKNS
a230      ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGD DAFNHPSSLAEAAKNS
           250      260      270      280      290      300

           310      320      330      340      350      360
m230.pep  GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
a230      GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
           310      320      330      340      350      360

           370      380
m230.pep  EEKTLPPFAEAKDAVRQAYIRTEAAKL
a230      EEKTLPPFAEAKDAVRQAYIRTEAAKL
           370      380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCGGCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACCTTTG TCGGCTTCGG CGTCAGCACG GTTTCCTATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGGG GTGTTCCAAT CCCTGCTGCA ACGCGCTTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATTGTGGACG ATCCCAATT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGTCTGAA GACCACTTGT
401 TCGAAGAAAT CCGCGATCAG TTGCTTTCG AGAATTTGGT AAGCCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAAGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 CGGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAAATATG
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGGCTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGA AAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAAGAA AAGCTGGGCG
851 ACGATGCGTT CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TGGAAACCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCCGGC ATGCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TCGGTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACCTTG CGAAAACAAG GCAAAAAGAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCAG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCCTATG TCAGACTGAC CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCTCCGG AGGATATTGC
1401 CGCAGACGTT CCTCTGCGA AACAGGCTTT GGCACAACAG CAGTCTGCCA
1451 ATACTTTCGA CCGTCTGATC CGCTATTTC ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGGCGAT GGTGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMI SVSSEGIKQM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMS DQFVEEIRDQ FALQNLVSLV

```

```

151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRKEVR EEKNLLFEFA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TPPEDIAAQL PPAKQALAQO QSANTFDLLI RYFNGKIKQT
501 KGAQSVDNQD GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCGTATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGGCGCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCAGCACA TCCGTTCCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA CGACACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCATTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCGCAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTGC TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAAACAAG GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAAGT ACAGGCTGTA ACCCCGCCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GGCGCAACAG CAGTCTGCCA
1451 ATACTTTTCA CTTGTTGATA CGTTATTTC ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTGCA CAACGGCGAC GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGA KLMI SVSSEIKQI
101 IVDNPNFHD NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRKEVR EEKTLFFAEA KDAVRQAYIR TEAAKLAENK AKDVLTQLNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TPPEDIAAQL PLAKQALAQO QSANTFDLLI RYFNGKIKQT
501 KGAQSVDNQD GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

	10	20	30	40	50	60
m230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230-1	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAIQNEQ					
	10	20	30	40	50	60
m230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGA KLMI SVSSEIKQIIVDDPNFHDANGKFDHALLN					
g230-1	ADGGSPWRDAVFQSLQRAYLKQGA KLMI SVSSEIKQIMIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGA KLMI SVSSEIKQIIVDDPNFHDANGKFDHALLN					
g230-1	ADGGSPWRDAVFQSLQRAYLKQGA KLMI SVSSEIKQIMIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230-1.pep	RYLSQRHMESEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN					
	130	140	150	160	170	180

524

```

g230-1      :|||||:|||||:|||||:|||||:|||||:
              QYLSQRHMSQDFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRITRSHTFN
              130      140      150      160      170      180

              190      200      210      220      230      240
m230-1.pep  PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g230-1      PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
              190      200      210      220      230      240

              250      260      270      280      290      300
m230-1.pep  ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g230-1      ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
              250      260      270      280      290      300

              310      320      330      340      350      360
m230-1.pep  GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g230-1      GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
              310      320      330      340      350      360

              370      380      390      400      410      420
m230-1.pep  EEKTLPF AEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVKWSEVSVLGAQQAR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g230-1      EEKNLLFEEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVKWSEVSVLGAQQAR
              370      380      390      400      410      420

              430      440      450      460      470      480
m230-1.pep  QSMPP EAYAE LLKAKPANGKPAYVRLIGLPAPVIVEVQAVTPPDDIAAQPLAKQALAAQ
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g230-1      QSMPP EAYAE LLKAKPANGKPAYVRLTGLPAPVIVEAQAVTPPEDIAAQLPPAKQALAAQ
              430      440      450      460      470      480

              490      500      510
m230-1.pep  QSANTFDLLIRYFNGKIKQTKGAQSV DNGDGGQX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g230-1      QSANTFDLLIRYFNGKIKQTKGAQSV DNGDGGQX
              490      500      510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 837>:

a230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CGTGATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCAGC GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC GCCTACCTTT CCAACGTCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTTCGA CACTTTC AAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAA AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCCTC AGCGAAACAG
701 AAGTGAAAAA TCGTTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTGC TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACTTGC CGAAAACAA GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGGCAA CCCGCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAAGT ACAGGCTGTA ACCCGCCCGG ATGATATCGC
1401 GCGACAGCTT CCGCTTGCAA AACAGGCTTT GCGCAACAG CAGCTCGCCA
1451 ATACTTTTCA CTTGTTGATA CGTTATTTCA ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFGVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGAKLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINA VF SDDVLKKKH SEVLTINSET
351 AWVVRKEVR EEKTLPFMEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWSE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPDDIAAQL PLAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNGD GQ*
```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFGVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ
m230-1	MFHSIEKYRTPAQVLLGLIALTFVGFGVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ
a230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN
m230-1	ADGGGSPSRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN
a230-1.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
m230-1	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
a230-1.pep	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE
m230-1	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
a230-1.pep	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
m230-1	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
a230-1.pep	GLKVETQETWLSRQDAQMSGMPENLINA VF SDDVLKKKH SEVLTINSETAWVVRKEVR
m230-1	GLKVETQETWLSRQDAQMSGMPENLINA VF SDDVLKKKH SEVLTINSETAWVVRKEVR
a230-1.pep	EEKTLPFMEA KDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVKWSEVSVLGAQQAR
m230-1	EEKTLPFMEA KDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVKWSEVSVLGAQQAR
a230-1.pep	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEVQAVTPPDDIAAQLPLAKQALAQQ
m230-1	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEVQAVTPPDDIAAQLPLAKQALAQQ
a230-1.pep	QSANTFDLLIRYFNGKIKQTKGAQSVNDNGDGQX
m230-1	QSANTFDLLIRYFNGKIKQTKGAQSVNDNGDGQX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

```
g231.seq
  1  atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
 51  gccgcggttg caaaataatc cgccatttta ccgtaaaaac cgccgcctga
101  acttttttat cgcggcagac ggcggttgcg cgtctccgca aaaatgcagg
151  gcgcgcggtt ttcagacggc atttgccgtt caaggccgtg cgggtgtcttt
201  accaaatgcc caaccattcg cccacggaat ccatccaatc cttattgccc
251  ccgcgcgtcc tgcctgcccg gcggtacgcc cacggcgctt gcggattttt
301  agctttccac aatcctttgc gttccctttc cgcctgaatt tgagcgtcgg
351  catagtcggc aaaatccgcc ttatcctgct gttcttttagc ataactttta
401  taatgccacg ccgcccgcgc ctgcacctgc atcaggttca aatcggtttt
451  gccggcggat acctgcgcca cttcgcgtg atagcggctg gtttcaaaca
501  cacgtacact gactttccta ccctccgccc ccgcgcgcag gttgtcgcgc
551  gaacgtgtac cgtaagcctg tttcatctcc ggtgcgtcga tatacgccat
601  ccgaatttta tgtttcgcgc cgtcgcgcgc gatgacgtga agggatcgcg
651  cgtcatagac tttggacacc gtgcctgtgt agctgtggcc ggatttcgcc
701  gatgcccgtc ggcgaaacggg cgcgtcgaaa cccacgtccc ctgcagtgcc
751  gagtacgtcg agtacggcaa ccgcccgtcc caccgcctca ctgtcatatc
801  ccgtataacc caacgcgccc aaaagcgaca gggcgacggg aagccatttc
851  atgatttttt taatctgcat atttttcaaa tgccgatgcc gtctgaacat
901  ctctga
```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

```
g231.pep
  1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51  ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101  SFQSFAPFP RLNLVGVIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151  AGGYLRHFAL IAVGFKHTYT DFPTLRRRAQ VVARTCTVSL FHLRCVDIRH
201  PNFMFRAVAV DDVKGIIVID FGHRACVAVA GFRRCPSANG RVETHVPCSA
251  EYVEYGNRRP HRLTVISRIT QRAQKRQGDG KPFHDFNLH IFQMMPSEH
301  L*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

```
m231.seq (partial)
  1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAAC
 51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101  ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151  GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGGTGTCTTT
201  ACCAAATGCC CAACATTTCG GC....
```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

```
m231.pep (partial)
  1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51  ARGFQTAFV QGRAVSLPNA QPFG....
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

```
m231/g231

      10      20      30      40      50      60
m231.pep  MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
g231      MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
      10      20      30      40      50      60

      70
m231.pep  QSRAVSLPNAQPFG
g231      QSRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPRLNLVGVIG
      70      80      90     100     110     120
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

527

a231.seq (partial)

```

1   ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTGTGGAACA
501 CGCGGACGCT GACTTTCCTG CCTTCCGCCG CCGCGCGCAG GTTGTGCGGC
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCCGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGTCGGC GCGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1   MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51  ARGFQTAFV  QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV  DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFG					
a231	QSRVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVSGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1   ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTCGCGCTG ATAGCGGTCG GTTTCAAACa
501 CaGgTaCaat gagtttcgta ccctccGCCG ccgcgcgCAG GTTGtcgcGC
551 GAACgTGTAC CGTAagcgtg Tttcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTtTa tGtttcgcgc cgtcgcCgtc gATGACGTGA AGGGtaticGC
651 CgtcATAGAC TTTGGACACC Gtgcctgcgt AGctGTGGCC GGATttcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1   MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51  ARGFQTAFV  QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```

101 SFPOSFAFPF RLNLVGVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
 151 AGGYLRHFAL IAVGFKHTYN EFRTLRRRAQ VVARTCTVSF FHLRCVDIRH
 201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGGTTGCG CGTCTCCGCA AAAATGCAGG
 151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
 201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCC
 251 CCGCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTT
 301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
 351 CATAATCGGC AAAATCGGCC TTATCCTGCT GTTCTTAGC ATAACTTTA
 401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTT
 451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTATCGAACA
 501 CGCGCACGCT GACTTTCCTG CCTTCGCGCG CCGCGCGCAG GTTGTGCGGC
 551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GCGCGCTCGA TATACGCCAT
 601 CCGGATTTTG TGTTCGCGC CGTCGCGGTC GATAACGTGA AGGGTGTGCG
 651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
 701 GATGCTCGGC GCGGGGCGGG CGCGTCGGAA CCCGCTCCC CTGCCGCGCC
 751 GAGTACGTCG AGTACGGCAA CCGCCGTCCG CACCGCTCG CTGCCGTACC
 801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC
 851 ATGATTTTTT TAATCTGCAT ATTTTCAA TGCCGATGCC GTCTGAACAT
 901 ATCGGAATCG GATTTAGAC GGCATCTTAA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep

1 MSKRKSINRP YQKPAELPPL QNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
 101 SFPOSFAFPF RLNLVGVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
 151 ADRNLRHFAL VAVGIEHAHA DFPFRRAQ VVARTRAVSL FHLRRVDIRH
 201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRCSAAG RVGTRVPCRA
 251 EYVEYGNRRP HRLAAVPRIT QRTQKRGD GPFHDFNLH IFQMPMPSEH
 301 IGIGFQTAS*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFAHGIHPILIAAPACPAVRPRRLRIFSFPOSFAFPFRLNLVGVG					
m231-1	QSRVSLPNAQPFAHGIHPILIAAPACSAVRPRRLRIFSFPOSFAFPFRLNLVSVGIIG					
	70	80	90	100	110	120
g231-1.pep	KIRLILFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFRTLRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVLHLHQVQIGFADNLRHFALVAVGIEHAHADFPFRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSFHLRCVDIRHPNFMFRAVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRRCASAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGGTTGCG CGTCTCCGCA AAAATGCAGG

529

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151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTAA
401 TAATGCCACG CCGCCCGGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCT GTGTCTGAACA
501 CGCGGACGCT GACTTTCCTG CCTTCGCGC CCGCGCGCAG GTTGTCTGCGC
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCTG TATACGCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCCGTC GATAACGTGA AGGGTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTGCGC
701 GATGCTCGGC GCGGGGCGGG CCGTCTCGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCGG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTT
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV  QSRVSLPNA QPFAHGIHPI LIAPAACP AVRPRLRIF
101 SFPQSFAFPF RNLNSVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFFAFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
a231-1.pep	QSRVSLPNAQPFAHGIHPILIAPAACPAPVVRPRLRIFSFPQSFAFPFRLNLSVGIIG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAACPASAVRPRLRIFSFPQSFAFPFRLNLSVGIIG					
	70	80	90	100	110	120
a231-1.pep	KIRLILFFSITFIMPRRPVHLHLQVQIGFADRNLRFALVAVGVEHADADFFAFRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVHLHLQVQIGFADRNLRFALVAVGIEHADADFFAFRRRAQ					
	130	140	150	160	170	180
a231-1.pep	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDENVKGVAVIDFGHRACVAVAGFRRCSAAGG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDENVKGVAVIDFGHRACVAVAGFRRCSAAGG					
	190	200	210	220	230	240
a231-1.pep	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300
a231-1.pep	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1  atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatectggt
51  tggtcagatt ttgggaacgg cggttgccgg cgcgccgct tatattgtcg
101 ggatactggt tttgctggtc gccgtcggag gaacggccgg cagcctggtt

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530

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151 atgccgtccg taccgcgcaa ggctgccgat acccaaatcg agtggaaatat
201 tgtccgtggt acaaaatccc tgctgcgtga aacggtgagg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggt tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggcaacga
351 taatgttttt aacctgatgc ttgctttggt ttccatcggg attgccgcgg
401 gttcgggtact gtgtgccaag ttcggcaggg aacggctgat gttggcttgg
451 gtaacgggtg gtgcgttggg ttcgacggtt tgcggcctgg ttttgggtg
501 gctgacgcac ggacaccggt ttgaagggtt gaacggcatt ttttgggttt
551 tatcgcaagg atgggcatac cccgtgatgg cggatgatgac gctgatcggc
601 tttttcggcg gatttttctc cgttccgctc tatacctggc tgcaaacccg
651 cagcagcgag actttccgcg cccgcgcggt tgccgccaac aatatcggtt
701 acggcatctt tatggtttcc gccgcggtt tgagcgcggt attgctgttt
751 ttggttgaca gcatttccct gctgtatctg attgtcgctt tgggcaatat
801 tccgttggcg gtatttttga ttaagcgaga aaggcggtt ttaggcgcgg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

```

g232.pep
  1 MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
 51 MPSVPAKAAD TQIEWNIVRG TKSLRETVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGNLGI FWFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAAIRKKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

```

m232.seq
  1 ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTCTG CCATCCTGTT
 51 CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTCGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGGAATAT
201 TGTCCGTGGC ACAAATCCC TGCTGCGTGA AACGGTGCGG CACAAGCCCCG
251 TTTTACC GC CATTATCGGT ATTTCTGGT TTTGGTTTGT CGGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTT AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAkGG AACGCCTGAT GTTGGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGT TGC GGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CGGTGATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTTCTC CGTTCGCTC TATACct(g)TG CAAACCGCCa
651 TAGCGAGaTT TCCGCGCCCg GCCGTGCGG CCAACAATAT CGTTAACGGT
701 ATTTTATG TTTCCGCTGC CGTTTGTAGC GCGGTGTTGC TGTTTTTGT
751 TGACAGCATT TCCTTGTGT ATCTGATTGT CGCTTGGGC AATATTCCGT
801 TGTCCGTATT TTTGATTAAG CGCGAAAGGC GGTTTTTAGG CGCGCGGCCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

```

m232.pep
  1 MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
 51 MPSVPAKAAD TQIEWNIVRG TKSLRETVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGNLGI FXFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

```

m232/g232
      10      20      30      40      50      60
m232.pep MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
          |||
g232      MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```

531

	10	20	30	40	50	60
	70	80	90	100	110	120
m232.pep	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	130	140	150	160	170	180
m232.pep	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	190	200	210	220	230	
m232.pep	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAANAANNIVNGIFMVS					
	240	250	260	270	280	289
m232.pep	AAVLSAVLLFLFDSISLLYLIVLALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIVLALGNIPLAVFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232.seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAAGCC GCCGTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTCA
101 AAACCGCGCT GTTTGTGATG ATTGGGTTT ACGGTTTGGG GCAAAACGGC
151 TTCCTGCCTG CCGGACAGAT GTTGAACCTG GCGCGTTGC TGTATTATT
201 GCCGTATTTT CTGTTTTCCT CGCTGTCGGG GCAGTTGGGT AACAAATTCG
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAAT GATCATTATG
301 GCGGTGCGCG CATACGGGTT TTATATCCGG TCTGCCCCGC TGCTTTTGGC
351 GTGTCTGTTT TGCATGGGCG CGCAATCGAC GCTGTTCCGG CCGCTGAAAT
401 ACGCCATCCT GCCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGGTAC GTTTGTGCGC ATCCTGTTTC GTGAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATTGTCGGG ATACTGGTTT
551 TGCTGTGTCG CGTAGGAGGC ACGGTCGGCA GCCTGTTTAT GCCGTCCGTA
601 CCCGCCAAGG CTGCCGATAC ACAAATTGAG TGGAATATTG TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CGGTGCGGCA CAAGCCCGTT TTTACCGCCA
701 TTATCGGTAT TTCGTGGTTT TGGTTTGTGC GCGCGGTTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTT CCATCGGTAT TGCCGCCGGT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGGAA CGGCTGAGGT TGGCTTGGT AACGGTTGGT
901 GCGTTGGGTT TGACGGTTTG CGGCTTGGT TTGGTGTGGC TGACGCACGG
951 ACACCGTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGCAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTTCGGCGGA
1051 TTTTCTCCG TTCCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCCGTTG CCGCCAACAA TATCGTTAAC GGTATTTTTA
1151 TGGTTTCCGC TGCCGTTTTG AGCGCGGTGT TGCTGTTTTT GTTTGACAGC
1201 ATTTCTTGT TGTATCTGAT TGTCGCTTTG GGCAATATTC CGTTGTCGGT
1251 ATTTTGTATT AAGCGGAAA GCGGTTTTT AGGCGCGGCG GCAATCAGGA
1301 AAAACCTTG A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232.pep
1  MYAKKGGLGL VKSRRFAPLF ATQFLGAFND NVFKTALFVM IGFYGLGQNG
51  FLPAGQMLNL GALLFILPYF LFSSLSGQLG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLLACLF CMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTFAV ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLFMPSV
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTALIGISWF WFGVAVYTTQ
251 LPTFTQIHLG GNDNVFNML ALFSIGIAAG SVLCAKFSRE RLRLAWVTVG

```

532

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAAVL SAVLLFLFDS
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP*

m232/a232 95.9% identity in 290 aa overlap

m232.pep					10	20	30
					MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLCMGAQSTLFGPLKYAILPDYLD	DDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP					
	120	130	140	150	160	170	
m232.pep		40	50	60	70	80	90
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
a232		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
	180	190	200	210	220	230	
m232.pep		100	110	120	130	140	150
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSXERLMLAW					
a232		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSRERLRLAW					
	240	250	260	270	280	290	
m232.pep		160	170	180	190	200	210
		VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMVMTLIGFFGGFFSVPL					
a232		VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMVMTLIGFFGGFFSVPL					
	300	310	320	330	340	350	
m232.pep		220	230	240	250	260	
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
a232		YTWLQTASSETFRARAVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
	360	370	380	390	400	410	
m232.pep	270	280	289				
	VFLIKRERRFLGAAAIRKKPX						
a232	VFLIKRERRFLGAAAIRKKPX						
	420	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq
 .1 atgaaacgca aaaatatcgc gctgattccc gccgccggca tcgggggtgcg
 51 tttcgggtgcg gacaaaacca agcaatatgt cgaaatcgga agcaaaaccg
 101 ttttagaaca tgtacttggg atttttgaac ggcattgaggc cgtcgatttg
 151 accgtcgttg tcgtctcgcc cgaagacacg tttgccgata aggttcagac
 201 ggcatttcca cagggttcggg tgtggaaaaa cggtaggacag acccgcgccg
 251 aaactgtccg caacgggtgtg gcaaaactgt tggaaaccgg tttggcggcg
 301 gaaaccgaca atattctggt acacgatgcc gcccgctgct gcctgccgtc
 351 tgaagctctg gcgcggttga tagaacaggc gggcaacgcc gccgaaggcg
 401 ggattttggc agttcccgtt gccgatacgc tcaagcgcg agaaagcggg
 451 caaatcagtg caactgtcga ccgttcgggg ctttggcagg cgcaaacgcc
 501 gcagcttttt caagcgggtt tgctgcaccg cgcattgggt gcggaaaact
 551 tgggcggcat taccgatgaa gcgtccgccg tggaaaaact ggggtgtgct
 601 ccgctactga tacaggcgca cgcgcgcaat ttgaaactga cgcagccgca
 651 ggacgcatac atcgtcaggc tgctgctcaa tgccgtctga

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep
 1 MKRKNIALIP AAGIGVRFGA DKPKQYVEIG SKTVLEHVLG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
 101 ETDNILVHDA ARCCLPSEAL ARLIEQAGNA AEGGILAVPV ADTLKRAESG

533

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR
 201 PLLIQGDARN LKLTQPDAY IVRLLLLNAV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC
 201 GGCATTTCGA CAGGTTCCGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG
 401 GGATTTTGGC AATTCCCAT TCCGATACGC TCAAGTGCGC GGACGGTGGG
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)
 1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFF QVRVWNGGQ TRAETVRNGV AKLLETGLAA
 101 ETDNILVHDA ARCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
	: : : : :					
g233	MKRKNIALIP AAGIGVRFADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m233.pep	FADKVQTAFFQVRVWNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
	: : : : :					
g233	FADKVQTAFFQVRVWNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
	70	80	90	100	110	120
	130	140	150			
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
	: : : :					
g233	ARLIEQAGNA AEGGILAVPVADTLKRAESGQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC
 201 GGCATTTCGA CAGGTTCCGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAAGTGTCCG CAACGGTGTG GCAAAATTGT TGGAAACCGG TTTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG
 401 GGATTTTGGC AATTCCCGTT TCCGATACGC TCAAGTGCGC GGACGGTGGG
 451 AACATTAGTG CAACCGTCGA GCGGACGAGC CTTTGGCAGG CGCAACGCC
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTGGCT GCGGAAACT
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCGC
 601 CCTTTGCTGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA

534

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDVAV*
```

m233/a233 99.3% identity in 152 aa overlap

```

10      20      30      40      50      60
m233.pep  MKRKNIALIPAAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
|||||
a233      MKRKNIALIPAAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
10      20      30      40      50      60

70      80      90      100     110     120
m233.pep  FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
|||||
a233      FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
70      80      90      100     110     120

130     140     150
m233.pep  TRLIEQAGNAAEGGILAIPIADTLKCADGGNI
|||||
a233      TRLIEQAGNAAEGGILAIPIADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA
130     140     150     160     170     180

a233      AENLDGITDEASAVEKLGIRPLLQGDARNLKLTPQDAYIVRLLLDVAVX
190     200     210     220     230
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg tttccgccgc catcgctttt gccgccgctg ccgtttcact
51  gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtgc
101 cctcctgcaa tacgcaatat cacggtgttc gcaccccgat ttccgtcgga
151 acattcgaca accgctccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaatccg gcatttccgg caaagcgag aacctgaaag gcgcagatta
351 tgctggtacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctatct
501 cacacagggc gcggggcgaat acgcactttc caaccgcaa atcatcggtt
551 tcggcggcac ttccggctac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaaccg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51  TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRFNV LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSNRE IIGFGTSGY DATLNGKVL D
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGGCG AATACGCACT TTCCAACCGT GAAATCATCG GTTTCGGCGG
51  CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTTA GACTTGGCAA
101 TCCGCGAAGC .gTCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng) from *N. gonorrhoeae*:

```

                                10      20      30
m234.pep                      GAGEYALSNREIIIGFGGTSGYDATLNGKVL
                                |||||
g234      LGRGKSQIAYAKVALNIVNVNTSEIVYSTQGAGEYALSNREIIIGFGGTSGYDATLNGKVL
      140      150      160      170      180      190

                                40      50
m234.pep      DLAIREAVNSLVQAVDNGAWQPNRX
              |||||:::||
g234      DLAIREAVDNLVQAVDNGAWQSNRX
      200      210      220

```

a234.seq (partial)

1	AACCGCACCT	ATTTGAACGC	ATTA AACACAG	GAATCCGGCA	TTTCCGGCAA
51	AGCGCATAAC	CTGAAAGGCG	CAAATTATGT	CGNNACCGGC	GATGTAACCG
101	AATTCGGACG	CANAGATGTC	GGCGATCATC	AGCTCTTCGG	CATTTTGGGT
151	CGCGGCAAAT	CGCAAATCGC	CTATGCAAAA	GTGGCTCTGA	ATATCGTCAA
201	CGTCAATACT	TCCGAAATCG	TCTATTCCGC	ACAGGGCGCG	GGCGAATACG
251	CAC TTTCCAA	CCGTGAAATC	ATCGGTTTCG	GCGGCACTTC	CGGCTACGAT
301	GCGACTTTGA	ACGGCAAAGT	TTTAGACTTG	GCAATCCGCG	AAGCCGTCAA
351	CAGCCTGGTT	CAGGCTGTTG	ACAACGGCGC	ATGGCAACCC	AACCGTTAA

a234.pep (partial)

1	NR TYLNALKQ	ESGISGKAHN	LKGANYVXTG	DVTEFGRXDV	GDHQLFGILG
51	RGKSQIAYAK	VALNIVNVNT	SEIVYSAQGA	GEYALSNREI	IGFGGTSGYD
101	ATLNGKVLDL	AIREAVNSLV	QAVDNGAWQP	NR*	

```

30                                     10                                     20
m234.pep
GAGEYALSNREIIGFGGTSGYDATLNGKVL

|||||
a234
LGRGKSQIAYAKVALNIVNVNTSEIVYSAQGAGEYALSNREIIGFGGTSGYDATLNGKVL
      50          60          70          80          90          100

          40          50
m234.pep    DLAIREAVNSLVQAVDNGAWQPNRX
            |||||
a234        DLAIREAVNSLVQAVDNGAWQPNRX
          110        120        130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:
q235.seq

g235 . pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235 . pep

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/g235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVOKAPDFDYTSFKESKPASILVVPPLNESPVDNGTWGVLAST					
	: : :					
g235	MKPLI LGLA AVLAL S AC QVR K APDL DY TS FK ES KP AS IL VV PP LN ES PD VN GT WGM LAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGY YVFPA AVVEET F KQN GLT NAADI HAVR PEKL HQIF GND A VL Y I TVTE YG TS					
	: :					
g235	AAP I SEAGY Y VF PA AV VE ET F K EN GL TNA ADI HA VR PE KL HQ IF GN DAV LY IT VT EYG TS					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
           130      140      150      160      170      180

           190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
           190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51 CCAAGTTCAA AAAGCGCCCG ATTCGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCTGC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51 NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVREKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
a235      MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
           10      20      30      40      50      60

           70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
a235      AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
           70      80      90      100     110     120

           130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
a235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           130     140     150     160     170     180

           190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq


```

1 ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51 CGGTTTCATA ACCTGCAACC GCGCCACAT CGCGGGTGTA ATGCCAGCAG
101 CGTTTCGATT TTTCGCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTCCGGCGC GGTAATTTCC
251 GCTTCCGCCT GCAAaggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTTACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTT
351 TCACCAgTTC GGCTTCGGCT TTTCGTTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTCGCGC TCGCGCGGGC GCGGCTGTGC
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGGAAAG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTTCAG CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCACC ATATCCGCCT GTTGCACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAAcagG AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTTCGGTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgcccgt gTAATCGGTG GATGCCGCCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTTCG TATAGACTTC CTGCGGCGCG ACGACGTTGC
951 CGATGGATTT CGACATTTTG CGGCCGTTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TCGCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1 MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAFAFFAV AGFGGNGKFI
51 TDFHFCFRHQ QGKAQFFAQS IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGLRAAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNV FHGEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAG
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1 ..TTGCACGGAC GAACCGACGG TTTTGTCCGC GCGCAAAGGC TCGATGGCGG
51 CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATTT TTTCACCACT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCKTCTTCGC CGCCGCCGwT GayGTCCAC GCTTCTTCGC
201 CGGTGAAGCA CAAAATCGGT GCAATCAAGA GAACCAAAC GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTCA GGATGTCGAG GTAGAACGCA CCAAGTCTT
351 CCGAGCAGAA AGAAACaTG TCTTTTACGG CAAAGTGGAa kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG AACTCTTGC AGCTGACGTG CCAATACCAC
451 GGCGTAGCGG TCGATTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTG AGGATTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCGC CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCTTC GCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GGCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1 ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVPMSME
51 EDAVXFAAAX DVPRFFAGEA QNRCNQENQT ACDVIQSLC AAACMAVCFG
101 GVEAVFQDVE VERTQVFRAE RNXFVYGKVE XITRIVIAQ TLLQLTCQYH
151 GVAVDFFHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQ
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236

539

m236 . pep				10	20	30
				LHGRTDGFVGAQRLDGGGYRFAGFADCRPF		
g236	FRHQQGKAQFFAQSIQIAGHFFRRGNFGFRLQGR	TDSFVGAQRLDSGGYCFARFADCRPF				
	60	70	80	90	100	110
m236 . pep		40	50	60	70	80
	FHQFGFGFFVDGRELVP	SMEEDAVXFAAAXD	VPRFFAGEAQNR	CNQENQTACD	VIQGS	LC
g236	FHQFGFGFFVDGRELVP	SMEEDAVFFAAADD	VPRFFAGEAQNR	CNQENQAARD	VVQGLR	
	120	130	140	150	160	170
m236 . pep		100	110	120	130	140
	AAACMAVCFGGVEAVFQD	VEVERTQVFRAERN	XVFGKVEXITR	IVIACQTL	LQLTCQYH	
g236	AAAGAAVFGGGVEAVFQD	VEVERAQVFRAERN	NVHFGEVEGI	ARIVTACQ	TLLQPPRQYQ	
	180	190	200	210	220	230
m236 . pep		160	170	180	190	200
	GVAVDFHHIRLLHGIFN	RIVKVAQVGKQKAQ	GIADTAVAFGYA	FEDFFGNRQFA	AVIGRCR	
g236	GVAVDFHHIRLLHGIFN	RIVKVAQIGKQEAQ	GIADAAVAFGNA	FEDFFGNRQFA	AVIGGCR	
	240	250	260	270	280	290
m236 . pep		220	230	240	250	259
	PQAQDVCAEFVINLLRC	NDVADGFRHFFAFA	VDNETMQQLFIR	RATHX		
g236	PQAQDVRAEFVIDFLR	DDVADGFRHFAA	VLNVHETVGQQL	FIRCASHG		
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

```

a236 . seq
1   ATGGCGCGTT  TCGCCTTCTC  CGCCGACATT  CTCTGCACAG  CGTTTGCAGA
51  CGGTTTCATG  GCCTGCAACC  GCGCCACAT  CGCGGGTGTA  GTGCCAGCAG
101 CGTTCGCATT  TTTCACCATC  ACTGGCTTTA  GCGGCAACGG  CAAGTTCGCT
151 GCCTACTTTC  ACTTCTGCTT  TAGACACCAG  CAAAGCAAAG  CGCAATTCTT
201 CGCCCAAAGC  ATTCAGATAG  CCGGCCATTT  CTTCCGGCGC  GGTAATTTCTG
251 GCTTCGGCTT  GCAAGGACGA  ACCGACGGTT  TTGTCGGCGC  GCAAAGGCTC
301 GATGGCGGCG  GTTACCGCTT  CGCGGGCTTC  GCGGATTGCC  GTCCATTTTT
351 TCACCAGTTC  GGCTTCGGCT  TTTTCGTTGA  TGGTCGGGAA  CTCGTGCCAA
401 GTATGGA AAA  GCACGCTGTC  TTCTGCGCCG  CCGCCGATGA  TGTCCACGCG
451 TTCTTCGCCG  GTGAAGCACA  AAATCGGTGC  AATCAAGAGA  ACCAGGCTGC
501 GCGTGATGTG  GTACAGGGCG  GTTTGCGCGC  TGCGGCGGGC  GCGGCTGTGC
551 GCTTTGGTGG  TATAGAGGCG  GTCTTTCAGG  ATATCGAGGT  AGAACGCGCC
601 CAAGTCTTCC  GAGCAGAAAG  AAACCATTTT  TTTCACGGCA  AAGTGGGAAG
651 CATAACGCGG  ATAAAAATCA  CCGGCAACGC  GTTCTTGCGC  CCGCCTTGCC
701 AACACCAAGG  CATAGCGGTC  GATTTCCACC  ATATCCGCCT  GTTGCACGGC
751 ATCTTCAATA  GGATTGAAGT  CGCTCAAGTT  GGCAAACAAA  AAGCTCAAGG
801 TATTGCGGAT  ACGGCGGTAG  CTTTCGGTTA  CGCGCTTGAG  GATTTCTTTG
851 GAAATCGCCA  ATTCGCCGCT  GTAATCGGTG  GATGCCGCCC  ACAGGCGCAG
901 GATGTCGCGC  CCGAACTCGT  TATACACTTC  TTGCGGCGCG  ACGACGTTGC
951 CGATGGATTT  CGACATTTTG  CGCCCGTTTT  GATCCACCAC  GAAACCATGG
1001 GTCAGCAGCT  GTTTGTACGG  CGCGCGACCC  ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

```

a236 . pep
1   MARFAFSADI  LCTAFADGFM  ACNRAHIAGV  VPAAFAFFTI  TGFSNGKFA
51  AYFHF CFRHQ  QSKAQFFAQ  S  IQIAGHFFRR  GNFGFGLQGR  TDGFVGAQRL
101 DGGGYRFAGF  ADCRPFFHQ  F  GFGFFVDGRE  LVPSMEKHAV  FCAAADDVPR
151 FFAGEAQNRC  NQENQAARDV  VQGGRLAAAG  AAVGFGGIEA  VFQDIEVERA
201 QVFRAERNHF  FHGKVEGIR  I  KITGNAFLQ  PPCQHQGI  AVDFHHIRLLHG
251 IFNRIEVAQV  GKQKAQGIAD  TAVAFGYALE  DFFGNRQFAA  VIGGCRPQAA
301 DVRAELVIHF  LRRDDVADGF  RHFAPVLIHH  ETMQQLFVR  RATH*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

1	atgcggggaca	aggttggcgg	taatatcgca	ctccccgcc	cacgaatat
51	cgattctaac	atcggcaagc	tgcggaaaaa	ctttaagcat	atcttggcgg
101	acaagctcgg	tcatacgcg	aggattgtcg	ataaattcgt	tatccttacc
151	gccgaaaagc	agcctgccgt	ccgcgctgag	gcggtataaa	tccaaaatat
201	ggcgcttgtc	gcatactgcc	atatgttgtc	ggataagccc	ttttgtgcgc
251	gcgcccaagc	gttcggtggc	aataataaag	gtgctgacgg	caatcgctt
301	gcgttcctaaa	ggccggaata	tcgggttcaa	accgacataa	gtattgacgg
351	catagaccac	atttttacac	tcgacgctgc	cttcggggcgt	gtaaaccagc
401	caaccgtttt	gatacggttc	gatgcgcgtc	atcggggatt	gctcgaaaa
451	ctgcgcgcgc	gcttcggcac	cggcgcgtgg	aacaccaac	tgtaatttga
501	cgcgatgaag	atccccggac	aagggatcga	actgtgcgcc	ttgttacata
551	tcgctgtcaa	gctgctgttt	caactcggct	ttatcccaaa	gttgataatg
601	actcgaccgc	taatgccgtt	gggcgtgttc	atgccactgc	tgcaactctt
651	ccaatgctg	cggacggacg	gcaaccgtgg	cataaccgcg	ctgccaatcg
701	caatcgatgg	catgtttgcg	gacgcgttgc	ttccaccagt	cgaccgcctg
751	caaagactgt	tgccaaaaac	attgcgcctg	ctccaaagcg	acctgttttt
801	caatttcccc	cataccgcag	cgctagtcgc	tgataacctg	cccgccactc
851	ctgcgcggacg	gcgcgaagcc	gatacgtgcg	gcttccaaaa	cgacggcttc
901	atgtccgtgt	tccgcacagc	gcaatgcggt	acacaaaccg	ctcaaacgcg
951	cgccgataat	gcaggtttcg	gcttttcagc	ggcattggag	tttcggataa
1001	acagtatcgg	gattaaccga	actaaaaata	taagaaggca	gatatctctg
1051	aaaatcaggg	cgaatcattg	tgtttgcctt	atcgggtata	ttttcggacg
1101	gaatgataca	gcagtgcggg	ccatatcgtc	caaacagaaa	atcggtttga

This corresponds to the amino acid sequence <SEQ ID 882; ORF 237.ng>:

1 MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51 AEKOPAVRAE AVIIQNMAVV AYCHIVADKP FCARAQFGG NNGKADGNRL

541

```

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN
151 LRAGFGSGAG NTQRVIERMK MPQGIELCA LVHIAVKLLF QLGFIPLIM
201 TRTVMLGVF MPLLQLFPLM RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF
301 MSVFRQRCQG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRRIQIFL
351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

```

m237.seq
1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TCGGAAAAA CTTAAGCAT ATCTGGCGG
101 ACAAGCTCGG TCATaCGTC AGGATTGTCG ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGTAATAA TCCAAAATAT
201 GGCGGTTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTGCGCGC
251 GCCCCAAGG GTTCGGTCGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGTTCCAAA GGCCGGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG
351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTCGGGCGT GTAAACCAGC
401 CAACCGTTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAT
451 CTGCGCACC GCTTCGGCAG CGGCACGAGC GATGCCCCAA GTGTAAGTGA
501 GCGGATGCAG GTGTCCGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG
601 ACTCGCACC TAATGCCGTT GGGCGTGTTT ATGCCACTGC TGCAACTCTT
651 CCCAATGCTG CGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA
701 CAATCGACGG CATGTTTGCG GACGCGTTCG TCCACCAGTT CGACCGCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT
801 CAATTTCCCC CATACCGCAG nCGTAATCGC TGATAACCTG CCCGCCACTC
851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCCAATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTCGCTTT ATCAGGTGTA TTTTCGGACG
1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAwACAGAAA ATCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

```

m237.pep
1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGHTL RIVDKLVILT
51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNKGADSNRL
101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN
151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFIPLIM
201 TRTVMLGVF MPLLQLFPLM RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRRAET DTRGFQHNRF
301 MSLLRQGQCS AQTTQSAADD TGIGFQTALK FRINSMRINR TEIIRRIQIFL
351 KIRANHCVCF IRCIFGRNDT GCRAISSXQK IG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

```

m237/g237
10 20 30 40 50 60
m237.pep MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE
|||||:|||||:|||||:|||||:|||||:|||||
g237 MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGHTRIVDKFVILTAEKQPAVRAE
10 20 30 40 50 60

70 80 90 100 110 120
m237.pep AVIIQNMAVVAYCHIVTDKPF CARPQGFGRNNKGADSNRLAFQRPEYRVQTCISIDSIDH
|||||:|||||:|||||:|||||:|||||:|||||
g237 AVIIQNMAVVAYCHIVADKPF CARAQGFGRNNKGADGNRLAFQRPEYRVQTDISIDGIDH
70 80 90 100 110 120

130 140 150 160 170 180
m237.pep IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP

```

542

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      ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 885>:

```

a237.seq
1   ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
51  CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTTAAGCAT ATCTTGGCGG
101 ACAAGCTCGG TCATACGCGC GGGATTGTCG ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT
201 GACGGTTGTC GCATACTGCC ATATTGTTGC GGATAAGCCC TTTTGCACGC
251 GCGCCCAAGG GTTCTGTGGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGCTCCAAA GGCTTGAATA TCGGATTCAA ACCGGCATAA GTATTGACGG
351 CGTACACCAG ATTTTTCATC TCGACGCTGC CTTCCGGGGT GTAAACCAGC
401 CAACCGTTTT GATAAGGTTT AATGCGTATC ATGGGAGAAT GCTCAAAAAT
451 CTTCGTACCA GCTTCGGCAG CGGCGCGGGC GATGCCCAAC GTGTAATTGA
501 GCGGATGGAG ATGCCCGGAC AAGGGATCGA ACTGTGCGCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGCTT CAGTTCAGTG TTATCCCAGA GTTGATAATG
601 AGTTGCACCG TAATATTTTT GGGCGTGCTC ATGCCATTGT TGCAATTCTT
651 CCCAATGCTG CGAACGGATG GCAACCGTGG CATAACCGCG CTGCCAATCG
701 CAATCAATGG CATGTTTGCG GACGCGTTCG TCCACCAGTT CGACCGCCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCTTG CTCCAAACCG ACCTGTTTTT
801 CAATTTCTCT CATACCGCAG GCGTAATCGC TGATAACCTG CCCGCCACTC
851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CTCAATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTCCGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCGGGTATA TTTTCCGACG
1101 GAATGATACA GGCTGTCGAG CCATATCGTC CAAACAGAAA ATCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 886; ORF 237.a>:

```

a237.pep
1   MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGHTR GIVDKLVILT
51  AEKQSAVRAE AVIIQNMTVV AYCHIVADKP FCTRAQGFCG NNKGADSNRL
101 ALQRLEYRIQ TGISIDGVHQ IFAFDAAFGG VNQPTVLIRE NAYHGRMLKN
151 LRTSFGSGAG DAQRVIERME MPQGQIELCA LVHIAVKLLL QFSVPIELIM
201 SCTVIFLGVL MPLLQFFPML RTDGNRGITA LPPIAINGMFA DAFVHQFDRL
251 QRLPKPLRL LQTDLFFNFI HTAGVIADNL PATPSRRAET DTRGFQHNRF
301 MSLLRQGQCS AQTTQSAADD TGIGFQTALK FRINSMRINR TEIIRRQIFL
351 KIRANHCVCF IGYIFGRNDT GCRAISSKQK IG*

```

m237/a237 85.6% identity in 382 aa overlap

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE					
a237	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTRGIVDKLVILTAEKQSAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMVAVYCHIVTDKPFCAQPGFGRNNKGADSNRLAFQRPYRVQTCISIDSIDH					
a237	AVIIQNMVAVYCHIVADKPFCTRAQGFQGNNGADSNRLALQRLYRIQTGISIDGVHQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDAHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					
a237	IFAFDAAFGRVNQPTVLIHFAYHGRMLKLNLRTSFGSGAGDAQRVIERMEMPGQGIELCA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m237.pep	LVHIAVKLLFQLGFIPKLIMTRTMPLGVFMPLQLFPMRLTDGNRGITALPITIDGMFA					
a237	LVHIAVKLLQFSVIPELIMSCTVIFLGVLMPQLLQFFPMRLTDGNRGITALPIAINGMFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m237.pep	DAFVHQFDRLQRLLPKPLRLLQADLFFNFPHPTAXVIADNLPATPSRAETDTRGFQHNRF					
a237	DAFVHQFDRLQRLLPKPLRLLQTDLFFNFLHTAGVIADNLPATPSRAETDTRGFQHNRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m237.pep	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVC					
a237	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVC					
	310	320	330	340	350	360
	370	380				
m237.pep	IRCI FGRNDTGCRAISSXQKIGX					
a237	IGYIFGRNDTGCRAISSXQKIGX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttggcag cggcaatatc
51  gatgctgcat atccccatta gtcatgcgaa cggtttggat gcccgtttgc
101 gcatgatgat gcaggcaaaa cactacgaac cgggtggcaa ataccatctg
151 tttggtaatg ctgcgcgagc tgtaaaaaat cgggttttgc ccgtccaaac
201 atttgatgca actgcggtcg gcccatact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtccgtt cgataatcat gattcaaaaa gcacttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttaccaa cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacgggcc tcaaggcggc
451 ggttatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tgttccgcaa gccctttttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttccgg ttttctcagc
601 cgtgcgggat aagcaggaaa actgatatgg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgtatgg atgatattcg cggcatcgtc caaggtgcgg
701 ttaatccttt tttaacgggt tttcaagggt tagggattgg ggcaattaca
751 gacagtgcgg taagcccggc cacagataga gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcacia cttgccgccg

```

```

851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgccttgcc gtagcagagg ccgcaggtac ggtttggcgc ggtaaaaaag
1001 tagaacttaa cccgaccaa tgggattggg ttaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacaatt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

```

g238.pep
1 MNLPIQKFMM LLAAAIISMLH IPISHANGLD ARLRDDMQAK HYEPGGKYHL
51 FGNARGSVKN RVCVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGTs TKTKINTVPQ APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPDKNWRN NRMDDIRGIV QGAVNPFLTG FQGVGIGAIT
251 DSAVSPVTDt AAQQTQLQGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGINS
301 ARQWADAHPN ITATAQTALA VAEAAGTVWR GKKVELNPTK WDWVKNtGYK
351 KPAARHMQTV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYt IDSNEKRNKI KNHGLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

```

m238.seq
1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGGTGTTATC GGTATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCACCTCTGA
351 TTCAGCGGC GGTGTAGACG GCGGTTTAC TGTTTACCAA CTTCATCGAA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCAGGAG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACTTCA ACAAAAAACA AGACTAATAT TGTCCTCAA GCCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCCTATGG ATGATGTTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTTAGGAA AATTAAAGTCC GGAAGCACAA CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCAG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCAAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TTAATAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAAATCTT TACCAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTCACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAATTTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTTACAAC AACAAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

```

m238.pep
1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPGGKYHL
51 FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

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```

151 DYPPPPGGARD IYSYVVKGTS TKTKTNIVPQ APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDVRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQQTLOGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGIN
301 AKQWADAHPN ITATAQTALS AAEAAGTVWR GKKVELNPTK WDWVKNTGYK
351 KPAARHMOTL DGEMAGGNKP IKSLPNSAAE KRKQNFEEKFN SNWSSASFDS
401 VHKTLPNAP GILSPDKVKT RYTSLDGKIT IIKDNENNYF RIHDNSRKQY
451 LDSNGNAVKT GNLOGKQAKD YLQQQTHIRN LDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 238 shows 86.0% identity over a 401 aa overlap with a predicted ORF (ORF 238.ng) from *N. gonorrhoeae*:

m238/g238

	10	20	30	40	50	60
m238.pep	MNLPIQKFMMLFAAAI SLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAAI SMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m238.pep	RVYAVQTFDATAVSPVLPITHERTGFEVIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
g238	RVCAVQTFDATAVGPILPITHERTGFEVIGYETHFSGHGHEVHSPFDNHSDSKSTSDFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGSYPPPPGGARDIYSYVVKGTSTKTKTNIVPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGYPEPQGARDIYSYHIKGTSTKTKINTVPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m238.pep	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDDVRGIVQGAVNPFLMG					
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPDKNWRANRMDDIRGIVQGAVNPFLTG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m238.pep	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQ LAAASLLQDS AFAVKDGIN					
g238	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQ LAAASLLQDS AFAVKDGIN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m238.pep	AKQWADAHPNITATAQTALSAAEAAGTVWRGKKVELNPTKWDVVKNTGYKKPAARHMOTL					
g238	ARQWADAHPNITATAQTALAVAEAAGTVWRGKKVELNPTKWDVVKNTGYKKPAARHMOTV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m238.pep	DGEMAGGNKPIKSLPNSAAEKRKQNFEEKFNSNWSSASFDSVHKTLPNAPGILSPDKVKT					
g238	DGEMAGGNRPPKSI-TSE GKANAATYPKLVNQLNEQNLNIAAQDPRLSLAIHEGKKNFP					
	370	380	390	400	410	
	430	440	450	460	470	480
m238.pep	RYTSLDGKITIIKDNENNYFRIHDNSRKQYLD SNGNAVKTGNLOGKQAKDYLQQQTHIRN					
g238	IGTATYEEADRLGKIWVGEGARQTSGGWLSRDGTRQYRPPTEKKSQFATTGIQANFETY					
	420	430	440	450	460	470

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

```
a238.seq (partial)
1   ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51  GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCG GCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTTGA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACTTCTGA
351 TTTCAGCGGC GGCCTAGACG GTGGTTTTAC CGTTTACCAA CTTCATCGGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGAGG AGCAAGGAT ATATACAGCT ACTATGTCAA
501 AGGAACCTCA ACAAAAACAA AGAGTAATAT TGTTCCTCGA GCCCATTTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATATTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGCGG TAAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCAAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAA TGGGATTGGG TAAAAAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTTG GATGGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA
```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

```
a238.pep (partial)
1   MNLPIQKFMM LFAAAISSLQ IPISHANGLD ARLRDDMQAK HYEPGGKYHL
51  FGNARGSVKN RYAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQQTLOGIN HLGNLSPQEQ LAAATLQDS AFAVKDGINS
301 ARQWADAHPN ITATAQTALA VAEAATTVWG GKKVELNPTK WDWVKNVTGYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ
```

m238/a238 91.9% identity in 385 aa overlap

	10	20	30	40	50	60
m238.pep	MNLPIQKFMM	LFAAAISSLQ	IPISHANGLD	ARLRDDMQAK	HYEPGGKYHL	FGNARGSVKK
a238	MNLPIQKFMM	LFAAAISSLQ	IPISHANGLD	ARLRDDMQAK	HYEPGGKYHL	FGNARGSVKN
	70	80	90	100	110	120
m238.pep	RYAVQTFDA	TAVSPVLPIT	HERTFEGVIG	YETHFSGHG	HEVHSPFDNH	DSKSTSDFSG
a238	RYAVQTFDA	TAVGPILPIT	HERTFEGVIG	YETHFSGHG	HEVHSPFDNH	DSKSTSDFSG
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYYVKGTS	TKTKSNIVPQ
a238	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYYVKGTS	TKTKSNIVPR
	190	200	210	220	230	240
m238.pep	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDVRGIV	QGAVNPFLMG
a238	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDIRGIV	QGAVNPFLMG
	250	260	270	280	290	300
m238.pep	FQGVGIGAIT	DSAVSPVTD	TAAQQTLOGI	NLDGKLSPEA	QLAAASLLQD	SAFAVKDGINS

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a238      |||||
          FQGVGIGAITDSAVSPVTDTAQQTLQGINHLGNLSPEAQLAAATALQDSFAFAVKDGIN
          250      260      270      280      290      300

m238.pep  310      320      330      340      350      360
          AKQWADAHPNITATAQTALSAEEAAGTVVRGKKVELNPTKWDVWKNTGYKKPAARHMQTL
a238      |||||
          ARQWADAHPNITATAQTALAVAEAAATTVWGGKKVELNPTKWDVWKNTGYKTPAVRTMHTL
          310      320      330      340      350      360

m238.pep  370      380      390      400      410      419
          DGEMAGGNKPIKSLP-NSAAEKRKQNFEEKFNSNWSSASFDSVHKTLTPNAPGILSPDKVK
          |||||:| ||: || |: |
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1  atgttccacc ataaagggtat tgcccgaaac cggcggatgg aggttttgtt
51  tttctgcegc cgcctgcatc gcttcgtgat tcgccaaacg cgcctgttgc
101 agcctcattt gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatacaca
201 cggaaaaagc ggaaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgcgc ttcagacggt tttctctggt attattccgg tatcggaccg
301 gcagtcgcgt ccgccacacg caaaactgcg ctctcgcgcc tcgggttggc
351 ggcaatttcc gcttcacccg gctttaatgc cctgccacg attttcaggg
401 gcggatcggg caaatccgct tctctgaccg ccgcccagct cggcaggggc
451 tcgtgttgcg aatatTTTTT gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaacgcgc gccctcttcc agacggcaca
551 tgacctgcgc caataccgcc cctacttctt caagctcgcg gttaataaag
601 atgcggattg cctggaagggt gcgctgcgca ggatcctgcc cccgctcgcg
651 agtacggacg ttttgtgcca cgatctgcgc cagcttgccg gttgtatcga
701 ttggactttc cgcccggttg gcgacaatgg cgcgcacaat ctggcggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1  MFHHKGIARN RRMEVLFFCR RPDRFVIRQT RLLQPHLRII LLQGDFLFFR
51  LVQSCEVEPV LVLLHHNGKS GNAHRKQQKE IRFVHCRSDV FLCYYSIGIP
101 AVRSATRFTA LLALGLAAIS ASPGFNALPT IFRGGSGKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARTIWR
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1  ATGCTCCACC ATAAAGGTmy kGCCCCGAAAC CGGCKGATGG AGGTTTTTGT
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCG GCCTCACCCG GCTTTAATGC CCTGCCACG ATTTTCAGGG
401 GCAGTCCGGG CAAATCCGCT TCCCTGACCG CCGCCACGCG CGGCAGGGG
451 GCGTGTGCG AATATTTTTT GACAAACTGC TTCACAATGC GATCTTCCAA
501 CGAATGGAAG GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTAATCTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTTGTGCCA CGATCTGCGC CAGCTTGCGG GTTGATATCGA
701 TTGGAATTTT CGCCCGTTGC GCAACAATGG CGCGCGCAAT CCGGCGGCTa
751 AACCGCTCTT CACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

548

m239.pep

```

1  MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
51  LIQSCEIEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
201 MRTAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIRRL
251 NRSSP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

m239/g239

	10	20	30	40	50	60
m239.pep	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRRIILQGDFLFFRLIQSCEIEPV					
	: : : :					
g239	MFHHKGIARNRRMEVLFFCRRPDRFVIRQTRLLQPHLRRIILQGDFLFFRLVQSCEVEPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTAALLALGLAAIS					
	: :					
g239	LVLLHHNGKSGNAHRKQOKEIRFVHCRSDVFLCYYSGIGPAVRSATRKTAALLALGLAAIS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	:					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMTCGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
g239	RRHMTCGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
	250					
m239.pep	ATMARAIRRLNRSSPX					
	:					
g239	ATMARTIWRRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

a239.seq

```

1  ATGCTCCACC ATAAAGGTAT TGCCCGAAAC CGGCGGATGG AGGTTTTGTT
51  TTTCTGCCGC CGCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTCG
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAGT TGAGCCTGTA CTGGTTTTGC TGCATACAAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTC AATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCTGCCCGCG ATTTTCAGGG
401 GCGGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCAGCG CGGCAGGGGC
451 GCGTGTTCG AATATTTTTT GACAACTGC TTCACAATGC GGTCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CCTACTTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGATTG CTTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTGTGCCA CGATCTGCGC CAGCTTGCGG GTTGTATCGA
701 TTGGACTTTC CGCCGTTGC GCAACAATGG CGCGCGCAAT CTGGCGGCTA
751 AACCGCTCTT CACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
  1 MLHHKGIARN RRMEVLFFCR RPDrfvvrQT RLLQPHLRII LLQGDFLFFR
 51 LIQSCEVEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTAL LALGLAAIS ASPGFNALPA IFRGSGSKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

	10	20	30	40	50	60
m239.pep	MLHHK	GXARNR	XMEVLFF	CRRPDR	fvvrQT	RLLQPHLR
a239	MLHHK	GIARNR	MEVLFF	CRRPDR	fvvrQT	RLLQPHLR
	70	80	90	100	110	120
m239.pep	LVLLH	HNGKSG	NAHRKQ	OKEIQF	VHCHSD	VFLCDCS
a239	LVLLH	HNGKSG	NAHRKQ	OKEIQF	VHCHSD	VFLCDCS
	130	140	150	160	170	180
m239.pep	ASPGF	NALPTI	FRGSSG	KSASLT	AAQRGR	GACCEY
a239	ASPGF	NALPAI	FRGSGS	KSASLT	AAQRGR	GACCEY
	190	200	210	220	230	240
m239.pep	RRHMT	CGNTAP	TSSSSR	LIKMRT	AWKVRV	AGSCPR
a239	RRHMT	CGNTAP	TSSSSR	LIKMRI	AWKVRV	AGSCPR
	250					
m239.pep	ATMAR	AIIRLN	NRSSPX			
a239	ATMAR	AIWRLN	NRSSPX			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
  1 atgatagaag tcatacat tttcttcg ggcgcc gaaacgcgca gacagtttgc
 51 ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
101 gggtaaacat gggatatcat gcgcacggga gacggtccga ttttataaag
151 ctgcgtattc agccgttcgt tcaaatcggg ttgcccgcga tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac caggttcgat catatcggtt
251 acggcacggg tgccgcgctg ttcgctgtct gcccgccggg gtctgttggg
301 atcgtaggcg ggcgtattgg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttcgg gcttttgctt gatggtattc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
501 ccacaatatt gccctgccgg tcccgcacaa caacttcgcg gccgtcttcg
551 ccatacaggc tgtcttcaag cgaaagtcc aaaccttcct gacctttgcc
601 gtcaatatcg gtaaatccga tgacgtgtgc aaacaggttg cccatcgggg
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
  1 MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
 51 LRIQPFVQIG FARIQCLRNH ERFDCRTRFD HIGYGTVAPL FAVCPAGSVG
101 IVGGRIGQGE DFPRAGIQNH HRSGFCLMVF DRLVQLFIGQ GLNPLIEGKD
151 DVFAVLRFCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFTQLTFA
```

201 VNIGKSDDVC KQVAHRVMAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

```
m240.seq
1  ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGCTGTCC CGGCCGGGCC TGTGTTGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 ArACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTaktGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCC ATCGGGTAAT
651 GCGGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 902; ORF 240>:

```
m240.pep
1  MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51  RIQPFVQIGF ARIQCLRNHK RFDCRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFXA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFTFLTFVAV
201 NIGKSDDVCK QVAHRVMAF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

```
m240/g240

      10      20      30      40      50      59
m240.pep  MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGI-AHGRRSDFIRLRIQPFVQIG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      MIEVIHFFGAETRRQFACADVGRFLHNAAH IQRGVNMGI IAHGRRSDFIRLRIQPFVQIG
          10      20      30      40      50      60

      60      70      80      90      100     110     119
m240.pep  FARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXH
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      FARIQCLRNHERFDCRTRFDHIGYGTVAPLFAVCPAGSVGIVGGRIGQGEDFPRAGIQNH
          70      80      90      100     110     120

      120     130     140     150     160     170     179
m240.pep  HRS GFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      HRS GFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRCFIARGVQAVHNIALPVPQNNFR
          130     140     150     160     170     180

      180     190     200     210     220
m240.pep  AVFAMQAVFKRKFTFLTFVAVNIGKSDDVCKQVAHRVMAFX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      AVFAIQAVFKRKFTFLTFVAVNIGKSDDVCKQVAHRVMAF
          190     200     210     220
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

```
a240.seq
1  ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
```

```

251 GCACGGTTGC GCGGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
  1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HRRSDFIRL
 51 RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFIA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHRRSDFIRLRIQPFVQIGF					
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHRRSDFIRLRIQPFVQIGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m240.pep	ARIQCLRNHKRFD CRTGFDH IGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXHH					
a240	ARIQCLRNHKRFD CRTGFDH IGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQNH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQNDFRA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQNDFRA					
	130	140	150	160	170	180
	190	200	210	220		
m240.pep	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
a240	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
  1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
 51 TTGTGCCGAC GTTGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCGGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
  1 MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

```

seq (paired)
1      . CCGCAATCAG TGGTGGTGAT GACCGTGC GG CCGGTGGACA TGACCGTGTG
51     CGATTTCCTC ATCGGATGCA TCGCGCACGC TTTCAACTGT AGCCTTAAAG
101    CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151    GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201    CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251    GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
301    GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351    CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
401    ATCGGTTCCT CGGTTTTGTC CAAAAGCTGA TTGTTGGCAT CATACATCTC
451    ATAATGCAGC GAAACCAACG AATTTTTCAC GATAGCCATA TTTGTCCTTT
501    CAGGAACAGC AGATTAATTA CAGGCGCATT CTA

```

```

1  ..RQSVVVMTVR AVDMTVCDFL IGCIAHAFNC SLKADFHACQ RMVAVHHRLA
51  VGNIGYTIDD NIAGFRIVGF KHHADFDfNR EHARIFDTDQ LRILLAERIV
101 GRQRHIDRIA GILTVQRLEH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

m241/g241

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

seq					
1	ATGCCAACAC	GTCCAAC TCG	CGCCGCAAAG	CATCCAACCC	CGCCAACCTG
51	GCTTCAGACG	GCATACTGCC	CTCGTCCGCC	ATATCGTCCG	CCGTCCGTGC
101	AAACGCATAC	ACCGCATGAA	CTCGGCTTCT	CAACCTGCGC	GGCAAAATCA
151	CGGAACCGAC	GGGAAAAATT	TTCGAATGCC	CAACCTGCAT	ACCTTCTCCA
201	TCCATCAAAAC	AAAAATGCCGT	CTGAAATGGA	ACAAACCTTT	TTCGACGGGC

553

```

251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCTCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```

a241.pep
1  MPTRPTRA AK HTPPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRREN FHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCD FL IGCIHTFN R SLKADFACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIV GF KHHADFDNR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRL FH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFR NS RLITGAF*

```

m241/a241 96.0% identity in 177 aa overlap

```

                                10      20      30
m241.pep                      RQSVVMTVR AVDMTVCD FLIGCIAH FNC
                                |||:|||||:|||||:|
a241      QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVMTVR TVDMTVCD FLIGCIAHTFN R
              70      80      90      100     110     120

              40      50      60      70      80      90
m241.pep    SLKADFACQ RMVAVHRLT VGNIGYTIDD NIAGFRIV GFKHHADFDNR EHARIFD TDQ
              |||:|||||:|||||:|||||:|||||:|
a241      SLKADFACQ RMVAVHRLT VGNIGYTIDD NIAGFRIV GFKHHADFDNR EHARIFD NTQ
              130     140     150     160     170     180

              100     110     120     130     140     150
m241.pep    LRILLAERIV GRKRHIDRIA GILTVQRL FHQRENAVVTAV QIRNRFFGFV QKLIVGIIHL
              |||:|||||:|||||:|||||:|||||:|
a241      LRILLAERIV GRKRHIDRIA GILTVQRL FHQRENAVVTAV QIRNRFFGFV QKLIVGIIHL
              190     200     210     220     230     240

              160     170
m241.pep    IMQRNHGIFH DSHICPFR NSRLITGAF X
              |||:|||||:|||||:|
a241      IMQRNHGILH DSHICPFR NSRLITGAF X
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>:

```

g241-1.seq
1  ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTC AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGTGTTT GCTGTCTGCC CGGCCGGGCC TGTTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCAAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCTCT TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTGCCCC ATCGGGTAAT
651 GGCCTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

g241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPPSC RQSVVVMTVR
101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

m241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCAGC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAACCCCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCGA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CGTGCAACG CCTCTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CCGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

m241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPPSC RQSVVVMTVR
101 AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVGF KHHADFDENR EHARIFDQDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFC
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSQTEQTLFRRHQIPPPSCRQSVVVMTVRAVDMTVCDLIGCIAHAFNC					
g241	QPTYLLHPSNKMPSQTEQTLFRRHQIPPPSCRQSVVVMTVRTVDMTVCDLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVVHRLAVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFDQDQ					
g241	SFKADFHACQRMVAVVHRLAVGNIGYTIDDNIAGFRIVRFKHTDLDFNRERARIFNTDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIAAGILTVQRLFHQRENAVVTAVQIRNRFFGFIQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

a241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

555

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CCGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CCGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1 MPTRPTRA AK HPTPTWLQT AYCPRPYP RP PSVQTHPHE PASSTCAAKS
51 ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPS RQSVVMTVR
101 TVDMTVCD FL IGCIATFNR SLKADFHACQ RMVAVHHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRA	ANPPTPPTWLQT	AYCPRPYP	RPPSVQTRTP	PREPASSTCAAKS	ANRRENSHNA
a241	MPTRPTRA	AKHPTPPTWLQT	AYCPRPYP	RPPSVQTHPHE	PASSTCAAKS	ANRRENFHNA
	10	20	30	40	50	60
	70	80	90	100	110	120
m241-1.pep	QPTYLLHPSN	KMPSETEQTL	FRRHQIPPS	RQSVVMTVR	AVDMTVCD	FLIGCIAHAFNC
a241	QPTYLLHPSN	KMPSEMEQTL	FRRHQIPPS	RQSVVMTVR	TVDMTVCD	FLIGCIAHTFNR
	70	80	90	100	110	120
	130	140	150	160	170	180
m241-1.pep	SLKADFHACQ	RMVAVHHRLAV	GNIGYTID	DNIA	GFRI	VGFKHHADFDENREHARIFD
a241	SLKADFHACQ	RMVAVHHRLT	VGNIGYTID	DNIA	GFRI	VGFKHHADFDENREHARIFNTDQ
	130	140	150	160	170	180
	190	200	210	220	230	240
m241-1.pep	LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV	QKLIVGIIHL
a241	LRILLAERIV	GRKRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV	QKLIVGIIHL
	190	200	210	220	230	240
	250	260				
m241-1.pep	IMQRNHGIFH	DSHICPFRNS	RLITGAF			
a241	IMQRNHGILH	DSHICPFRNS	RLITGAF			
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1 atgatcgggc aactgttgt tttgttcgtg atcgagcact tcaagcaacg
51 cgctggcggg atcgccccga aagtcgctgc ccaatttgtc gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccg cggatttcgc
201 tttcgctcgc cacgccgcc aaggccatac ggacataatt ccgccccgtt
251 gctttggcga tggattcgcc caaagagggt ttgccacgc ccggagggcc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttgagcgg
351 cgaggtattc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtcgggc tttggcgatg tctttgctga cgcgggattt
451 tttcttcac gccagtcgga gcagggtgtc gatgtagttg cgtacgacgg

```

501 tggattcggc agacatcggc ggcattattt tgagtttttt cagttcggac
551 aggcattttt ctccgccttc tttagtcata cccgcctttt tgatgcctgc
601 ctccaaggca tccagttcgc cgttttcgtc ttcttcgccc aatcttttgt
651 gtatcgcttt aatctgttcg ttcagataat attcgcggtg ggatttttcc
701 atttggcggt tgacgcgttc gcgatgcgt ttttcggcct gcataatgtc
751 gagttcggat tccagctttc ccagcaggaa ttccatccgt ttgccgattt
801 cgggaatctc caaaatctgt tggcgttgcg ccagtttcaa ctgcaaattc
851 gctgcgaccg tatcggttag

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

g242.pcp

1	MIGELVVLV	IEHFKQRAGG	IAPKVAAQFV	DFVEQEQRVS	YACFCHILQN
51	LAGHRADIGT	AVPADFAFVA	HAAQGHTDIF	PPRCFGDGFA	QRGFAHARRA
101	DQTQNRTEFL	VHTFLDGEVF	QNPFFDFFQA	VVVGIIQHQS	FGDVFADAGF
151	FLPRQSEQGV	DVVAYDGGFG	RHRRHHEFF	QFGQAFFFRF	FGHTRLFDAC
201	LQGIQFAVF	FFAQFFVYRF	NLFVQII FAL	GGFFLAFFDAS	AYAFFGLHNV
251	EFGFQLCQQE	FHPFADFGNL	QNLLALRQFQ	LQMRCDRIG*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

m242.seq

1	ATGATCGGCA	AAC TTGTTGT	TTTGTTCGGG	ATC GAGCACT	TCGAGCAACG
51	CGCTGGCGGG	ATCGCCTCGG	AAGTCGTTAC	CCAATTTGTC	GATTTTCGTCG
101	AGCAGGAACA	AGGGGTTTTT	CACGCCGGCT	TTTGCCATAT	TCTGCAAAAT
151	CTTACCGGGC	ATAGAGCCGA	TATAGGTGCG	CGCGTGTCCC	CTGATTTTCG
201	TTTCGTCGCG	CACGCGCCCC	AAAGCCATGC	GGACATATTT	CCGCCCCGTT
251	GCTTTGGCGA	TGGATTCGCC	CAAAGAGGTT	TTGCCCACGC	CCGAGGGGCC
301	GACCAGGCAC	AGAATCGGGC	CTTTGAGTTT	GTCCATACGT	TTTTGGACGG
351	CGAGGTATTC	CAAAATCCGT	TCTTTGACTT	TTTCAGGCC	GTAGTGGTCG
401	GCATCCAGCA	CCAGTCCGGC	TTTGCGCATG	TCTTTGCTGA	CGCGGGATTT
451	TTTCTTCCAC	GGCAGCTCGA	GCAAAGTGTC	GATGTAGTTG	CGTACGACGG
501	TGGATTCCGC	AGACATCGGT	GGCATCATTT	TGAGCTTTTT	CAGTTCGGAC
551	AGGCATTTTT	CTTCCGCTTC	TTTGCTCATA	CCCGCCTTTT	TGATATCTGC
601	TTCCAAGGCA	TCCAGTTCGC	CGTTTTTCGT	TTCTTCGCCC	AGTTCTTTGT
651	GTATCGCTTT	AATCTGTTTC	TTCAGATAAT	ATTGCGCGTG	GGATTTTTCC
701	ATTTGGCGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
751	GAGTTCCGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TTGCCGATTT
801	CGGGAATTT	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAAAATG
851	GCTGCGACCG	TATCGGTTAG			

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

m242.pcp

1	MIGKLVVLFG	IEHFEQRAGG	IASEVVQTFV	DFVEQEQGVF	HAGFCHILQN
51	LTGHRADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHARRA
101	DQAQNRAFEF	VHTFLDGEVF	QNPFFDFFQA	VVVGIQHQSG	FGDVFADAGF
151	FLPQRLQESV	DVVAYDGGFR	RHRWHHFEL	QFGQAFFFR	FGHTRLFDIC
201	FGRQIQFAVF	FFAQVDFVYR	NLFVQIIFAL	GFHFALFDAS	AYAFFGLHNV
251	EFGFQLCQVE	FHPFADFNGF	QNLLARQFQ	LQMRCDRIG*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

m242/g24290.3% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVVLFGLIEHFEQRAGGIASEVVTQFVDFVEQEQQGVFHAGFCHILQNLTGHRADIGA					
	: : : : : : :					
g242	MIGELVVLVFIHFKQRAGGIAPKVAAQFVDFVEQEQRVSYACFCHILQNLGHRADIGT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVAHAAQSHADI FPPRCFGDGF AQRGFAHARRADQAQNRAFEFVHTFLDGEVF					
	: : : : :					
g242	AVPADFAFVAHAAQGHDTDFPPRCFGDGF AQRGFAHARRADQTQNRTFELVHTFLDGEVF					
	70	80	90	100	110	120

a242.seq

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

a242.pcp

m242/a242 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVVLF	GLGIEHFEQ	RAGGIASEV	VTVFVDFVE	QEQGVFHA	GFCFCHILQ
a242	MIGELVVLL	GLGIKHFEQ	RAGGIAPVAX	QFVDFVEQ	EQVVFYAG	FCHILQNL
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFV	AHAQSHADI	FPPRCFGDG	FAGRGFAH	ARRADQAQ	NRAFEFVHT
a242	AVSPDFAFV	AHAQSHADI	FPPRCFGDG	FAGRGFAH	AWRADQAQ	NRAFEFVHT
	70	80	90	100	110	120
	130	140	150	160	170	180
m242.pep	QNPFFDFFQ	AVVVGIQH	QSGFGDV	FADAGFFL	PRQLEQSV	DVVAYDGG

558

```

a242      QNPFFDFQAVVVGIQHQSFGFQVDFADAGFFLPRQFEQGVVDVAYDGGFGRHRRHHFELF
           130      140      150      160      170      180
           190      200      210      220      230      240
m242 . pep QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNFVQIIIFALGFFHLAFDAS
           |||||
a242      QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNFVQIIIFALGFFHLAFDAS
           190      200      210      220      230      240
           250      260      270      280      290
m242 . pep AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNQNLALRQFQLQMRCDRIGX
           |||||
a242      AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNQNLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243 . seq
1  ATGGTaatcg tctGGTTGcC cgAGTTaccg CCGATGCCCG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAACA GGTCTTCCTC
201 TTCTTGCAAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCc tgCCGATGAG CTTTTGTGTT
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243 . pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51  IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243 . seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCCG CGACGATGGG
51  CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGyGGT TTTTCACCGA ATCCCACACG GGGGCGAAyA GGTCTTCCTC
201 TTCTTGCAAA CCCGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTGTGTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243 . pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

```

m243/g243
           10      20      30      40      50      60
m243 . pep MVIVWLPELPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||||
g243      MVIVWLPELPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
           10      20      30      40      50      60
           70      80      90      100     110
m243 . pep GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||||
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTTGTTC
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMPL SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSEFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMPLSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAAATIFSMPLSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX					
	: :					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPMSEFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgcctg aagcccgccg ggcgggttca gacggcattg ccgctttact
51  tcgacgcggt tatacgcgaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcagggctt cttccgtgcc accgtaacca tagccgggag
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgcctg atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga tttgcgtggc
301 atcaaagcgc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcacgcaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acatttccac ggcaaaactt tgtccggcga acttggtgct
451 atcggaattt tctgctggtt ggcggcgagg caggttttgc tcggttgcca
501 aagcgcgcag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacggtttc caccgcctcc acattttcaa
651 ccgcttcttc actggtttgc tgctgtgctt gttcgctcat atcgatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgcgcgc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LPCHRNHSRA
51  QHTVGQGITL LHHTNHGIGF LLTGHRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFORIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFLRFQF GNPRQLILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLLCLEFAH IVSLKTNWKS KSGYYPISKIR
251 TFSRNFQORQ EISHPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq

560

```

1  ATGCCGTCCTG AAGCCCGACA GGCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTG
101 CCCAGACGCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTCATCACA CCCACCACGG
201 TATTCGGCTC CTGTTCGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGGTTG ATTTCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACCTT TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GGCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTTCT GCACACCGTC
601 CGCATTTTCT ACTGTTTTCG CGGTTTCCAC CGCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGCTGC TGTGTCTGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAKCAGAGA ATTTCAAATT CATTTTCAAA
801 TCCCCTACCG AAAAAATAAT ATAGACGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 932; ORF 244>:

```

m244 . pep
1  MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLRHRNHSRA
51  QHAVGQRITL LHHTHHGIRL LFACHRLHRL MDIRIELIAR FRVDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAL LVFQLRFQLG NPRLQILISR LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFFT VLLLCLFAHI VSLKTNWKS SSYYPRKIRT
251 FSRNFXQXQR ISNSFSNPLP KKXYRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

	10	20	30	40	50	60
m244 . pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLPCHRNHSRAQHTVGGGITL					
	10	20	30	40	50	60
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244 . pep	IAALIQKRHFQIILDRQHFHKGKLLSGELVRIRNFLLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHKGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVQLRFQL					
	130	140	150	160	170	180
m244 . pep	IAALIQKRHFQIILDRQHFHKGKLLSGELVRIRNFLLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHKGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVQLRFQL					
	130	140	150	160	170	180
m244 . pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVRISYCLDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244 . pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVRISYCLDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244 . pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
g244	KSGYYPKIRTFSRNFKQRQEISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1   ATGCCGTCTG AAGCCCGACA GGCgggttca GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTTCATCAGC CCCACCACGG
201 TATTGGGTTC CTGTTCGCTT GCCACGCCTT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCCCTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGTCTGT GGCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTGC TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAAAACAAA TTGGAAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1   MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFE GKLLSGELVR
151 IRNFLLVAAA QVLVLCQSAQ LLVFQLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244.pep	IAALIQKRHFQIILDRQHFEHGKLLSGELVRIRNFLLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQKRHFQIILDRQHFEHGKLLSGELVRIRNFLLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	239
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
a244	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	240	250	260	270		
m244.pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1   atgccgcctg aagcccgcc gccgggttca gacggcattg ccgctttact
```


562

```

51  tcgatcggtt  tatacgcaaa  acgcgcttca  ggaaataaat  cagattattc
101 cccagacgcc  ttcaggcttc  cttccgtgcc  accgtaacca  tagccgggcg
151 caacacacgg  tcggacaggg  tataaccctt  cttcatcaca  ccaaccacgg
201 tattgggttc  ctgctcactg  gccaccgect  gcategcctg  atggatattc
251 ggatcgagct  ttcgcccgc  tttaggattg  atttccttga  ttgctgggc
301 atcaaacgcc  tttcgcaact  cattcaaagt  catctgcaca  cccattttca
351 gcgcacgaa  attaccgctc  tgatccaaaa  gcgccatttc  cagataatcc
401 ttgaccggca  acatttcac  ggcaaaactc  tgccggcgca  acttgtgcgt
451 atcggcaatt  tcctgctggt  ggcgcgcgcg  caggttttgc  tcgtttgcc
501 aagcgcgcag  ttgttcgtct  ttcaactgcg  cttccagctc  ggcaatccgc
551 gcctgcaaat  cctcataagc  cggctcggcg  gcagcctgtt  cctgtacacc
601 gtcgcgattt  cctactgtct  cgacgggttc  caccgctcc  acattttcaa
651 ccgcttcttc  actgttttgc  tgctgtgtct  gttcgctcat  atcgatcccc
701 tcaaaacaaa  ttggaaatca  aaatccgggt  attaccggag  caagataagg
751 acattttcaa  gaaacttcaa  gcaaaggcag  gaaatttcac  atccgcccgc
801 gaatacccta  ccgcaaaaac  catataaacg  gtaa

```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

g244-1.pep

```

1  MPPEARPAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LPCHRNHSRA
51  QHTVGGQGITL  LHHTNHGIGF  LLTGHLRL  MDIRIELIAR  FRIDFLDLRG
101 IKRLLQLIQS  HLHTHFQRIE  ITALIQKRHF  QIILDRQHFH  GKLLSGELVR
151 IGNFLLVAAA  QVLLVCQSAQ  LFFVQLRFQL  GNPRLQILIS  RLGGSLFLYT
201 VRISYCLDGF  HRLHIFNRFF  TVLLCLFAH  IVSLKTNWKS  KSGYPSKIR
251 TFSRNFQKQ  EISHPPPNTL  PQPKYKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

m244-1.seq

```

1  ATGCCGTCTG  AAGCCCGACA  GCGGGTTC  GACGGCATTG  CCGCTTACT
51  TCGATCGGTT  TATACGCAAA  ACGCGCTTCA  GGAAATAAAT  CAGATTATTC
101 CCCAGACGCC  TTCAGGCTTC  CTTCTGCGCC  ACCGTAACCA  TAGCCGGGCG
151 CAACACGCGG  TCGGACAGCG  TATAACCCTT  CTTTCATACA  CCCACCACGG
201 TATTCGGCTC  CTGTTCGCTT  GCCACGCCT  GCATCGCCTG  ATGGATATTC
251 GGATCGAGCT  TATCGCCCGC  TTTAGGGTTG  ATTCCTTGA  TTTGCGTAGC
301 ATCAAATGCT  TTCTGCAACT  CGTTCAAAGT  CATCTGCACG  CCCATTTTCA
351 GCGCATCGAA  ATTGCCGCTC  TGATCCAAAA  GCGCCATTTC  CAGATAATCC
401 TTGACCGGCA  GCATTTCAC  GGCAAACCTC  TGTCCGGCGA  ACTTGTGCGT
451 ATCCGCAATT  TyCTGCTGGT  GGCGCGGCG  CAGGTTTTGC  TCGTTTGCCA
501 AAGCGCGCTG  CTCGTCTTTC  AACTGCGTTT  CCAGCTCGGC  AATCCGCGCC
551 TGCAAAATCCT  CATAAGCCGG  CTCTGCGGCA  GCCTGTTCT  GCACACCGTC
601 CGCATTTCTT  ACTGTTTCGA  CGGTTTCCAC  CGCTCCACA  TTTTCAACCG
651 CTTCTTCACT  GTTTTGCTGC  TGTGCTGTT  CGCTCATATC  GTATCCCTTA
701 AAACAAATTG  GAAATCAAAA  TCCAGTTATT  ACCCGCGCAA  GATAAGGACA
751 TTTTCAAGAA  ACTTCAAKCA  AAKCAGAGA  ATTTCAAATT  CATTTTCAAA
801 TCCCTACCG  AAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pep

```

1  MPSEARQAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LLRHRNHSRA
51  QHAVGQRITL  LHHTHHGIRL  LFACHRLHRL  MDIRIELIAR  FRVDFDLRS
101 IKCFLQLVQS  HLHAHFQRIE  IAALIQKRHF  QIILDRQHFH  GKLLSGELVR
151 IRNLLVAAA  QVLLVCQSAL  LVFQLRFQLG  NPRLQILIS  LCGSLFLHTV
201 RISYCFDGFH  RLHIFNRFFT  VLLCLFAHI  VSLKTNWKS  SSYYPKIR
251 FSRNFXQQR  ISNSFSNPLP  KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLPCHRNHSRAQHTVGGQGITL					
	10	20	30	40	50	60
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
g244-1	LHHTNHGIGFLLTGHLRLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120



	130	140	150	160	170	180
m244-1.pep	IAALIQRHFQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAALLVFQLR	FQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAALLVFQLR	FQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAALLVFQLR	FQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAALLVFQLR	FQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAALLVFQLR	FQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAALLVFQLR
g244-1	ITALIQKRHFQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAQLFVFQLR	FQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAQLFVFQLR	FQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAQLFVFQLR	FQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAQLFVFQLR	FQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAQLFVFQLR	FQIILDRQHFHGKLLSGELVRIRNFFLLVAAQVLLVCQSAQLFVFQLR
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVIRISYCFDGFHRLHIFNRF	FTVLLCLFAHIVSLKTNWKS	FTVLLCLFAHIVSLKTNWKS	FTVLLCLFAHIVSLKTNWKS	FTVLLCLFAHIVSLKTNWKS	FTVLLCLFAHIVSLKTNWKS
g244-1	GNPRLQILISRLCGSLFLTYVIRISYCLDGFHRLHIFNRF	FTVLLCLFAHIVSLKTNWKS	FTVLLCLFAHIVSLKTNWKS	FTVLLCLFAHIVSLKTNWKS	FTVLLCLFAHIVSLKTNWKS	FTVLLCLFAHIVSLKTNWKS
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKX	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKX	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKX	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKX	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKX	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKX
g244-1	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPYKR	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPYKR	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPYKR	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPYKR	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPYKR	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPYKR
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1. seq

```
1 ATGCGCTCTG AAGCCCGACA GCGGGTTCA GACGGCATTG CCGCTTTACT
51 TCGATCGGGT TATAGCAAAA ACGCGTTCA GGAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCTT CTTATCATCG CCACACCGG
201 TATTGGGTTG CTTCTCGCTT GCCACGCC T GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCTTGA TTTGCGTAGC
301 ATCAAAATGT TTTGCAACT CGTTCAAAGT CATCTGCAGC CCGATTATTC
351 GCGCATGCAA ATTGCGCCTT TGATCAAAA GCGCCATTTC CAGATAATCA
401 TTGACCGGCA GCATTTCCAC GGCAAATTC TGTCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCTCTGCTGT GCGCGCGCGC CAGGTTTTC TCGTTTGCCA
501 AAGCGCTGCG CTGCTCTGTCT TTCAACTCTG CTTCCAGCTC GCGAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCGCGATTT CTTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTTG TGCTGTGTCT GCTTGCCTAT ATCGTATCCC
701 TTA AAACAAA TTGGAATCA AAATCCAGTT ATTACCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGCGAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

1	MPSEARQAGS	DGIAALLRSV	YTQNALQEIN	QIIPQTPSGF	LLCHRNHSRA
51	QHAVGQRITL	LHHAHHGIGF	LFACHRLHRL	MDIRIELIAR	FRIDFLDLSR
101	IKCFLQLVQS	HLHAHFQRIE	IAALQKRHF	QIILDRQHFP	GKLLSGELVR
151	IRNFLVAAA	<u>QVLLVCQSAQ</u>	LLVFQLRFQL	GNPRLQILIS	RLCGSLFLHT
201	VRISYCLDGF	HLRHIFNRF	<u>TVLLCLFAH</u>	<u>IVSLKTNWKS</u>	KSSYYPRKIR
251	FRSRNFKORG	RISNFSNPL	PKK*		

m244-1/a244-1 96.8% identity in 274 aa overlap

		10	20	30	40	50	60
m244-1.pep		MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTSPSGFLLRHRNHSRAQHAVGQRITL					
a244-1		MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTSPSGFLLCHRNHSRAQHAVGQRITL					
		10	20	30	40	50	60
		70	80	90	100	110	120
m244-1.pep		LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
		: :					
a244-1		LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
		70	80	90	100	110	120
		130	140	150	160	170	179
m244-1.pep		IAALIQRKHFQIILDRQHFHKGKLLSGELVRI RNFLVAAAQVLLVCQSA-LLVFQLRFQL					
a244-1		IAALIQRKHFQIILDRQHFHKGKLLSGELVRI RNFLVAAAQVLLVCQSAQLLVFQLRFQL					
		130	140	150	160	170	180
	180	190	200	210	220	230	239
m244-1.pep		GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLLLCLFAHIVSLKTNWKS					
a244-1		GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLLLCLFAHIVSLKTNWKS					
		190	200	210	220	230	240

```
g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgccct tcgttttcga
51  ccagacacag cgtgcccgtt tcggcaacgg cgaagtttac gccgctcaag
101 ccgacatcgg cagtgcctga aatatcgcgc agggctttgc gggcgaatcc
151 ggtcagttgg tccacgtcgt ctgtaagcgg tgtgcccagg ttttggctga
201 acagttcgtg gacctgtctt ttggttttat ggattgcggg catcacgtga
251 tgggtcgggt tttcgccctgc catttggacg ataaactcgc ccaagtcgct
301 ttccaccgcc ttaatgcctt ttgcttcaag ataatggttc agctcgattt
351 cttcgctgac catggatttg cctttgacca tcagcttgcc gtttttggct
401 gtgatgatgt cgtggataat ttggcaggct tcggcagggg tttccgccca
451 gtgtactttc acgcccaact tagtcagggt ttcttccaac tgctccagca
501 qcqcaggtaa
```

g246.pep

1	MYGRNGSTQA	AVAFVFDQTO	RARFGNGEVY	AAQADIGSAV	NIAQGFAGES
51	GQLVHVVCCKR	CAEVLVEQFA	DLFFGFMDCG	HHDMGRFFAC	HLLDKLAQVA
101	FHRLNAFCFK	IMVQLDDFFD	HGFAFDHQLA	VFGCDDVSLN	LAGFGRGRFP
151	VYFHAOLSOV	FFOLLQSG*			

```
m246.seq      (partial)
      1  ATGCACGGGC  GGTACGGTGG  TACTCAAGCG  ACCGTTgCTT  CGTTTTCCAC
     51  CAGACACAGC  GTACCTGTTT  CAGCAACGGC  AAAGTTTACG  CCACTCAAAC
    101  CGACATCGGC  AGTGCTGTAA  ATATCGCGCA  GTGCTTTACG  GGCGAAGCCG
    151  GTCAGTTGGT  CTACATCGTC  TGTCAGCGGC  GTACCGAGGT  TTTGGTGGAA
    201  CAGTTCGCTA  ACCTGTTCTT  TGGTTTTGTG  GATAGCAGGC  ATCACGATAT
    251  GGGTCGGTTT  TTCGCCTGCC  ATTTGGACGA  TGAACTCGCC  CAAGTCGCTT
    301  TCTACCGCTT  TAATGcYttt  TGCTTCAAGA  TAATGrTTCA  GCTCGATTTT
    351  CTCGCTGACC  ATCGATTTCG  CTTTGACCAT  CAGCTTGCCG  TTTTGTGGTG
    401  TGATGATGTC  GTGGATAATT  GTGCAGGCTT  CGGTTCGGGT  TTCTGCCCG...
```

```
m246.pep (partial)
  1  MHGRYGGTQA TVAFVFHQTO RTCFSNGKVV ATQTDIGSAV NIAQCFTGEA
 51  GQLVYIVCQR RTEVLVEQFA NLFFGFVDSR HHDMGRFFAC HLDDELAQVA
101  FYRENAFCFK IMXOLDFLAD HRFAEDHOLA VFGCDVVDN LAGEGRGFCR...
```

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng) from *N. gonorrhoeae*:

m246/g246		10	20	30	40	50	60
m246 . pep		MHGRYGGTQATVAFVFHQ	RTQRTCF	SNGKVYATQT	DIGSAVNIAQC	FTGEAGQLVYIV	CQR
		: :	:	:	:	:	:
g246		MYGRNGSTQA	AVAFVFDQT	QRRARFGNGE	VYAAQADIG	SAVNIAQGF	FAGESGQLVHV
		10	20	30	40	50	60
		70	80	90	100	110	120
m246 . pep		RTEVLVEQFANLFF	GGFVDSRH	HDMGRFFACH	LDD	ELAQVAFYR	FNAFCFKIMXQ
g246		CAEVLVEQFADLFF	GGFMDCGH	HDMGRFFACH	LDDKLAQV	AFHRLNAFC	FKIMVQLDFF

565

	70	80	90	100	110	120
	130	140	150			
m246 . pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246 . seq (partial)

1	ATGCACGGGC	GGAACGGTGG	TACTCAAGCG	ACCGTTGCCT	TCGTTTCCA
51	CCAGACACAG	CGTACCTGTT	TCAGCAACGG	CGAAGTTCAC	GCCACTCAAA
101	CCGACATCGG	CAGTGCTGTA	AATATCGCGC	AGTGCTTTAC	GGGCGAAGCC
151	GGTCAGTTGG	TCTACGTCGT	CCGTTAACGG	TGTGCCGAGG	TTTTGGTGGA
201	ACAGTTCGCT	AACCTGTTCT	TTGGTTTTAT	GGATTGCGGG	CATCACGATA
251	TGGGTCGGTT	TTTCACCTGC	CATTGGACG	ATGAACTCGC	CCAAGTCGCT
301	TTCCACCGCT	TTAATGCCTT	TTGCTTCAAG	ATAATGGTTC	AGCTCGATTT
351	CCTCGCTGAC	CATCGATTTC	CCTTTGACCA	TCAGCTTGCC	GTTTTGGCT
401	GTGATGATGT	CGTGGATGAT	TTGCGAGGCT	TCGGCCGGTG	TTTCCGCCCA
451	GTGTACTTTT	ACGCCCAACT	TGGTCAGGTT	TTCTTCCAGC	TGCTCCAGCA
501	G				

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246 . pep (partial)

1	MHGRNGGTQA	TVAFVFHQTO	RTCFNNGEVH	ATQTDIGSAV	NIAQCFTGEA
51	GQLVYVVR*R	CAEVLVEQFA	NLFFGFMDCG	HHDMGRFFTC	HLDDELAQVA
101	FHRFNAFCFK	IMVQLDFLAD	HRFAFDHQLA	VFGCDDVVDD	FAGFGRCFRP
151	VYFYAQLGQV	FFQLLQQ			

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVFHQTRTCFSNKGVIATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQTRTCFSNNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246 . pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFTCCHLDDELAQVAFHRFNAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246 . pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
a246	HRFAFDHQLAVFGCDDVVDVDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247 . seq

1	atgaaacgta	aaatgctaaa	cgtaccaaag	ggcggttatg	atggtatgaa
51	gggttttacc	attgttgaat	ttctggttgc	gggcctgctc	agtataattg
101	tcctgatagc	ggctgatcgc	agttacttta	catcccggaa	attaaatgat
151	gtggcaaacg	agcgtcttgc	cattcaacag	gatttgcgga	atgcggcaac
201	attaattgtc	cgcatgcaa	gaatggcggg	gagcttcggt	tgtttcaata
251	tgcccgagca	tactaaagac	gatattgttg	attcaagtaa	tcaaactcaa
301	tctaaccctg	caaaaaccgg	tgccaaacaa	gaaaatcccc	ttttttcctt
351	aaaaaggagc	ggcatggata	aacaactgat	tcccgttgct	gaatccatag
401	atattaaata	tccgggtttt	atccagcgcc	ttaacgcatt	ggttttccaa
451	tacggtatcg	atgatcttga	tgcgagtgc	gagactgttg	tagtcagcag
501	ctgttccaaa	atagcaaaac	cgggtaagaa	aatatctacc	ttgcaagaag
551	caaagagtgc	attacagatt	actaatgatg	ataaacaaaa	tggaaatc

g247.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 949>:

m247.seq (partial)

This corresponds to the amino acid sequence <SEQ ID 950; ORF 247>:

m247.pep (partial)

1	XRRKMLNVXX	GSYDGMKGFT	IIIEFLVAGLL	SMIVLMAVGS	SYFTSRKLND
51	AANERLAAQQ	DLRNAATLIV	RDARMAGGFG	CFNMSEHPAT	DVIPDTTQQN
101	SPFSLKRNIG	DKLIPIAESS	NINYQNFFQV	GSALIFYQYI	DDVNASTATT
151	VVSSCAAISK	PGKQIPTLED	AKKELKIPDQ	DKEQNGNIAR	QRHVVNAYAV
201	GRIADEESLF	RFQOLDKGKW	GNPQL...		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/q247

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTTIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAAERLAAQQ					
	: :	: :	: :	: : :	:	:
g247	MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIAVVSSYFTSRKLNDVANERLAIQQ					
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSPFSLKRN					
			::		::	
g247	DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAKPGAKQENPLFSLKRS					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	GIDK-LIPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISKPGKQIPT					
	:: :	: :	: :	: :	: :	: :

g247 GMDKQLIPVAESIDIKYPGFIQRLNALVFQYGIDDLDAEAEVTVSSCSKIAPGKKIST
130 140 150 160 170 180

m247.ppep 170 180 190 200 210 220
LEDAKKELKIPDQDK EQNGNIARQRHVVNAYAVGRIAD-EESLFRFQLDDKGKWGNPQL
|::||: |:| ::|| |||||:|:||||| |:: ||||| |

g247 LQEAKSALQITNDDK-QNGNITRQKHVVNAYAVGRFGNN EESLFRFQLDDKGKWGNPQLL
190 200 210 220 230

g247 VKVKVRMDVRYIYVSGCPEDEDAGKEEFRTYNKFDSKNAVTTPAGVEVL LDSGLNAKIA
240 250 260 270 280 290

```
a247.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCTC  AGTATGATTG
101 TCCTGATGGC  GGTCCGATCG  AGTTACTTCA  CATCCCGGAA  ATTAATGATG
151 GCGGCAAAACG  AGCGTCTTTC  CGCGCAACAG  GATTTGCGGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGGT  TGTTTCAATA
251 TGTCCGAGCA  TACTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAACT
301 CAACATGTCC  CTGTAAAACC  CGGTGCCAAA  CAAGAAAATC  CCCCTTTTTT
351 TTTAGAGTGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCCTATTGC  TGAATCCACA  GATATTAAAT  ATCCGGGTTT  TGCCAGGCT
451 CGTCCGGCAT  TGATTTTCCA  ATACGGCATC  GATGATCTTG  ATGCGAGTGC
501 TGAGACTGTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CCGGGTAAGA
551 AAATATCTAC  CTTGCAAGAA  GCAAAGAGTG  CATTACAGAT  TACTAATGAT
601 GATAAACAAA  ATGGAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCCTA
651 TGCGGTCCGC  AGGATTGCCG  GTGAGGAAGG  TTTGTTCCGC  TTCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCCTCAGT  TGCTCGTGAA  AAAGATTAGA
751 CATATGAAAG  TGCGGTATAT  CTATGTTTCC  GACTGTCCTG  AAGATGACGA
801 TGCCGGCAAA  GAGGAAAAAT  TCAAATATAG  GGGTACATTG  GACAGCTCCA
851 CAAATGCTGT  TAGCCCGGCC  GGGGTGATAG  TTTTATTGAT  TANCGGTACT
901 GATACCAAGA  TTGCCGCTTC  TTCAGACAAT  CATATTTATG  CTTACCGTAT
951 CGATGCGACA  ATACGCGGGG  GAAATGTATG  CGCAAACAGA  ACACTTTGA
```

a247.pep

1	<u>MRRKMLNVPK</u>	<u>GNYDGMKGFT</u>	<u>IIIEFLVAGML</u>	<u>SMIVLMAVGS</u>	<u>SYFTSRKRLND</u>
51	<u>AAANERLSAQQ</u>	<u>DLRNAATLIV</u>	<u>RDARMAGGFG</u>	<u>CFNMSEHTKN</u>	<u>DIIVDSPSKQT</u>
101	<u>QHVPVKEGAK</u>	<u>QENPLFSLEW</u>	<u>ANTNNTNNNT</u>	<u>AKLIPIAEST</u>	<u>DIKYPGFAQA</u>
151	<u>RPALIFQYGI</u>	<u>DDLDAEAETV</u>	<u>VVSSCSKIAK</u>	<u>PGKKISTLQE</u>	<u>AKSALQITND</u>
201	<u>DKQNGNITRQ</u>	<u>RHVVNAYAVG</u>	<u>RIAGEEGLFR</u>	<u>FQLDDKGKWG</u>	<u>NPQLLVKKIR</u>
251	<u>HMKVRYIYVS</u>	<u>DCPEDDDAGK</u>	<u>EEKFKYTGTG</u>	<u>DDSTNAVTPA</u>	<u>GVEVLLSXGT</u>
301	<u>DTKIAASDN</u>	<u>HIYAYRIDAT</u>	<u>IRGGNVCANR</u>	<u>TL*</u>	

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTTIEFLVAGLLSMIVLMVAGSSYFTSRKLNDAANERLAAQQ					
		1:				
a247	MRRKMLNVPKGNYDGMKGFTTIEFLVAGMLSMIVLMVAGSSYFTSRKLNDAANERLSAQQ					
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSPFSLK-					
a247	DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDPSKQTQHPVPKPGAKQENPLFSLEW					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	-----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISK					
	:		:	:		:
a247	ANTNNTNNNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDASETVVVSSCSKIAK					
	130	140	150	160	170	180

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```

                170      180      190      200      210      220
m247 . pep      PGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVNAYAVGRIADEESLFRFQLDDKGKW
                |||:| ||::||: ||:| ::|| ||||:||||| ||||| ||: ||||| |||||
a247            PGKKISTLQEAKSALQITNDDK-QNGNITRQRHVVNAYAVGRIAGEEGLFRFQLDDKGKW
                190      200      210      220      230

m247 . pep      GNPQL
                |||||
a247            GNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEKFKYTGTDFSSTNAVTPAGVEVLLSXG
                240      250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

```

g247-1.seq (partial) ..
1  CCCGGTGCCA AACAAAGAAAA TCCCCTTTT TCCTTAAAA GGAGCGGCAT
51  GGATAAACAA CTGATTCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATGCGA GTGCTGAGAC TGTGTAGTC AGCAGCTGTT CCAAAATAGC
201 AAAACCGGGT AAGAAAATAT CTACCTTGCA AGAAGCAAAG AGTGCATTAC
251 AGATTACTAA TGATGATAAA CAAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATCGCGT CGGCAGGTTT GGCAATAATG AGGAAAGTTT
351 GTTCCGCTTC CAATTGGATG ATAAGGGCAA GTGGGGTAAT CCTCAGTTCG
401 TCGTGAAAAA GGTAAACGCT ATGGATGTGC GGTATATTTA TGTTTCCGGT
451 TGTCCTGAAG ATGAAGATGC CGGCAAAGAG GAAAAATCA GATATACGAA
501 TAAATTCGAC AAATCCAAAA ATGCTGTTAC GCCTGCCGGG GTGGAGGTTT
551 TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TCGACAATA CGCGGGGAA ATGTATGCGC
651 AAACAGAACA CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

```

g247-1.pep (partial) ..
1  PGAKQENPLF SLKRSMDKQ LIPVAESIDI KYPGFIQRLN ALVFQYIGDD
51  LDASAETVVV SSSSKIAPKG KKISTLQEAK SALQITNDDK QNGNITRQKH
101 VVNAYAVGRF GNNEESLFRF QLDDKGKWN PQLLVKKVKR MDVRYIYVSG
151 CPEDEDAGKE EKFRYTNKFD KSKNAVTPAG VEVLLDSGLN AKIAASSDNS
201 IYAYRINATI RGNVNCANRT L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

```

m247-1.seq
1  ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAGTTATG ATGGTATGAA
51  AGGTTTTACC ATTATTGAAT TTTTGGTTGC GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCCGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAAACG AGCGTCTTGC CGCGCAACAG GATTTGCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTTCAATA
251 TGTCCGAGCA CCTTCAACT GATGTTATTC CCGATACGAC GCAACAAAT
301 TCTCCTTTT CCTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTTCA ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTCAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATG CCGATGAGGA AGGTTTGTTT CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGAATCCTC AGTTGCTCGT GAAAAAGGTT AGACATATGA
701 AAGTGCGGTA TATCTATGTT TCCGGCTGTC CTGAAGATGA CGATGCCGGC
751 AAAGAGGAAA CATTCAAATA TACGGATAAA TTCGACAGCG CCCAAAATGC
801 TATTACGCCC GCGGGGTGG AGGTTTATT GAGTAGCGGT ACTGATACCA
851 AGATTGCCGC TTCTTCAGAC AATCATATT ATGCTTACCG TATCGATGCG
901 ACAATACGCG GGGGAAATGT ATGCGCAAAC AGAACACTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

```

m247-1.pep
1  MRRKMLNVPK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51  AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPDTTQON
101 SPFSLKRRNGI DKLIPIAESS NINYQNFFQV GSALIFQYGI DDVNASTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEEGLF RFQLDDKGKW GNPQLLVKKV RHMKVRYIYV SGCPEDDDAG
251 KEETFKYTDK FDSAQNAVTP AGVEVLLSSG TDTKIAASSD NHIYAYRIDA
301 TIRGGNVCAN RTL*

```

	70	80	90	100	110	120
m247-1.pep	NAATLIVRDARMAGGFGCFNMSEHPATDVI	PDTTQQNSPFLSRNGIDK-LIPIAESSNI	:	:	:	:
g247-1				PGAKQENPLFSLKRSGMDKQLIPVAESIDI		
				10	20	30
	130	140	150	160	170	180
m247-1.pep	NYQNFFQVGSALIFQYIGIDDVNASTATTVVSSCAAISKPGKIPTLED	AKKELKIPDQDK	:	:	:	:
g247-1	KYPGFQIRLNALVFQYGIDDLDAEAETVVVSSCKIAKPGKKISTLQEAKSALQITNDDK					
	40	50	60	70	80	90
	190	200	210	220	230	240
m247-1.pep	EQNGNIARQRHVVNAYAVGRIAD-EEGLFRFQLDDKGWGNPQLLVKKVRHMKVRYIYVS					
g247-1	-QNGNITRQKHVVVNAYAVGRFGNNEESLFRFQLDDKGWGNPQLLVKKVKRMVDVRYIYVS					
	100	110	120	130	140	
	250	260	270	280	290	300
m247-1.pep	GCPEDDDAGKEETFKYTDKFDSAQNAVTPAGVEVLSSGTDTKIAASSDNHIYAYRIDAT					
g247-1	GCPEDDEDAGKEEFRTYNKFDSKNNAVTPAGVEVLDSGLNAKIAASSDNSIYAYRINAT					
	150	160	170	180	190	200
	310					
m247-1.pep	IRGGNVCANRTLX					
g247-1	IRGGNVCANRTLX					
	210	220				

a247-1.seq (partial)

This corresponds to the amino acid sequence <SEQ ID 958; ORF 247-1.a>:

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLDSA ETVVVSSCSK
51  IAKPGKIST LQEAKSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQLDDKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEKFKYT
151 TFGDSSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNVC
201 ANRTL*

```

[illegible]

570

```

m247-1      YAVGRIADEEGLFRFQLDDKGKWNQPLLKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFDSSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            | |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m247-1      TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            260      270      280      290      300      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1   atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgccagc tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggttttgcg
201 ggagggcgaa tttcaggttt tggatttggg atatgctgcg gacagtaaag
251 ttacgtttag cgaaaactgt gaaaaagggtc tgtgtaccgc agtgaatgtg
301 cggacaaata ataatggtag tgaagaggct ttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttcttgccct gcaaagtctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aagggcgcgg caggcgctcg caaaatgccg cgctatatta tcgaatatatt
501 aggcgtgaag aacggacaaa atgtttatcg gggtactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcataaat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1   MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFLLVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNGSSEA FGNIVVQKP AVEAVKRSCP AKSGKNSTDL CIDNKGMEYN
151 KGAAGVSKMP RYIIIEYLVK NGQNVYRVTA KAWGKNANTV VVLQSYVGNN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1   ..GGGTTTGCAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.TyWT
51  gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGCTT TGGCCGAGKc GkCTwTGCGG
151 GAAGGCGAAC TTCAGGTTTT GGATTTGGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAAACGTGT GAAAAGGTCT GTsTGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301 AAGCCACCG TTGAGGCGGT GAAGCGTTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GGwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCAC.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAACGGA
451 GAAATGTTT ATCGGGTTAC TGCCAAGGCT TGGGGtAAGA ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1   ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXXR
51  EGELQVLDLE YDTSKVTFs ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGXKEYKKG TRSVTKMPRY IIEYLVGXNG
151 ENVYRVTAKA WGKNANTVVV LQSYVSNND *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

```

m248/g248
m248.pep
            10      20      30      40
GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
| ||:|||| | ||| | ||||| ||||| ||||| |||||

```

571

```

g248      MRKQNTLTGIPTSDGQRGSALFIVLMVMIVVAFVVTAAQSYNTEQRI SANESDRKLALS
           10      20      30      40      50      60
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNND-NEEAFDNIVVQGKP
           50      60      70      80      90      100
g248      LAEAAALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNGSEEAFGNIVVQGKP
           70      80      90      100      110      120
m248.pep  TVEAVKRSCPA-----NSTDLCLDKKXKEYKKGTRSVTKMPRYII EYLGXNGENVYRVTA
           110      120      130      140      150
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYII EYLGXVKNQNVYRVTA
           130      140      150      160      170      180
m248.pep  KAWGKNANTVVVLQSYVSNNDX
           160      170      180
g248      KAWGKNANTVVVLQSYVGNNDQX
           190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51 GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEAAALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSC TA KSTGLCIDNK GMEYKKGTQS
151 VSKMPRYIIE YLGXNGENV YRVTA KAWGK NANTVVVLQS YVSNND*

```

m248/a248 89.4% identity in 180 aa overlap

```

m248.pep      GFALLIVLMVXIVVAFXXVTAAQSYNTEQRI SXNESDRKLAXS
                10      20      30      40
a248      MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRI SANESDRKLALS
                10      20      30      40      50      60
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNNDNEEAFDNIVVQGKPT
                50      60      70      80      90      100
a248      LAEAAALREGEFQVLDLEYDTSKVTFSENCGKGLCTAVNVRTNNDNEEAFDNIVVQGKPT
                70      80      90      100      110      120
m248.pep  VEAVKRSCPANSTDLCIDKKXKEYKKGTRSVTKMPRYII EYLGXNGENVYRVTA KAWGK
                110      120      130      140      150      160
a248      VEAVKRSC TAKSTGLCIDNKGMEYKKGTQSVSKMPRYII EYLGXVKNQNVYRVTA KAWGK
                130      140      150      160      170      180
m248.pep  NANTVVVLQSYVSNNDX
                170      180

```

572

|||||
a248 NANTVVVLQSYVSNNDX
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq

```

1  ATGCGCAAAC AGAACAACCTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGTTTGTAAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAGGTC TGTGTGCCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep

```

1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEAAALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSCPA NSTDLCKK GMEYKKGTRS
151 VSKMPRYIE YLGVKNGENV YRVTAKEGK NANTVVVLQSYVSNND*

```

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
g248	MRKQNTLTGIPTSDGQRGSAFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	119
m248-1.pep	LAEAAALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNND-NEEAFDNIVVQGKPT					
g248	LAEAAALREGE FQVLDLEYAADS KVTFSENCEKGLCTAVNVRTNNGS EEA FGNIVVQGKPT					
	70	80	90	100	110	120

	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA---NSTDLCKK GMEYKKGTRSVSKMPRYIE YLGVKNGENVYRVTA					
g248	AVEAVKRSCPAKSGKNSTDLCKK GMEYNKGAAGVSKMPRYIE YLGVKNQNVYRVTA					
	130	140	150	160	170	180

	180	190
m248-1.pep	KAWGKNANTVVVLQSYVSNNDX	
g248	KAWGKNANTVVVLQSYVGNNDQX	
	190	200

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m248-1.pep	LAEAAALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNNDNEEAFDNIVVQGKPT					
a248	LAEAAALREGE LQVLDLEYDTDSKVTFSENC GKGLCTAVNVRTNNDNEEAFDNIVVQGKPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDLCKK GMEYKKGTRSVSKMPRYIE YLGVKNGENVYRVTAKEGK					
a248	VEAVKRSC TAKSTGLCKK GMEYKKGTSVSKMPRYIE YLGVKNGENVYRVTAKEGK					
	130	140	150	160	170	180

```

                190
m248-1.pep    NANTVVVLQSYVSNNDEX
              |||||
a248          NANTVVVLQSYVSNNDEX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```

g249.seq
1   atgaagaata atgattgctt ggcctgaaa aatccccagt ccggtatggc
51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtatttttg
101 cattgctgtc cgtacagttg cggacagtcg cttccgtcag ggaggcggaa
151 acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaatggt
201 gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgccggatgc ggtagctatt cattacgccg
401 tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcgggtgt
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagttag cggcgacaat atcgtatata cctatcaggc aagggtcggg
601 ggtcgtgaat ga

```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

```

g249.pep
1   MKNNDCLRLK NPQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDLDSNKK YSLYMGKQTL SAVDGEFMLD
101 AEKSKAQLAE EQLKRFSHEL KNALPDAVAI HYAVCKDSSG DAPTLSDSGA
151 FSSNCDNKAN GDTLIKVLWV NDSAGDS DIS RTNLEVSGDN IVYTYQARVG
201 GRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```

m249.seq
1   ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGTTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CGGACAGTCN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATT TGCATTGAT
301 GCCATGAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTAG
351 TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTCGGCAG GGGATTCCGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCCGAGGT
601 CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```

m249.pep
1   MKNNDCFRLK DSQSGMALIE VLVAMLVLT I GILALLSVQL RTVXXXXXXXX
51  XXXXXXXXXXX XLMEGMLMNP TIDSDSNKK YNLYMGNHTL SAVDGDFAID
101 AMKTKGQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLGNAF
151 SSNCDNKANG DTLIKVLWVN DSAGDS DIS TNLEVSGDNI VYTYQARVG
201 RE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

```

m249/g249
                10      20      30      40      50      60
m249.pep      MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXX
              |||::|::|: ||||| ||||| ||||| ||||| ||||| : : :

```

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10          20          30          40          50          60
           70          80          90          100         110         120
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNHTLSAVDGDFAIDAMKTKGQLAEAQLKRFSYEL
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g249      NLMEGMLMNPTIDLDSNKKNYSLYMGKQTL SAVDGEFMLDAEKSQAQLAEELKRFSHEL
           70          80          90          100         110         120
           130         140         150         160         170         179
m249.pep  KNALPDAAAIH YAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVND SAGDSDIS
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g249      KNALPDAVAIH YAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVND SAGDSDIS
           130         140         150         160         170         180
           180         190         200
m249.pep  RTNLEVSGDNIVYTYQARVGGREX
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g249      RTNLEVSGDNIVYTYQARVGGREX
           190         200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```
a249.seq
1  ATGAAGAATA  ATGATTGCTT  CCGCCTGAAA  AACCCCCAGT  CCGGTATGGC
51  GCTGATAGAA  GTCTTGGTGC  CTATGCTCGT  TCTGCCACAT  GGTATTTTGG
101 CACTATTGTC  TGTTCAAGTG  CGGACAGTCG  CTTCCGTGAG  GGAGGCAGAG
151 ACGCAAAACA  TCGTCAGTCA  AATCACGCAA  AACCTGATGG  AAGGAATGTT
201 GATGAATCCG  ACCATTGATT  CGGACAGCAA  CAAGAAAAAC  TATAATCTTT
251 ACATGGGAAA  CCATCATGCA  CTATCAGTTG  TGGATGGCGA  TTTTCAGGTT
301 GATGCCATAA  AAACAAAGAC  CGAGTTGGCA  GAGGCACAAT  TGAAGAGATT
351 TAGTTATGAG  CTGAAAAATG  CCTGCCGGA  TGCGGCAGCC  ATCCATTACG
401 CCGTCTGCAA  GGATTGTCG  GGTGTTGCGC  CGACATTGTC  CGCCGGCAGT
451 ACTTTTCTT  CAAATTGCGA  TGGTAGTGCA  AATGGGGATA  CTTTGATTAA
501 AGTATTGTGG  GTAAATGATT  CGGCAGGGGA  TTCGGATATC  GCCCGTACGA
551 ATCTTGAGAC  GAACGGCAAC  AATATCGTAT  ATACCTATCA  GGCAAGGGTC
601 GGAGTCCGGG  AATGA
```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

a249.pep

1	MKNND C FR L K	NPQSGMALIE	<u>VIVAMLVLT</u> I	<u>GILALLSVQL</u>	RTVASVREAE
51	TQTIVSQITQ	NLMEGMLMNP	TIDSDSNKKK	YNLYMGNNHA	LSVVDGDFQV
101	DAIKTKTQLA	EAQLKRFSYE	LKNALPDAAA	IHYAVCKDSS	GVAP T LSAGS
151	TFSSNCDGSA	NGDTLIKVLW	VNDSAGDS D I	ARTNLETNGN	NIVYTYQARV
201	GGRE*				

m249/a249 81.9% identity in 204 aa overlap

	10	20	30	40	50	60							
m249.pep	MKNND	CFRLK	DSQSG	MA	LIEVL	VAMLV	LTIGI	LALLS	VQLRT	VXXXX	XXXXXXXXXXXXXXXXXXXX		
a249	MKNND	CFRLK	NPQSG	MA	LIEVL	VAMLV	LTIGI	LALLS	VQLRT	VASVR	EAEQT	IVSQITQ	
	10	20	30	40	50	60							
	70	80	90	100	110	119							
m249.pep	XLMEG	MLMNP	TIDSD	SNKKN	YNLYM	GNH-TLS	AVDGD	FAIDAM	KTGKQ	LAEAL	KRFSYE		
a249	NLMEG	MLMNP	TIDSD	SNKKN	YNLYM	GNHHALS	VVDGDF	QVDAIK	TKTQL	AELAL	KRFSYE		
	70	80	90	100	110	120							
	120	130	140	150	160	170							
m249.pep	LKNAL	PDAAA	IHYAV	CKDSS	GNAPT	LS-GNA	FSSNC	DNKAN	GDTLI	KVLWV	ND	SAGDS	SDI
a249	LKNAL	PDAAA	IHYAV	CKDSS	GVAPT	LSAGS	TSSNC	DGSAN	GDTLI	KVLWV	ND	SAGDS	SDI
	130	140	150	160	170	180							

```
m249.pep      180          190          200
               SRTNLEVSGDNIVYTYQARVGGRGX
               :|:|||||:|:|||||
a249           ARTNLETNGNNIVYTYQARVGGRGX
               190          200
```

1	ATGAAGAATA	ATGATTGCTT	CCGCGTGAAA	GATTCCCAGT	CCGGTATGGC
51	GCTGATAGAA	GTCTTGGTGT	CTATGCTCGT	TCTGACCATC	GGTATTTTGG
101	CACATATTGT	TGTACAGTTG	CGGACAGTCG	CTTCCGTCAG	GGAGGCGGAG
151	ACACTAAACCA	TCGTGACCCA	AATCAGCGAA	AACCTGATGG	AGGGAATGTT
201	GATGAATCCG	ACCATTGATT	CGGACAGCAA	CAAGAAAAAC	TATAATCTTT
251	ACATGGGAAA	CCATACACTA	TCAGCTGTGG	ATGGCGATTT	TGCGATTGAT
301	GCCATGAAAA	CTAAGGGGCA	ATTGGCAGAG	GCACAATTGA	AGAGATTTAG
351	TTATGAGCTG	AAAAATGCCT	TGCCGGATGC	GCGAGCCATC	CATTACGCCG
401	TCTGCAAGGA	TTCGTCGGGT	AACGCGCCGA	CATTGTCCGG	CAATGCTTTT
451	TCTTCAAATT	GCGACAATAA	GGCAACGGG	GATTACTTTAA	TTAAAGTATT
501	GTGGGTAAAT	GATTCGGCAG	GGGATTCCGA	TATTTCCCGT	ACGAATCTTG
551	AGGTGAGCGG	CGACAATATC	GTATATACTT	ATCAGGCAAG	GGTCGGAGGT
601	CGGGAATGA				

1	MKNNDCFRLK	DSQSGMALIE	<u>VLVAMLVLT</u>	<u>GILALLSVQL</u>	RTVASVREAE
51	TQTIVSQITQ	NLMEGMLMNP	TIDSDSNKKN	YNLYMGNNHTL	SAVDGDFAFID
101	AMKTKQGLAE	AQLKRFSEYL	KNALPDAAAI	HYAVCKDSSG	NAPTLSGNAF
151	SSNCDNKANG	DTLKVLVVN	DSAGSDSISR	TNLEVSGDNI	VYTYQARVGG
201	RE*				

	10	20	30	40	50	60
m249-1.pep	MKNND	CFLKDSQ	SGMALIE	VLVAM	LVLTIGI	LALLSVQ
g249	MKNND	CLRLKNP	QSGMALI	EVLVAM	LVLTIGI	LALLSVQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m249-1.pep	NLMEG	MLMNP	PTIDSD	SNKKNY	NLYMG	NHTLSA
g249	NLMEG	MLMNP	PTIDL	SDSNKK	NYSLY	MKGQTL
	70	80	90	100	110	120
	130	140	150	160	170	179
m249-1.pep	KNALP	DAAAI	HYAVCK	DSSGNA	PTLSGN	-AFSSN
g249	KNALP	DAVAI	HYAVCK	DSSGDA	PTLSDS	GAFSSN
	130	140	150	160	170	180

Query: 13 QSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQIVSQITONLMEGMLMNPTI 72
 QSG ++IEVLVA+L+++IG+L ++++Q +T+ ++ + + + NL+E M +P
 Sbjct: 12 QSGFSMIEVLVALLLISIGVLGMIAMQGKTIQYTADSVERNKAAMLGSNLLES MRASPKA 71

Query: 73 DSDSNKKKNYNLYMGNHHALSVDVGDFQVDAIKTKTOLAE---QLKRFSYELKNALPDAA 129

576

D + M G A + T L +A +L ++ ++KN LP A
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAKGSAPFTAPSSCTPLPDAIKDRLGCVAEQVKNELPGAG 126
 Query: 130 AI---HYAVCKDSSGVAPTL SAGSTFSSNCDGSANGDTL-IKVLWVND SAGSDIARTNL 185
 + Y +C+ S +CDG G L I++ W + A ++
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSML EIRLAWRGKQGACVNAADSSA 172
 Query: 186 ETN 188
 +T+
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLK	DSQSG	MALIE	VLVAM	LVLTIG
a249	MKNND	CFRLK	NPQSG	MALIE	VLVAM	LVLTIG
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLMEG	MLMNP	TIDSD	SNKKY	NLYMG	NH-TLS
a249	NLMEG	MLMNP	TIDSD	SNKKY	NLYMG	NH-HALS
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKNAL	PDAAI	HYAVC	KDSSG	NAPTLS	-GNAF
a249	LKNAL	PDAAI	HYAVC	KDSSG	VAPTL	SAGSTF
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRTN	LEVSG	DNIVY	TYQAR	VGGREX	
a249	ARTN	LETNG	NNIVY	TYQAR	VGGREX	
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1 atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51 aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggtg
101 tgcagggcgg gcaaaaaggt atggggccggc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacgggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcggcatac cctgatgggg ggcggcgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1 MHTTASPRDE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51 GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRRARV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1 ATGCACACCT TCCCCGCATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51 CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAACTACT CGGTATGCAG
101 GGCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCACTAT
151 GAACCTTCGCC GCGGCTCCG AGTTGCCAC GGTCAACCTG TGGGCGsGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1 MHTPSPHNEF IRGIKESSPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51 MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRRARTVF YV*
  
```

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

```

      10      20      30      40      50      59
m250.pep  MHTSPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWSLEMLLMTSMNFAGGSEF
          |||::|||
g250      MHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMGRLEMLLMTGMNFAGGSEF
          10      20      30      40      50      60

      60      70      80      90      100     110
m250.pep  ATVNLWAEPLPILLIATVTFMINSRHILMGGGACPAAPERNTAEKSRARTVFYVX
          |||::|||
g250      ATVNLWAEPLPILLIATITFMINSRHILMGGGACHAHERNTAEKSRARAVFYV
          70      80      90      100     110

```

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTGCCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGT
101	TGCAGGGTGG	ACAAAAAGGC	ATGAGCTGGC	TGGAAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGGCGG	CTCCGAGTTT	GCCACGGTCA	ACCTGTGGGC
201	GGAACTCTG	CCGATACTGG	TTATCGCCAC	CGTAACCTTA	ATGATTAATT
251	CTCGGCATAT	CCTGATGGGG	G.CGGCACTT	CCCCCGCACC	TGAAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACTGTT	TTTTATGTGT	GA

```

1  MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMQGQKG MSWLEMLLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATVTF MINSRHILMG XGTC PAPERN
101 TAEKSARTV FYV*

```

```

59          10          20          30          40          50
m250.pep
MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTSMNFAGGSEF
          |
||:|||||||||||||||||||||||||||||||||:|||||||
a250
MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTGMNFAGGSEF
          10          20          30          40          50
60
          60          70          80          90          100          110
m250.pep
ATVNLWAEPLPILLIATVTFMINSRHILMGGGACPAAPERNTAEKSRARTVFYVX
|||||
a250
ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCPAAPERNTAEKSRARTVFYVX
          70          80          90          100          110

```

1	atgcctgacc	caatagggat	tcttttcgct	gccgtcgggg	ttgatttttt
51	tgccgttggt	ttgagggggc	gttttcaacg	aataggcgcg	gttggcatgt
101	tgataataat	aatcctgatg	gcggaqgtcg	qaaccaaacc	ggtcgtaacc

q251.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/q251

m251.pep TVDAARRAVRISIVAQAADLPRNDISPAYGDP
IGAGFTAVGADFFAVVLRGRVRRIGAVG
g251 MPDPIGILFAAVGVDFFAVVLRGRFQIRIGAVG

40 50 60 70 80 90
10 20 30

579

	100	110	120	130	140	150
m251.pep	MLIIIIILMAEIRAKAVKPEIHAQVVADFGGIEGFFECRLQEPVAFPNHAIGFVIGKRLV					
	: : : : : : : : :					
g251	MLIIIIILMAEVGKTCTVTEVDAQVVADFGGIEGFFECRLQEPVAFPNHAVGVVGRRLV					
	40	50	60	70	80	90
	160	170	180	190	200	210
m251.pep	GTRAAIFVRTVGRTRVLLKMIQTDALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
	: : : : : :					
g251	GTRAAIFVRTVGGTVRLLKMIVQTDALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
	100	110	120	130	140	150
	220	230	240	250	260	270
m251.pep	VKHARTVFRAHQRTVFAVGKQSAVFVVARVFAVTGQRTLFFICIKNRLGQECRNRHIAR					
	: : : : : :					
g251	VKHARTVFRAHLRTVFTVGNQPAVFAARVFAVASYSR-VFFIFIKNRLGQECRNRHIAR					
	160	170	180	190	200	210
	280	290	300			
m251.pep	VESLLRVFEYAADVPLILKTKTRAEQPRPAFVX					
	: : : : :					
g251	VESLLRAFEYAADVVPFVKTKTRAEQPRPAFVX					
	220	230	240			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 985>:

```

a251.seq
1   ATGCGTGTCTG  CGGTAGTCGT  AGCGCAACCC  CGCGCCGACA  TCCGCCACC
51  TGCCCAAACG   GACATTGTCC  CGAACTGCCG  CGTAATAGCT  TTGCGCGTTG
101 ATGCTGCGCG   GCGTGCAGTC  CGTATAAGTA  TTGTTGCCCA  AGCGGCAGAT
151 TTGCCCCGTA   ACCACATTTT  CCCTGCCTAT  GCTGACCCAA  TAGGGTTGGT
201 CCTTGCCGCC   GTTGGGGTTG  GCGGTTTTAG  GGGGCGTTTT  CGACGAATAG
251 GCGCGGTTGG   CATGTTGATA  ATAATAATCC  TGATGGCGGA  GATTAGATC
301 AAAGCGGTCA   AAACCGAGAT  TCACGCTCAG  GTTGTGGCGG  ATTTTGGCGG
351 TATCGAAGGA   TTTTTTGAAT  GCCGCCTGCA  AGAGCCTGTG  GCTTTCCCCG
401 TAAATCACGC   GGTCCGATTT  GTAGTAGGAA  AACGGCTTGT  CGGCACTCGG
451 GCGGCAATAT   TTGTCCGAAC  CGTCGGCAGA  ACAGTGCGTC  TGCTGAAAT
501 GATTGTCCAA   ACCGATGCCC  TGCCGGTCTG  AAGAGAGGCG  GGCATAATCC
551 ACCCAAGTGT   CTTTATCGGC  ATTGGTATAG  ACATATTCCA  AACCCTAGCG
601 GCTTTTGGTG   TGCGTCTCGT  CGTAAACAC  GCCCGTACCG  TATTCGCGC
651 CCACCAGCGC   ACCGTTTTTC  CCGTTGGTAA  ACAGACCGCC  GTATTTGTGG
701 TCGCCCGCGT   ATTTGCCGTT  GCCTCTTATC  GGTCCGTATT  TTCTATTTTC
751 ATCAAAAACC   GCCTTGGTCA  GGAATGCCGG  AACCCTCATA  TCGCGCGTGT
801 CGAAAGTTTG   TTGCGTGTGT  TCGAGTATGC  CGCCGATGTA  GTGCCGTTTG
851 TTTTCAAAC    GAAAACCCGG  GCGGAACAGC  CACGATCGGC  TTTCGTATGA

```

This corresponds to the amino acid sequence <SEQ ID 986; ORF 251.a>:

```

a251.pep
1   MRAAVVVAQP  RADIRPPAQT  DIVPNCRVIA  FAVDAARRAV  RISIVAQAAD
51  LPRNHISPAY  ADPIGLVLA  VGVGGFRGRF  RRIGAVGMLI  IIILMAEIRV
101 KAVKTEIHAQ  VVADFGGIEG  FFECRLQEPV  AFPVNHAVGF  VVGKRLVGTR
151 AAIFVRTVGR  TVRLLKMIVQ  TDALPVVREA  GIIHPSVFIG  IGIDIFQTVA
201 AFGVRLVVKH  ARTVFRAHQR  TVFAVGKQTA  VFVVARVFAV  ASYRSVSFIF
251 IKNRLGQECR  NRHIARVESL  LRVFEYAADV  VPFVFKTKTR  AEQPRSAFV*

```

m251/a251 88.5% identity in 304 aa overlap

	10	20	30	40	50	60
m251.pep	MRAAVVVAQARADIRPPAQTDIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPAY					
	: : : : :					
a251	MRAAVVVAQPRADIRPPAQTDIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m251.pep	GDPIGAGFTAVGADFFAVVLRGRVRRIGAVGMLIIIIILMAEIRAKAVKPEIHAQVVADFG					
	: : : : :					

```

a251      ADPIGLVLAAVGVGGF----RGRFRIRIGAVGMLIIIIILMAEIRVKAVKTEIHAQVVADFG
              70              80              90              100             110

              130              140              150              160              170              180
m251.pep  GIEGFFECLRLQEPVAFPNHAIGFVIGKRLVGTRAAIFVRTVGRTVRLKMIQTALPV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      GIEGFFECLRLQEPVAFPNHAGFVVGKRLVGTRAAIFVRTVGRTVRLKMIQTDALPV
              120              130              140              150              160              170

              190              200              210              220              230              240
m251.pep  VREAGIIRPSVFIGIGIDIFQTVAAGFVRLVVKHARTVFRAHQRTVFAVGKQSAVFVVAR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VREAGIIHPSVFIGIGIDIFQTVAAGFVRLVVKHARTVFRAHQRTVFAVGKQTAVFVVAR
              180              190              200              210              220              230

              250              260              270              280              290              300
m251.pep  VFAVTGQRTLFFFIKRNRLGQECRNRIARVESLLRVFEYAADVPLILKTKTRAQPR
              ||||:|:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VFAVASYSR-VFSIFIKRNRLGQECRNRIARVESLLRVFEYAADVVPFVKTKTRAQPR
              240              250              260              270              280              290

m251.pep  PAFVX
              |||
a251      SAFVX
              300

```

```
g253.seq
1 atgatcgaca gggaccgtat gttgcgggac acgttggaac gtgtgctgtc
51 ggggtcgttc tggttatggg tgggtggtggc atcgatgatg ttaccgccg
101 gattttcagg cacttatctt ctgatggaca atcaggggct gaattttctt
151 ttagtcttgg cgggatgtgt gggcatgaat acgttgatgc tgcagtagt
201 gttggcaacg ttgttctgtc gcgtgaaagt gggacggttt ttcagcagtc
251 cggcgacgtg gtttcggggc aaaggccctg taaatcaggc ggtgttgctg
301 ctgtatgcgg accagtggcg gcaaccttcg gtacgatgga aaataggcgc
351 aacggcgcac agcttgtggc tctgcacgct gctcggaatg ctggtgtcgg
401 tattgctgct gcttttgggt cggcaatata cgttcaactg ggaaagcacg
451 ctgttgagca atgcgcgttc ggtacgcgcg gtggaatatg ttgcattggc
501 gccgtcgaaa ctcggtttcc ctgtcccga tgcgcggcg gctatcgaag
551 gtcgtctgaa cggcaatatt gccgatgcmc gggcttggtc ggggctgctg
601 gtcggcagta tcgtctgcta cggcatctcg ccgcgcctct tggcttgggt
651 agtgtgtaaa atccttttga aaacaagcga aaacggattg gatttggaaa
701 aaacctatta tcaggcggtc atccgcgcgt ggcagaacaa aatcaccgat
751 gcggatacgc gtcgggaaac cgtgtccgcc gtttccgccg aaatcgtctt
801 gaacgatgcg ccgaaatggg cgtctatgct ggagaccgag ttgagggacg
851 gccaatgggt cgagggcagg ctggcgagg aatggctgga taagggcgtt
901 gccgccaatc gggaacaggt tgccgcgctg gagacagagc tgaagcagaa
951 accggcgcaa ctgcttatcg gcgtacgcgc ccaaactgtg ccggaccggg
1001 gcgtgctgcg gcagattgtg cggttttggc aagcggcgca gggcggcgcg
1051 gtggtgcagc ttttggcgga acagggcctt tcagacgacc tttcgaaaaa
1101 gctggaacat ttgctgaacg cgtagaccga atcggcgcg cggtggctgt
1151 agcctgacag ggtggcgca ggaaggcgtt tgaaagacca ataa
```

g253.pep

1	MIDRDRMLRD	TLERVAGSF	WLWVVVASMM	FTAGFSGYTL	LMDNQGLNFF
51	<u>LVLAVGLGMN</u>	<u>TLMLAVLAT</u>	LFLRVKVGRF	FSSPATWFRG	KGPNQAVLR
101	LYADQWRQPS	VRWKIGATAH	SLWLCTLLGM	LVSVLLLLLV	RQYTFNWEST
151	LLSNAASVRA	PEMLAWLPST	LGFPVPDARA	VIEGRNLNGNI	ADARAWSGLL
201	<u>VGSIVCYGIL</u>	<u>PRLLAWVCK</u>	ILLKTSENGL	DLEKTYQYQAV	IRRWQNKITD
251	ADTRRETVSA	VSPKIVLNDA	PKWALMLETE	WDQGWQFEGR	LAQEWLDKGV

m253.seq

1	ATGATTGACA	GGAACCGTAT	GCTGCGGGAG	ACGTTGGAAC	GTGTGCGTGC
51	GGGGTCGTTC	TGGTTGTGGG	TGGTGGCGGC	GACGTTTGCA	TTTTTTACCG
101	GTTTTTCAGT	CACTTATCTT	CTAATGGACA	ATCAGGGTCT	GAATTTCTTT
151	TTGGTTTTGG	CGGGCGTGTT	GGGCATGAAT	ACGCTGATGC	TGGCAGTATG
201	GTTGGCAATG	TTGTTCTCTG	GTGTGAAAGT	GGGGCGTTTT	TTACGAGCTC
251	CGGCGACGTG	GTTTCGGGGC	AAAGACCGTG	TAAATCAGGC	GGTGTTGCGG
301	CTGTATGCGG	ACGAGTGGCG	GCAACCTTCG	GTACGTTGGA	AAATAGGCGC
351	AACGTCGCAC	AGCCTGTGGC	TCTGCACGCT	GCTCGGAATG	CTGGTGTGCG
401	TATTGTTGCT	GCTTTTGGTG	CGGCAATATA	CGTTCAACTG	GGAAAGCACG
451	CTGTTGAGCA	ATGCCGCTTC	GGTACGCGCG	GTGGAATGTG	TGGCATGGAT
501	GCCGTCGAAA	CTCGGTTTCC	CTGTCCCCGA	TGCGCGGGCG	GTCATCGAAG
551	GCCGCTCTGA	CGGCAATATT	CGCGATGCGC	GGGCTTGGTC	GGGGCTGCTG
601	GTCGGCAGTA	TCGCCTGCTA	CGGCATCCTG	CCGCGCCTGC	TGGCTTGGGT
651	AGTGTGTAAG	ATCCTTTTGA	AAACAAGCGA	AAACGGATTG	GATTTGGAAG
701	AGCCCTATTA	TCAGGCGGTC	ATCCGCCGCT	GGCAGAACAA	AATCACCGAT
751	GCGGATACGC	GTCGGGAAAC	CGTGTCCGCT	GTTTACCAGG	AAATCATCTT
801	GAACGATCGC	CCGAAATGGG	CGGTCATGCT	GGAGACCGAG	TGGCAGGACG
851	GCGAATGTTT	CGAGGGCAGG	CTGGCGCAGG	AATGGCTGGA	TAAAGGCGTT
901	GCCACCAATC	GGGAACAGGT	TGCCGCGCTG	GAGACAGAGC	TGAAGCAGAA
951	ACCGGCGCAA	CTGCTTATCG	GCGTGCGCGC	CCAAACTGTG	CCGACCGCGC
1001	GCGTGTTGCG	GCAGATTGTC	CGACTCTCGG	AAGCGGCGCA	GGGCGGCGCG
1051	GTGGTGACAG	TTTTGGCGGA	ACAGGGGCTT	TCAGACGACC	TTTCGGAATA
1101	GCTTGAACAT	TGGCGTAAAG	CAGGTGGCCG	ATGCGGCGCG	CGGTGGCTTG
1151	AGCCTGACAG	GGCGGCGCAG	GAAGGGCGTT	TGAAAGACCA	ATAA

m253 . pep

1	MIDRNRMLRE	TLERVAGSF	WLWVVAATFA	FFTGFSVTYL	LMDNQGLNFF
51	<u>LVLAGVLGMN</u>	<u>TLMLAVWLAM</u>	LFLRVKVRGF	FSSPATWFRG	KDPVNVAVLR
101	LYADEWRQPS	VRWKIGATSH	<u>SLWLCTLLGM</u>	<u>LVSLLLLLLV</u>	RQYTFNWEST
151	LLSNAASVRA	VEMLAWLP SK	LGFPVPDARA	VIEGRLNGNI	ADARAWSGLL
201	<u>VGSIACYGIL</u>	<u>PRLLAWVVCK</u>	ILLKTSENGL	DLEKPYQAV	IRRWQNKITD
251	ADTRRETQVA	VSPKIIILNDA	PKWAVMLETE	WQDGEWFEGR	LAQEAWLDKGV
301	ATNREQVAAL	ETELKQKPAQ	LLIGVRAQTV	PDRGWLRIQV	RLESEAQQGA
351	VVOLLAEQGL	SDDLSEKLEH	WRNALAECGA	AWLEPDRAAO	EGRLKDO*

Homology with a predicted ORF from *N. gonorrhoeae*

m253/q253

	10	20	30	40	50	60
m253 . pep	MIDRNRMLRETLEVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFVLVLAGVLGMN					
	: : : : : :					
g253	MIDRDRMLRDTLEVRAGSFWLWVVASMMFTAGFSGTYLLMDNQGLNFFVLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253 . pep	TLMLAVWLAMLFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	: : : : : : : :					
g253	TLMLAVWLATLFLRVKVGRRFFSSPATWFRGKGPVNQAVLRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253 . pep	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
	: : : : : : :					
g253	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m253 . pep	VIEGRNLNGNIADARAWSGLLVGS	IACYGILPRLLAWVVKILLKTSE	NGLDLEKPYQAV			
g253	VIEGRNLNGNIADARAWSGLLVGS	IVCYGILPRLLAWVVKILLKTSE	NGLDLEKTYQAV			
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 . pep	IRRWQNKITDADTRRET	VS AVSPKII	LNDA PKWAVMLETE	WQDGEWFEGRLAQEW	LDKGV	
g253	IRRWQNKITDADTRRET	VS AVSPKIV	LNDA PKWALMLETE	WQDGEWFEGRLAQEW	LDKGV	
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 . pep	ATNREQVAAL	ETELKQKPAQL	LLIGVRAQTV	PDRGVLRQIVRL	SEAAQGGAVVQL	LAEQGL
g253	AANREQVAAL	ETELKQKPAQL	LLIGVRAQTV	PDRGVLRQIVRL	SEAAQGGAVVQL	LAEQGL
	310	320	330	340	350	360
	370	380	390			
m253 . pep	SDDLSEKLEHWRNAL	AECGAWLEP	PDRAAQEGR	LKDQX		
g253	SDDLSEKLEHWRNAL	TECGAWLEP	PDRAAQEGR	LKDQX		
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

a253 . seq	1	ATGATCGACA	GGAACCGTAT	GCTGCGGGAG	ACGTTGGAAC	GTGTGCGTGC
	51	GGGGTCGTTC	TGGTTGTGGG	TGGCGGCGGC	GACGTTTGCG	TTTTTTACCG
	101	GTTTTTCAGT	TACTTATCTT	CTAATGGACA	ATCAGGGTCT	GAATTTCTTT
	151	TTGGTTTTGG	CGGGCGTGTT	GGGCATGAAT	ACGCTGATGC	TGGCAGTATG
	201	GTTGGCAATG	TTGTTCTCTG	GCGTGAAAGT	GGGGCGTTTT	TTCAGCAGTC
	251	CGGCGACGTG	GTTCGGGGG	AAAGACCCCTG	TCAATCAGGC	GGTGTTCGGG
	301	CTGTATGCGG	ACGAGTGGCG	GCAACCTTCG	GTACGTTGGA	AAATAGGCGC
	351	AACGTGCGAC	AGCCTGTGGC	TCTGCAAGCT	GCTCGGAATG	CTGGTGTCTG
	401	TATTGTTGCT	GCTTTTGGTG	CGGCAATATA	CGTTCAACTG	GGAAAGCACG
	451	CTGTTGGGCG	ATTCGTCTTC	GGTACGGCTG	GTGGAAATGT	TGGCATGGCT
	501	GCTTCGCAAA	CTGGGTTTTT	CCGTGCCTGA	TGCGCGGGCG	GTCATCGAAG
	551	GTCGTCTGAA	CGGCAATATT	GCCGATGCGC	GGGCTTGGTC	GGGGCTGCTG
	601	GTCGGCAGTA	TCGCCTGCTA	CGGCATCCTG	CCGCGCCTCT	TGGCTTGGGC
	651	GGTATGCAAA	ATCCTTTTGA	AAACAAGCGA	AAACGGCTTG	GATTTGGAAA
	701	AGCCCTATTA	TCAGGCGGTC	ATCCGCCGCT	GGCAGAACAA	AATCACCGAT
	751	GCGGATACGC	GTCGGGAAAC	CGTGTCGCGC	GTTTCGCCGA	AAATCGTCTT
	801	GAACGATGCG	CCGAAATGGG	CGGTCATGCT	GGAGACCGAA	TGGCAGGACG
	851	GCGAATGGTT	CGAGGGCAGG	CTGGCGCAGG	AATGGCTGGA	TAAGGGCGTT
	901	GCCGCCAATC	GGGAACAGGT	TGCCGCGCTG	GAGACAGAGC	TGAAGCAGAA
	951	ACCGGCGCAA	CTGCTTATCG	GCGTGCGCGC	CCAAACTGTG	CCCGACCGCG
	1001	GCGTGTTGCG	GCAGATCGTC	CGACTTTCGG	AAGCGGCGCA	GGGCGGCGCG
	1051	GTGGTGCAGC	TTTTGGCGGA	ACAGGGGCTT	TCAGACGACC	TTTCGGAAAA
	1101	GCTGGAACAT	TGGCGTAACG	CGCTGACCGA	ATGCGGCGCG	GCGTGGCTGG
	1151	AACCCGACAG	AGCGGCGCAG	GAAGGCCGTC	TGAAAACCAA	CGACCGCACT
	1201	TGA				

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

a253 . pep	1	MIDRNRMLRE	TLERVAGSF	WLWVAATFA	FFTGFSVTYL	LMDNQGLNFF
	51	LVLAVGLGMN	TLMLAVWLAM	LFLRVKVGRF	FSSPATWFRG	KDPVNQAVLR
	101	LYADEWRQPS	VRWKIGATSH	SLWLCTLLGM	LVSVLLLLLV	RQYTFNWEST
	151	LLGDSSSVRL	VEMLAWLPAK	LGFPVPDARA	VIEGRNLNGNI	ADARAWSGLL
	201	VGSIACYGIL	PRLLAWAVCK	ILLKTSENGL	DLEKPYQAV	IRRWQNKITD
	251	ADTRRET	VSA VSPKIVL	NDAP KWAVMLETE	WQDGEWFEGR	LAQEWLDKGV
	301	AANREQVAAL	ETELKQKPAQ	LLIGVRAQTV	PDRGVLRQIV	RLSEAAQGGA
	351	VVQLLAEQGL	SDDLSEKLEH	WRNALTECGA	AWLEPDRAAQ	EGRLKTNDR
	401	*				

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
a253	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMFLRVKVGRRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMFLRVKVGRRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m253.pep	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLAWVVKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253.pep	IRRWNQKITDADTRRETAVSAVSPKIILNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253	IRRWNQKITDADTRRETAVSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253.pep	ATNREQVAALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	:					
a253	AANREQVAALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRDKQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRKTNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcaggtttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg ttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcactggttt ctttgagaaa cgggcccgggc
301 tggacgggat tttcactgtc ctggctgctg gcggctgcag gaatcgaca
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggctcttg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtatttg gcggcagcat aacccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```

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```

51  LLYLSSSLYH GIAAGKLKSI LKKTDHCFMIY VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYIVMGW MVLAVMKSLT
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

```

m254.seq (partial)
1  ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT
51  GTACCACGGA ATTGCAGCCG GAAACTGAA AAGCATTTTG AAAAAACCG
101 ACCACTGCAT GATTTATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA
151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG
201 GCTGCTGGCG GCTGCAGGAA TCGACAAGA ACTCACCATC GGACGGAAAA
251 GCGAAAAACG TCTGCTGTCT ATTGTGATTT ATGTCGTCAT GGGTTGGATG
301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT
351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTCCGC ATTTACTGGT
401 TTGTAAACGA TGAAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTC
451 GTATTGGGCG GCAGCATCAC CCAATTGTG AGCGTGTACG GTTACGTAAT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

```

m254.pep (partial)
1  ..VSVYGISLLL LYLSSWLYHG IAAGKLKSIK KTDHCFMIYV LIAGSYTPFA
51  LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLLS IYIYVVMGWM
101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEKI RHGHGIWHLF
151 VLGGSITQFV SVYGYVI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254 . pep					10	20	30
					VSVYGISLLLLYLSSWLYHGIAAGKLKSIL		
g254							
	20	30	40	50	60	70	
m254 . pep		40	50	60	70	80	90
		KKTDHCFMIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS					
g254							
	80	90	100	110	120	130	
m254 . pep		100	110	120	130	140	150
		IYIYVVMGWMVLAVMKSLTASLPSAGLAWLAAGGMLYSVG IYWFVNDEKIRHGHGIWHLF					
g254		: : :					
	140	150	160	170	180	190	
m254 . pep		160					
		VLGGSITQFVSVYGYVIX					
g254							
		VLGGSITQFVSVYGYVIX					
		200					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

```

a254 . seq
1  ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTGTA GCGGTTTGAT
51  TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG
101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT
151 CTGCTCTATT TGAGTTCCTC GCTGTACCAC GGAATTGCAG CCGGAAAACCT
201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTAT GTGCTGATTG
251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGGCCGGGC

```

585

```

301  TGGACGGTAT  TTTCACGTGC  CTGGCTGCTG  GCGGCTGCAG  GAATCGCACA
351  AGAACTCACC  ATTGGACGGA  AAAGCGAAAA  ACGACTGCTG  TCTATTGCGA
401  TTTATATCGT  AATGGGCTGG  ATGGTCTTGG  CGGTAATGAA  ATCCCTGACA
451  GCCTCACTCC  CGCCGGCAGG  ACTGGCTTGG  CTGGCGGCAG  GCGGTATGCT
501  GTACAGCGTC  GGCATTTACT  GGTTTGTAAA  CGATGAAAAA  ATCCGACACG
551  GGCACGGAAT  CTGGCATCTG  TTCGTATTGG  GCGGCAGCAT  CACCCAATTT
601  GTCAGCGTGT  ACGGTTACGT  AATCTGA

```

This corresponds to the amino acid sequence <SEQ ID 998; ORF 254.a>:

a254 . pep

```

1  MYTGERFNTY SHLSGLILAA AGLALMLLKT IGHGDGYRIF SVSVYGISLL
51  LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLL SIAIYIVMGW MVLAVMKSLT
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

m254/a254 97.6% identity in 167 aa overlap

					10		20
30							
m254 . pep							
VS	V	S	V	G	I	S	L
VS	V	S	V	G	I	S	L
a254							
H	L	S	G	L	I	L	A
		20		30		40	
70							60
		40		50		60	
90							80
m254 . pep							
K	K	T	D	H	C	M	I
K	K	T	D	H	C	M	I
a254							
K	K	T	D	H	C	M	I
		80		90		100	
130							120
		100		110		120	
150							140
m254 . pep							
I	V	I	Y	V	M	G	W
I	V	I	Y	V	M	G	W
a254							
I	A	I	Y	I	V	M	G
		140		150		160	
190							180
		160					
m254 . pep		V	L	G	G	S	I
		V	L	G	G	S	I
a254		V	L	G	G	S	I
		200					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

586

g255.seq
 1 atggttggac aggaagcctt gcggggtcag ttcgtcgccg tggtcgctgc
 51 cgcggttgcg tacgctgtca aaacctgcgc cgatttccac gcctttgacg
 101 gcgttgatgc ccatcatcgc gtaggcgatt tcggcatcga ggcggtcgaa
 151 aacgggttcg cccaaaccga cggggacgtt ggcggttcg atatgcagtt
 201 tcgcgccgac ggaatccaag gatttgcgca caccgtccat atagtgttcc
 251 agttcggcga tttggctttg gttggcggca aaaaaaggat tttgggaaat
 301 gtgttcgctg ccttcaaacc ggattttttt ttcgcccact tgggtaacgt
 351 aggcggtgat ttccgtgccg aatttttctt tcagccattt tttggcaacg
 401 gctccggcgg caacgcgggc tgcggtttcg cggcggaac tcctgccgcc
 451 gccccggtag tcgcgctac cgtatttctg ccaataggta tagtcggcgt
 501 gtccggggcg gaaggcggcg gcgatgtcgc cgtagtcttc gctgcgctgg
 551 tcggtgttgc ggattag

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

g255.pep
 1 MVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAAHR VGDFGIEAVE
 51 NGFAQTDGDV GGFDMQFRAD GIQGFATVH IVFQFGDLAL VGGKKRILGN
 101 VFAAFKPDPF FADLGNVGGD FRAEFFFQPF FGNGSGGNAG CGFAGGTPAA
 151 APVVARVVFV PIGIVGVSGA EGGDVAVVF AALVGVAD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1001>:

m255.seq
 1 GTGGTTGGAC AGGAAGCCTT GCGGGGTCAG TTCGTGCGCG TGTTGCTGCG
 51 CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCAC GCCTTTGACG
 101 GCGTTGATGC CCATCATCGC GTAGGCGATT TCGGCATCGA GGCGGTCAAA
 151 AACAGGTTTCG CCCAAGCCGA CAGGGACATT GGCTGCTTCG ATATGCAGCT
 201 TCGCGCCGAC GGAATCCAAG GATTGCGCA CGCTGTCCAT ATAGTTTTC
 251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
 301 GTGTTGCGAG CTTCAAACC GGATTCTTTT TTCGCCGACT TGGGTAACGT
 351 AGGCGGTGAT TTCCGTGCCG AATTTTCTT TCAACCATT TTTGGCAACG
 401 GCTCCGGCAG CAACGCGGGC GCGGTTTCA CGGCGGAGC TCCTGCCGCC
 451 GCCCGGTTAG TCGCGCTGC CGTATTGTG CCAATAGGTA TAGTCGGCGT
 501 GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
 551 TCGGTATTGC GGATTAA

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

m255.pep
 1 VVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAAHR VGDFGIEAVK
 51 NRFAQADRI GCFDMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN
 101 VFAAFKPDPF FADLGNVGGD FRAEFFFQPF FGNGSGSNAG GGFTGGAPAA
 151 AAVVARAVVF PIGIVGVAGA EAGGDVAVVF AALVGIAD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

m255/g255

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAAHRVGDFGIEAVKNRFAQADRI					
g255	MVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAAHRVGDFGIEAVENGFAQTDGDV					
	10	20	30	40	50	60
m255.pep	GCFDMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDPFFADLGNVGGD					
g255	GGFDMQFRADGIQGFATVHIVFQFGDLALVGGKKRILGNVFAAFKPDPFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	FRAEFFFQPFNGSGSNAGGGFTGGAPAAAAVVARAVFVPIGIVGVAGAEAGGDVAVVF					
g255	FRAEFFFQPFNGSGGNAGCGFAGGTPAAAPVVARVVFPIGIVGVSGAEGGDVAVVF					

587

	130	140	150	160	170	180
	189					
m255 . pep	AALVGIADX					
	:					
g255	AALVGVADX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```

a255 . seq
  1  GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCGG TGTTGCTGTC
 51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCAC GCCTTTGACG
101  GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GGCGGTCGAA
151  TACGGGTTTCG CCAAGCCGA CGGGACGTT GGCGGCTTCA ATATGCAGCT
201  TCGCGCCGAC GGAATCCAAG GATTGCGCA CGCTGTCCAT ATAGTTTCC
251  AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301  GTGTTGCGAG CCTTCAAACC GGATTCTTT TCGCCGACT TGGGTAACGT
351  AGGCGGTGAT TTCCGTGCCG AATTTTCTT TCAACCATTT TTTGGCAACG
401  GCTCCGGCGG CAACGCGGGC GCGGTTTCG CGGGCGGAAC TCCTGCCGCC
451  GCCCCGGTAG TCGCGCGTGC CGTATTGTG CCAATAGGTA TAGTCGCGCT
501  GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551  TCGGTATTGC GGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```

a255 . pep
  1  VVGQEALRGE FVAVFAAALR YAVKTCADFH AFDGVDHHR VGDFGIEAVE
 51  YGFAQADGDV GGFNMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN
101  VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNGSGNAG GGFAGGTPAA
151  APVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*

```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255 . pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVKNRFAQADRDI					
	: : : : : :					
a255	VVGQEALRGEFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVEYGFADGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m255 . pep	GCFDMLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	: : : : : : : : : : :					
a255	GGFNMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m255 . pep	FRAEFFFQPF FGNGSGSNAGGGFTGGAPAAA VVARAVFVPIGIVGVAGAEAGGDVAVVF					
	: : : : : : : : : :					
a255	FRAEFFFQPF FGNGSGSNAGGGFTGGAPAAA VVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
	189					
m255 . pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```

g256 . seq
  1  atgctcgcgg tacgcaatcg gggttggcac ggcgcagtcg tccatttcgg
 51  cagctcgggc ggcgtagcga acaccgcccc ggtgttctac cacttgggtg
101  ataccgccga aatcgccctt gctttggaca cgctcaccgc gcgttaccgt
151  gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201  tttgggcgaa cagggcaaaa aggcattgcc gcacgcctcg gccgccgtat
251  ccgccccgt tgatgcagag gcggcaggca gccgcttcga cagcggcatc
301  acgcggctgc tctacacgcg ctacttcttc cgcacactga taccctaaag

```

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```

351 acgttcgctc caaggttttc agacggcatt tgccgcaggg tgcaaaacac
401 tgggcgagtt tgacgaccgt ttcaccgcac cgctgcacgg ctttgccgac
451 cggcacgact actaccgcca aacttcctgc aaaccgctgc tcaaacacgt
501 tgccaaaccg ctgctcctgc tcaatgccgc caacgacccc ttcctgccgc
551 ccgaagccct gccccgtgca gacgaagcgt ccgaagccgt taccctgttc
601 caacctgcac acggcgggca cgcgggcttt gtgagcagca ccggcgagcag
651 gctgcacctg caatggctgc cgcagaccgt cctgtcctat tttgacagct
701 tccgcacaaa caggcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

```

g256.pep
  1 MLAVNRNGWH GAVVHFRSCG GVANTAPVIFY HLGDTAEIAF ALDTLTARYR
 51 EIYAVGVSLG GNAPAKYLGE QGKKALPHAS AAVSAPVDAE AAGSRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNAANDP FLPPEALPRA DEASEAVTLF
201 QPAHGGHAGF VSSTGGRLLH QWLPQTVLSY FDSFRNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

```

m256.seq
  1 ATGCTTGCGG TACGCGATCG GGGTTGGCAC GCGGTAGTCG TCCATTTCGG
 51 CAGCTGCGGC GGCATTGCCA ACACCGCTCC GGTGTTCTAC CA.CTtGGCG
101 ATACCGCCGA AATCGCCTTT ACTTTGGACA CGTTCGCCGC GCGTTACCGT
151 GAAAtATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCAAAA AGGCATTGCC GCAAGCCGCT GCCGTCATCT
251 CCGCCCCCGT CGATGCAGAG GCGGCAGGCA GACGCTTCGA CAGCGGCATC
301 ACGCGGCTGC TCTACACGCG CTACTTCCTC CGCACCTGA TACCCAAAGC
351 AAAATCGCTC CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGC TTCACCGCAC CGCTGCACGG CTTTGCCGAC
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCCCT GCCCGCGCA GACGAAGTAT CCGAAGCCGT TACCCTGTTC
601 CAGCCGGCAT ATGGTGGTCA TGTGGGCTTT GTCAGCAGCA CCGGCGGAG
651 GCTGCACCTG CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

```

m256.pep
  1 MLAVRDRGWH GVVHFRSCG GIANTAPVIFY XLGDTAEIAF TLDTFAARYR
 51 EIYAVGVSLG GNALAKYLGE QGKKALPQAA AVISAPVDAE AAGRRFDSGI
101 TRLLYTRYFL RTLIPKAKSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPAYGGHGVF VSSTGGRLLH QWLPQTVLSY FDSFRNRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

```

m256/g256
      10      20      30      40      50      60
m256.pep MLAVRDRGWHGVVHFRSCGGIANTAPVIFYHLGDTAEIAFTLDTFAARYREIYAVGVSLG
      |||||:|||||:|||||||:|||||||:|||||||:|||||||:|||||||
g256      MLAVNRNGWHGAVVHFRSCGGVANTAPVIFYHLGDTAEIAFALDTLTARYREIYAVGVSLG
      10      20      30      40      50      60

      70      80      90     100     110     120
m256.pep GNALAKYLGEQGKKALPQAAVISAPVDAEAAGRRFDSGITRLLYTRYFLRTLIPKAKSL
      ||| |||||:|||||:|:|:|:||||| |||||:|||||:|||||:|
g256      GNAPAKYLGEQGKKALPHASAAVSAPVDAEAAGSRFDSGITRLLYTRYFLRTLIPKARSL
      70      80      90     100     110     120

      130     140     150     160     170     180
m256.pep QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLLNAVNDP
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|
g256      QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLLNAANDP

```

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	130	140	150	160	170	180
	190	200	210	220	230	240
m256 . pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

```

a256 . seq
1   ATGCTCGCGG TACGCGATCG GGGTTGGAAC GGCCTAGTCG TCCATTTCCG
51  CAGCTGCGGC GCGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACCGCCGA AATTGCCTTT ACTTTGGACA CGCTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGCTGCC GCAAGCCGCC GCCGTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCCGCGCA GACGAAGTGT CCGAAGCCGT TACCCTGTTC
601 CAGCCGACAC ACGGTGGTCA TGTGGGCTTT GTCGGCAGCA CCGGCGGCAG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

```

a256 . pep
1   MLAVRDRGWN GVVVHFRSCG GVANTAPVFY HLGDTAEIAF TLDTLAARYR
51  EIYAVGVSLG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSCI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVGF VGSTGGRLHL QWLPQTVLSY FDSFRTNRR*

```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256 . pep	MLAVRDRGWHGVVVHFRSCGGIANTAPVFYXLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
a256	MLAVRDRGWNGVVVHFRSCGGVANTAPVFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256 . pep	GNALAKYLGEQKKALPQAAVISAPVDAEAAGRFRD SGITRLLYTRYFLRTLIPKARSL					
	: : : : :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAAGRFRD SGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256 . pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRH DYYRQTSC KPLLKHVAKP LLLNNAVNDP					
	: : : : :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRH DYYRQTSC KPLLKHVAKP LLLNNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256 . pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGFVGSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

```

g256-1 . seq
1   ATGATTTTGA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACA CCGGCACCC GCATACCGCC

```

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```

101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CCAAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTTCGCC CGATGCGCCG CTGGTCGTGC TGTTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTCGAACTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GGCGCAGTCG TCCATTTCGG CAGCTGCGGC
301 GGCGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACCGC GCGTTACCGT GAAATATACG
401 CCGTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCCTCG GCCGCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACGCCCA AACTTCCTGC AAACCGCTGC TCAAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCTTGCCGC CCGAAGCCCT
801 GCGCCGTGCA GACGAAGCGT CCGAAGCCGT TACCCTGTTT CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CCGGCGGCAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTTGACAGCT TCCGCACAAA
951 CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVNRGWH GAVVHFRSCG
101 GVANTAPVFI HLGDTAEIAF ALDTLTARYR EIYAVGVSLG GNAPAKYLGE
151 QGKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG KTLGEFDDR FTAPLHGFAD RHDYRQTSC KPLLKHVAKP
251 LLLNAANDP FLPEALPRA DEASEAVTLF QPAHGGHAGF VSSTGGRLHL
301 QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCCGCGCCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTGCCCCGA TGGCGCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGCAGCC ATTACGCGGT CGAACTGATG CTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTCCGCGAG CTGCGGCGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAATATTT GGGCGAACAG
451 GGCACAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCGTCGA
501 TGAGAGGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAGC CGGCTGCTCT
551 ACACGCGCTA CTCTCTCCGC ACCCTGATAC CCAAAGCAA ATCGCTCCAA
601 GGTTTTCAGA CGCATTTCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCTTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCGGCCCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CCTGTTCCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGCTGCCGC AGACCGTCCT GTCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVRDRGWHG VVVHFRSCGG
101 IANTAPVFIH LGDTAEIAFT LDTFAARYRE IYAVGVSLGG NALAKYLGEQ
151 GKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFADR HDYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHVGFEV SSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

          10      20      30      40      50      59
m256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
          |||||:|||||:|||||:|||||:|||||:|||||
g256-1      MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
          10      20      30      40      50      60
          60      70      80      90     100     110     119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVRDRGWHGVVHFRSCGGIANTAPVFIHLGDTAEIAF

```

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```

g256-1      |||||:|||||:|||||:|||||:|||||:|||||:
            LVVLFHGLEGSSRSYAVELMLAVRNRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
            70      80      90      100     110     120

m256-1.pep  120      130      140      150      160      170      179
            TLDTF AARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAAGRFRFDSGI
            :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1      ALDRTLARYREIYAVGVSLGGNAPAKYLGEQKKALPHASAAVSAPVDAEAAGSRFDSGI
            130      140      150      160      170      180

m256-1.pep  180      190      200      210      220      230      239
            TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRF TAPLHGFADRHDYYRQTSC
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1      TRLLYTRYFLRTLIPKARS LQGFQTAFAAGCKTLGEFDDRF TAPLHGFADRHDYYRQTSC
            190      200      210      220      230      240

m256-1.pep  240      250      260      270      280      290      299
            KP LLKHVAKP LLLNAVNDPFLPPEALPRAD E VSEAVTLFQPAYGGHVG FVSSTGGRLHL
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1      KP LLKHVAKP LLLNAANDPFLPPEALPRAD EASEAVTLFQPAHGGHAG FVSSTGGRLHL
            250      260      270      280      290      300

m256-1.pep  300      310      319
            QWLPQTVLSYFDSFRTNRRX
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1      QWLPQTVLSYFDSFRTNRRX
            310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1.seq
1  ATGATTTTGA CACCGCCGGA CACACCCTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACG CTCCGCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAACCGC CTACGACTTT
151 TCAGACGGCA TTTGCCCCGA TCGCGCGCTG GTCGTGCTGT TTCACGTTT
201 GGAGGGCGGC AGTGGCAGCC ATTACGCGGT CGAACTGATG CTCGCGGTAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGCGCGC
301 GTAGCGAACA CCGCCCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 TGCCTTTACT TTGGACACGC TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAAATATT GGGCGAACAG
451 GGGCGAAACG CGTGCCGCA AGCCGCGGCC GTCATCTCCG CACCCGTCGA
501 TGCAGAGGCG GCAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGC AACTGATAC CCAAAGCAGG GTCGCTCCAA
601 GGTTCAGCA CGGCATTTGC CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGTTTC ACCGACCCGC TGCACGGCTT TGCCGATCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCGCTGCC
801 CCGCGCAGAC GAAGTGTCG AAGCCGTTAC CCTGTTCCAG CCGACACACG
851 GTGGTCATGT CGGCTTTGTC GGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGTTGCCGC AGACCGTCCT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1.pep
1  MILTPPDTPF FLRNGNADTI AAKFLQRSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVDRGWNG VVVHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVSLGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSGIT RLLYTRYFLR TLI PKARSLQ
201 GFQTAFAGC KTLGEFDDRF TAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PTHGGHVG FV GSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

a256-1.pep  10      20      30      40      50      60
            MILTPPDTPF FLRNGNADTI AAKFLQRSAPAYRRELLPDSTGKTKTAYDFS DGISPDAPL
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m256-1      MILTPPDTPF FLRNGNADTI AAKFLQRPAPAYRRELLPDSTGKTKVAYDFS DGISPDAPL
            10      20      30      40      50      60

a256-1.pep  70      80      90      100     110     120
            VVLFHGLEGGSGSHYAVELMLAVDRGWNGVVVHFRSCGGVANTAPVFYHLGDTAEIAFT
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m256-1      VVLFHGLEGSSRSYAVELMLAVDRGWNGVVVHFRSCGGIANTAPVFYHLGDTAEIAFT

```

592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAAVISAPVDAEAAAGNRFDSGIT					
m256-1	LDTFAARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAAAGRRFDSGIT					
	130	140	150	160	170	180
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYRQTSCK					
m256-1	RLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYRQTSCK					
	190	200	210	220	230	240
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPTHGGHVGFVGSTGGRLHLQ					
m256-1	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGFVSSTGGRLHLQ					
	250	260	270	280	290	300
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	WLPQTVLSYFDSFRTNRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

```

g257.seq
1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaacg caacatggat aaaaaacgcg atgaaaatgt gtttttctgg
151 aaagggtgctg cgctgggttc cggcgcgagg ctgcgcctgt tcggcggtgga
201 cgacagacag gcggcggatt tgggtcaataa ggttttggcg gaagtggcgc
251 gtttggaataa aatgttcagc ctttaccgtg aagacagcct gatcagccgt
301 ctgaaccgcg acggttatct gacttcgcct ccggcggatt ttttgaact
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

```

g257.pep
1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMFS LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIFTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

```

m257.seq
1  ATGGGCAGGC ATTTTCGGGCG .CAGCGTTTT CTGACGGTTG CCGCCGTTGC
51  GGCGGGGgAc. GCGGcGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAAATGT GTTTTTCTGG
151 AAAGGTGTCG CACTGGGTTC CGGTGCGGa. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA ATTGTTTACG CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCCG TCGGCGGATT TTTTGGAACT
351 GkTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

```

m257.pep
1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNMD EKRDENVFFW
51  KGVALGSGAX LRLFGVDDRR AADLVNKLVA EVARLEKLFS LYREDSLISR
101 LNRDGYLTSP SADFLELXSL AAIFTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10

20

30

40

50

60

593

```

m257.pep  MGRHFGRRFLTVAAVAAGTAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALLGSGAD
          |||||:||||:||||:||||| |||||:||||:||||:|||||
g257      MGRHFGRRRFLTAAAVAVAGAAVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVALLGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDLSISRLNRDGYLTSPSADFLLELXSL
          |||||:||||:||||:||||| |||||:||||:||||:|||||
g257      LRLFGVDDRQAADLVNKKVLAEEVARLEKMFSLYREDLSISRLNRDGYLTSPPADFLLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC  ATTTTCGGGCG  CAGGCGTTTT  TTGACAGTTG  CCGCCGTTGC
51  GCGGCGGGGC  GCGGCGGTTT  CTTTCCTGCC  GAATCCTTTT  GCCGCCGATG
101 ATGAAAAACG  CAATAAAGAT  GAAAAACGCA  ATGAAAATGT  GTTTTTCTGG
151 AAAGGTGTCG  CACTGGGTTC  CGGTGCGGAG  CTCCGTCTGT  TCGGTGTGGA
201 CGACAGGCGT  GCGGCGGATT  TGGTCAACAA  GGTTTTGGCG  GAAGTGGCGC
251 GTTTGGAAAA  AATGTTTCAGC  CTTTACCGTG  AAGACAGCCT  GATCAGCCGT
301 CTGAACCGTG  ACGGTTATTT  GACTTCGCCG  CCGGCGGATT  TTTTGGAAC
351 GTTGAGCCTG  GCCGTGATAT  TCACGCGCTG  A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF  LTVAAVAAAG  AAVSFLPNPF  AADDEKRNKD  EKRNENVFFW
51  KGVALGSGAE  LRLFGVDDRR  AADLVNKKVLA  EVARLEKMFS  LYREDLSISR
101 LNRDGYLTSP  PADFLELLSL  AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGXQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALLGSGAX
          |||||      :|||||||:      |||||
|||
a257      MGRHFGRRRFLTVAAVAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALLGSGAE
          10      20      30      40      50
60

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDLSISRLNRDGYLTSPSADFLLELXSL
          |||||:||||:||||:||||| |||||:||||:||||:|||||
||
a257      LRLFGVDDRRRAADLVNKKVLAEEVARLEKMFSLYREDLSISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTXX
          |||||
a257      AVIFTRX

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

```

g258.seq
1   atgcgccgct tcctaccgat cgcagccata tgcgccgtcg tcctgctgta
51  cggattgacg gcggcgaccg gcagcaccag ttcgctggcg gattattttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctgggtgt gtccgccggt
151 ttggcacggt atgtcatatt gctgttgaaa gacaggcgca acggcgtggt
201 cggttcgtag attgccaaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttctcg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggccgcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgcccc
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgaccaaatc cgaccagccg cttcccgaca aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgtaa agcataggcg gcgtattgta
651 cgcgcaggga tggttgtcgg caggtacgca caacggggcg gattacgcgc
701 tgttcttccg ccagccgatt cccgaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gaaaaaagg
801 tttgcagacc tttttctggt taaccctgct gattgcctcg ctgctgtcga
851 ttttcttgcg gctggtaatg gcaactgtat ttgcccgcg tttcgtcgaa
901 cccattctgt cgtttgccga gggcgcaaag gcggtggcgc aggggtgattt
951 cagccagacg cgccccgtat tgcgcaacga cgagttcgga cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcgga ggaagccgcc cgtcactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctentacccc ctctcttggt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctcccctct ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

```

g258.pep
1   MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVL SAV
51  LARYVILLK  DRRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVVPQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGVSRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKKGLQT FFLVTLIIAS LLSIFLALVM ALYFARRFVE
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVDLG LTTGVVVSYP LSCCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

```

m258.seq
1   ATGCGCCGTT TTCTACCGAT CGCAGCCATA TCGCCCGTCG TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTTCT
101 GGTGGATTGT TCGGTCAGC GCAATGCTGC TGCTGGTGTG GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTCGCAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCCG CGTGTTTCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTTG AGCAAGTCCG CATTGAATTT GCGGCGAGAC AACGCCCTCG
401 GCAACGCCGT CCCCCTGCAG ATAGACCTCA TCGGCGCGCG TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGCG TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCTT
701 TGTTTTCCG TCGCCGCTT CCCAAAGGCG TGGCAGAGGA TGCCGCTTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTCTCTGG CAACCCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCGCGCG TTTCGTCGAA
901 CCCGTCCTAT CGCTTGCCGA GGGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TCGCAACGA CGAGTTCGGA CGCTTGACCA

```

595

```

1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGGCATTATC TTGAATGCGT
1101 GTTGAGAGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAACsTT CAACAAAGCG GCGGAACAGA TTyTGGGGAT GCCGCTTACC
1201 CCCcTGTGGG GCAGCAGCCG GCACGGTTGG CACGCGCTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGCAACg GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAAA GAAGCCGCGT
1451 GGGGCGAAgT GGCGaAgCGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCCGCCGA ACgGsTGGCG TkGAAATTGG GCGGGAAGCT
1551 GGATGAGCAG GATGCGCAAA TCCTGACGCG TTCGACCGAC ACCATCGTCA
1601 AACAGGTGGC GGCATTGAAG GAAATGGTCG AAGCATTCCG CAATTATGCG
1651 CGTTCCCTT CGCTCAAATT GGAAAATCAG GATTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTATG AAGCCGGTCC GTGCCGTTTT GCGGCGGACT
1751 TGCCGGCGAA CCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

m258.pep

```

1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51 LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSQAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAVVPQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QRAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEFVFAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERXA XKLGGKLEDEQ DAQILTRSTD TIVKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AADLPANR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

m258/g258

```

              10      20      30      40      50      60
m258.pep  MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAVLARYVILLLK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVSFS AMLLLVLSAVLARYVILLLK
              10      20      30      40      50      60

              70      80      90     100     110     120
m258.pep  DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSQAQFINGTINSWFGNDTHEALERSLNL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      DRRNGVFGSQIAKRLSGMFTLVAVLPGFLFLFGISAQFINGTINSWFGNDTHEALERSLNL
              70      80      90     100     110     120

              130     140     150     160     170     180
m258.pep  SKSALNLAADNALGNAVVPQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      SKSALDLAADNAVSNVAVPQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK
              130     140     150     160     170     180

              190     200     210     220     230     240
m258.pep  SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGR DYALFFRQPV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      SINPHQFDQPLPDKEHWEIQQTGSVRSLESIGGVLYAQGWLSAGTHNGR DYALFFRQPI
              190     200     210     220     230     240

```

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	250	260	270	280	290	300
m258 . pep	PKGVAEDAVLIEKARAKYAELSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE					
g258	PENVAQDAVLIEKARAKYAELSYSKKGLQTFVLVTLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258 . pep	PVLSLAEGAKAVAQGDIFSQTRPVLNRNDEFGRLTCLFNHMTQLSIAKEADERNRRREEAA					
g258	PILSLAEGAKAVAQGDIFSQTRPVLNRNDEFGRLTCLFNHMTQLSIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258 . pep	RHYLECVLEGLTTGVVVFDEQGCLKTFNKAEEQILGMPLTPLWGSSRHGWHGVSAQQSLL					
g258	RHYLECVLDGLTTGVVVSYPVLSCCRTAVFSTCHSSPLSYFX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1027>:

```

a258 . seq
1   ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTTCT
101 GGTGGATTGT TCGGTTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGCAG ATTGCCAAAC GCCTTTCGCG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTTTCTG TTCGGCGTTT CCGCACAGTT TATCAACGGC
301 ACGATTAATT CGTGTTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTG AGCAAGTCCG CATTGAATCT GGCGGCAGAC AACGCCCTTG
401 GCAACGCCAT CCCCCTGCAG ATAGACCTCA TCGCGCGCGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACAGGCGG GTTCGGTCAG GGATTTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CAGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTTCCTGG CAACCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCGCGCG TTTCGTCGAA
901 CCCGTCCTAT CGCTTGCCGA GGGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TGCGCAACGA CGAGTTCGGA CGCTTGACCA
1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGACATTATC TCGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACCTT CAACAAAGCG GCGGAACAGA TTTTGGGGAT GCCGCTTACC
1201 CCCCTGTGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACG GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAAA GAAGCCGCGT
1451 GGGGCGAAGT GGCAAAACGG CTGGCACACG AAATCCGCAA TCCGCTCAGC
1501 CCCATCCAGC TTTCTGCCGA ACGGCTGGCG TGGAAATTGG GCGGGAAGCT
1551 GGACGAGCAG GACGCGCAA TCCTGACACG TTCGACCGAC ACCATCATCA
1601 AACAAGTGGC GGCATTAAAA GAAATGGTCG AGGCATTCCG CAATTACGCG
1651 CGTTCCCTT CGCTCAAATT GGAAAATCAG GATTTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTACG AAGCTGGTCC GTGCCGTTT GCGGCGGAAC
1751 TTGCCGGCGA ACCGCTGATG ATGGCGGCGG ATACGACCGC CATGCGGCAG
1801 GTGCTGCACA ATATTTTCAA AAATGCCGCC GAAGCGGCGG AAGAAGCCGA
1851 TGTGCCCCGAA GTCAGGGTAA AATCGGAAGC GGGGAGGAC GGACGGATTG
1901 TCCTGACAGT TTGCGACAAC GGCAAGGGGT TCGGAGGGA AATGCTGCAC
1951 AATGCTTCG AGCGTATGT AACGGACAAA CCGGCTGGAA CCGGATTGGG
2001 ACTGCCCGTG GTGAAAAAAA TCATTGAAGA ACACGGCGGC CGCATCAGCC
2051 TGAGCAATCA GGATGCGGGC GGCGCGTGTG TCAGAATCAT CTTGCCAAAA
2101 ACGGTAGAAA CTTATGCGTA G

```

m258/a258 99.0% identity in 584 aa overlap

		10	20	30	40	50	60
m258.pep		MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVAFSAML	LLVL	SAVLARYVILL	LLK		
a258		MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVAFSAML	LLVL	SAVLARYVILL	LLK		
		10	20	30	40	50	60
		70	80	90	100	110	120
m258.pep		DRRDGVFGSQIAKRLSGMFTLVAVLP	PGVFLFGV	SAQFINGTINSWFGNDTHEALERS	LN		
a258		DRRDGVFGSQIAKRLSGMFTLVAVLP	PGVFLFGV	SAQFINGTINSWFGNDTHEALERS	LN		
		70	80	90	100	110	120
		130	140	150	160	170	180
m258.pep		SKSALNLAADNALGNAV	PVQIDLIGAASLP	PGDMGRVLEHYAGSG	FAQLALYNAASG	KIEK	
a258		SKSALNLAADNALGNAI	PVQIDLIGAASLP	PGDMGRVLEHYAGSG	FAQLALYNAASG	KIEK	
		130	140	150	160	170	180
		190	200	210	220	230	240
m258.pep		SINPHKLDQPFPGKARWEKI	QRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQ	PV			
a258		SINPHKLDQPFPGKARWEKI	QAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQ	PV			
		190	200	210	220	230	240
		250	260	270	280	290	300
m258.pep		PKGVAEDAVLIEKARAKYAEL	SYSKGLQTF	FLATLLIASLLSIFLALVMALYFARRFVE			
a258		PKGVAEDAVLIEKARAKYAEL	SYSKGLQTF	FLATLLIASLLSIFLALVMALYFARRFVE			
		250	260	270	280	290	300
		310	320	330	340	350	360
m258.pep		PVLSLAEGAKAVAQGD	FSQTRPVLNRNDEFGR	LTKLFNHMT	EQLSIAKEADERNRRREEAA		
a258		PVLSLAEGAKAVAQGD	FSQTRPVLNRNDEFGR	LTKLFNHMT	EQLSIAKEADERNRRREEAA		
		310	320	330	340	350	360
		370	380	390	400	410	420
m258.pep		RHYLECVLEGLTTGVVV	FDEQGCLKTFNKAAEQILGMPLT	PLWGSSRHGWHGVSAQQSLL			
a258		RHYLECVLEGLTTGVVV	FDEQGCLKTFNKAAEQILGMPLT	PLWGSSRHGWHGVSAQQSLL			
		370	380	390	400	410	420
		430	440	450	460	470	480
m258.pep		AEVFAAIGAAAGTDKPVHV	KYAAPPDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK				
a258		AEVFAAIGAAAGTDKPVHV	KYAAPPDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK				

598

	430	440	450	460	470	480
	490	500	510	520	530	540
m258.pep	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDITIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDITIKQVAALK					
	490	500	510	520	530	540
	550	560	570	580	589	
m258.pep	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNIFKNAAEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

g259.seq

```

1  atgatgatgc acgcttctgt ccaaagtcgt ttgcgaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaactctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgccgtc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaattgctc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccg acgacgaaga cgcgcgcacg attgccgccg
401 agttggcaaa aatggatatg ttgcgattgg ggacggacgc ggtcgccctc
451 ggcgaaacct atgggcgcgt gttcgccgat attttcgagt tgcggcgccg
501 tttggaagg cgcgcggtca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtga gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

g259.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKKHLRRC LPFGNGVGF
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

m259.seq (partial)

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTCGTG TCGGCGCGTT CAAAGGCCAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTcAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACkGACGC GGTcGCCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGmGGC
501 TTTGGAAGGG CGCGCGTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGmGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

m259.pep (partial)

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```

599

151 GETYGRVFAD IFELSALEG RAFKGLMLKT AEYKXHLRRC LPFGNGVGVG
 201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAFAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAFAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGKMAEQVRFKAE					
	:					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGKMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSALEGRAFKGMLKLT					
g259	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALERRAFKGILKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRC LPFGNGVGVGRTQSGVAGDFKNIR					
g259	AEYKXHLRRC LPFGNGVGVGRTQSGVAGDFKNIR					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1	ATGATGATGC	ACGCTTCTGT	CCAAAGCCGT	TTCGCACCGA	TACTTTATGT
51	TTTGATTTTC	TTTGCCGGTT	TTTTGACCGC	GCAAATCTGG	TTCAATCAGA
101	AAGCCTATAC	TGAAGAGCTG	CCTCCGCTTC	TGTCCGCATT	GTCCGCCGTC
151	GCGCTGGTGT	GGCTGGCGTG	GGCGTTCGTG	TCGGCGCGTT	CAAAGGCTAA
201	GGCGGAAAAG	TTCTACCGCG	AAAAAATGAT	ACAGAACGAA	AGCATACACC
251	CCGTCCTGCA	CGCTTCTTTG	CAACACTTGG	AACACAAGCC	GCAAATGCTC
301	GCCCTGCTGG	TCAAAAACCA	CGGCAAAGGG	ATGGCGGAAC	AGGTCAGGTT
351	CAAGGCGGAA	GTGCTGCCCG	ACGACGAAGA	CGCGCGCACG	ATTGCCGCCG
401	AGTTGGCAAA	AATGGATATG	TTTGCAATTG	GGACGGACGC	GGTCGCCTCG
451	GGCGAAACCT	ATGGACGCGT	GTTCGCCGAT	ATTTTCGAGT	TGTCGGCGGC
501	TTTGGAAGGG	CGCGCGTTCA	AAGGAATGTT	GAAACTGACG	GCGGAATATA
551	AAAA.CATCT	TCGCGGATGC	CTGCCGTTTC	GAAACGGCGT	TGGAGTTGGG
601	CGCGCTCAAT	CAGGCGTTGC	AGGAGATTTT	AAAAACATCG	GAAAAGTCCA
651	A				

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1	MMMHASVQSR	FAPILYVLIF	FAGFLTAQIW	FNQKAYTEEL	PPLLSALSAV
51	ALVWLAFAFV	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQML
101	ALLVKNHKGK	MAEQVRFKAE	VLPDDEDART	IAAELAKMDM	FALGTD AVAS
151	GETYGRVFAD	IFELSALEG	RAFKGMLKLT	AEYKXHLRRC	LPFGNGVGVG
201	RAQSGVAGDF	KNIGKVQ			

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAFAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAFAFV					

600

	10	20	30	40	50	60
m259.pep	70	80	90	100	110	120
	SARSKAKAEKFYREKMIQNESIHVPVXHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
a259						
	SARSKAKAEKFYREKMIQNESIHVPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
m259.pep	130	140	150	160	170	180
	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSALEGRAFGMLKLT					
a259						
	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSAALEGRAFGMLKLT					
	130	140	150	160	170	180
m259.pep	190	200	210			
	AEYKXHLRRCLPFGNGVGVGRTQSGVAGDFKNIR					
a259						
	AEYKXHLRRCLPFGNGVGVGRAQSGVAGDFKNIGKVQ					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCGTG TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCAGAACCT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCAGAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGCGCATGCC TGCCGTTCGG AAACGGCGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTTC A AACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKMLKLT AEYKNIFGDA CRSETALELG
201 ALNQAQLEIS KTSEKSKRIF Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

```

      10      20      30      40      50      60
g259-1.pep  MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
|||||
m259-1      MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
      10      20      30      40      50      60

      70      80      90     100     110     120
g259-1.pep  SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE
|:|||||
m259-1      SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE
      70      80      90     100     110     120

      130     140     150     160     169
g259-1.pep  VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSAALE
|||||
m259-1      VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSAALEGRAFGMLKLT
      130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

```

a259-1.seq
1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCGATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCGTG TCGCGCGGTT CAAAGGCTAA
201 GCGCGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGCGGCG
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCCG AAACGCGGTT GGAGTTGGGC
601 GCGCTCAATC AGGCGTTGCA GGAGATTCA AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

```

a259-1.pep
1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQLAQEIS KTSEKSKRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

```

      10      20      30      40      50      60
a259-1.pep  MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
|||||
m259-1      MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
      10      20      30      40      50      60

      70      80      90     100     110     120
a259-1.pep  SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE
|||||
m259-1      SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE
      70      80      90     100     110     120

      130     140     150     160     170     180
a259-1.pep  VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSAALEGRAFGMLKLT
|||||
m259-1      VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSAALEGRAFGMLKLT
      130     140     150     160     170     180

      190     200     210     220
a259-1.pep  AEYKNIFGDACRSETALELGALNQLAQEISKTSKSKRIFYX
|||||
m259-1      AEYKNIFGDACRSETALELGALNQLAQEISKTSKSKRIFYX
      190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

602

```

1  atgggtgctg  gtgtagtatt  cgttgctctt  cagccgttct  tcagcctggt
51  tcgagcggtg  ttcgagggcg  gagtcggtat  agtcgagggg  gcgcacgatg
101 ccgctgaatg  cgacttcttg  tccgaggaat  ttaccctgat  ccggatcggt
151 gatgttttta  ttgattcggg  aggtcagata  acggcccggg  tctttcaggg
201 ctttggtgta  aaccctggcg  cctttgggtg  acagcagcct  gccttccggg
251 cccgagagca  ggcgcgggcg  ggcagcggtt  tctttgctgg  aaacgatttg
301 cgggtgctgc  ataaagacgc  ggtagaagtt  gacatcgatg  gcgggaatac
351 cgtatccgga  cacttcctta  tccggactga  ttttgacgac  ggggatgccc
401 tctgtctggt  ccaagccgag  gcgcgggttc  ccgccaacgt  agcgcaacac
451 caatacctgg  cccggataaa  tcaggtcggg  attgtggatt  tgatcccggg
501 tcgcgcccc  caggggggga  ccattgccac  gggctgtaca  ggtatttgcc
551 cgaaataccc  cacagggtgt  cgccctgttt  ga

```

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

g260.pep

```

1  MGAGVVFVVF  QPFFSLFRAL  FEGGVGIVEG  AHDAAECDL  SEEFTRIRIG
51  DVFIDSVGQI  TARFFQAFGV  NPGAFGVQQP  AFRAREQARR  GSGFFAGNDL
101 RVLHKDAVEV  DIDGGNTVSG  HFLIRTFDD  GDAVCLFQAE  ARFAANVAQH
151 QYLARINQVG  IVDLIPVRAP  QGGTIATGCT  GICPKYPTGC  RPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

```

1  ATGGGTGCGG  GTATGGTATT  CGTTGTCTTT  CGGCCGTTCT  CCAGCCTGTT
51  TCGAGCGTTG  TTCGAGGACA  GAGTCGGTAT  AGTCGAGGGA  GCGCACGATG
101 CCGCTGAATG  CGACTTCCTG  CCCGAGGAAT  TTACCCGTAT  CCGGATCGGT
151 GATGTTTSTA  TTGATTCGGT  AGGTCAGGTA  GCGGCCCGGC  TCTTTCAGGC
201 CTTTGGTGTA  AACCCTGGTG  CCTTGGTGT  ACAGCAGCCT  GCCTTCCGGG
251 CCCGAGwCA  SGCGCGGyGC  GGCAGCGGTT  TCTTTCGGG  AAACGATTTG
301 CGGATCCGCG  ATAAAGATGC  GGTAGAAGTT  GACATCGATG  GCGGGAATAC
351 CGTATCCGGA  CACTTCCTTA  TCCGGACTCA  TTTTGACGAC  GGGGATGCCG
401 TCTGTCTGTT  CCAAGCCGAG  GCGCGGTTTC  CCGTCAACGT  GGCGCAACAC
451 CAATACCTGG  TCCGATAAAA  TCAGGTCGGG  ATTGTGGATT  TGATCCCGGT
501 TCGCGTyCCA  CAG

```

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260.pep

```

1  MGAGMVVFVVF  RPFSSLFRL  FEDRVGIVEG  AHDAAECDL  PEEFTRIRIG
51  DVFIDSVGVV  AARLFQAFGV  NPGAFGVQQP  AFRARXXARX  GSGFFAGNDL
101 RMPHKDAVEV  DIDGGNTVSG  HFLIRTHFDD  GDAVCLFQAE  ARFAVNVAQH
151 QYLVRINQVG  IVDLIPVRVP  Q

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFSSLFRLFEDRVGIVEGAHDAAECDLPEEFTRIRIGDVFIDSVGVV					
	: : :					
g260	MGAGVVFVVFQPFFSLFRALFEGGVGIVEGAHDAAECDLSEEFTRIRIGDVFIDSVGQI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
	: : :					
g260	TARFFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVLHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVRINQVGIVDLIPVRVPQ					
	: : :					
g260	HFLIRTFDDGDAVCLFQAEARFAANVAQHQYLARINQVGIVDLIPVRAPQGGTIATGCT					
	130	140	150	160	170	180

603

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

```
a260.seq
  1 ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
 51 TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CCACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GGCGCGGCGC GGCAGCGGTT TCTTTGCGGG AAACGATTGT
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTTC CCGTCAACGT GGCGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTTGCC
551 CGAAATGCCC CACAGGTGTG CGCCCTGTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

```
a260.pep
  1 MGAGMVFFVF RPFSSLFRAL FEDRVGIVEG AHDAAECDLF PEEFTRIRIG
 51 DVFIDSVGQV AARLFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVPKDAVEV DIDGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*
```

m260/a260 97.1% identity in 171 aa overlap

```

      10      20      30      40      50      60
m260.pep  MGAGMVFFVFRPFSSLFRALFEDRVGIVEGAHDAAECDLFPEEFTRIRIGDVFIDSVGQV
          |||
a260      MGAGMVFFVFRPFSSLFRALFEDRVGIVEGAHDAAECDLFPEEFTRIRIGDVFIDSVGQV
          |||

      70      80      90     100     110     120
m260.pep  AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGNTVSG
          |||
a260      AARLFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGNTVSG
          |||

      130     140     150     160     170
m260.pep  HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVRINQVGIVDLIPVRVPQ
          |||
a260      HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVINQVGIVDLIPVRVPQAAXIATGCT
          |||

a260      GICPKCPTGCRPVX
          190
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

```
g261.seq
  1 atggagcttg ggcataatcgt attccttctg ctttgcgcg gttcagacgg
 51 cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctcgggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctgttcgctg atgtagtcca acacgcccac ttcgtccgcc aacgcccacg
201 tttgcgcctt ggtcaggtag atcagcgggc tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcacg gatttgacga acacgcccgcg
301 gcagtcggga tagcccgaaa aatcggttgc gcacacgccc gcgatgatgt
351 gccggatacc ctgcccttgg gcaaaaatgg cggcgtaaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgttg cggcggtttc
451 gatggcggcg gtttcgatgg cggcggttgc gtccatcagg gcgttgtgctg
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttccagc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgccgtag gtttgattg
```

604

651 cctgaatcag gcaggtgggc gaatcctgac cgcccagaaa gatgaccaag
701 gctttttggt ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep
1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG
51 LFADVQHAH FVRQRPRLRL GQVHQRRVDL KIVVHRQIKG NVHGFDEHAA
101 AVGIARKIGF AHARDDVPDT LPFGKNGGVK QEKRVTPVHK GIGNAVVGGF
151 DGGGFDGGGF VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP
201 VSEGDLDFV APVGLDCLNQ AGGRILTARE DDQGFLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq
1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTCGCGCT GTTCAGACGG
51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGcCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCACGCCCAT TTCGTCCGCC AACGCCACG
201 TTTGCGCCTT GGTCAGATAC ATCAGCGCGC TGTGGATTG AAAATCATAG
251 TCCATCGCCA AATTAAGGGT AACGTCATC GATTTGACAA ACACGTCGCG
301 GCAGTCGCGA TAGCCGGAGA AGTCGGTTTC GCACACGCCG GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 gCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GgCTcAAGTC GAGTACGGTT TGTTTGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GCCTTGGACG TTTTCGCGCC CGTAGGTTT GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep
1 MELGHIVFLM VCACSDGLFT FOIFRQPAFA QDTARAFAAA ADDAVIAGVG
51 LLADIVQHAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHRFDKHVA
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAPVGL DCLNQAGGRI LTARKDDQGL LV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/g261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
	:: ::: ::					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVQHAH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA AVGIAGEVGF AHARDDVPYP					
	:: :: ::					
g261	FVRQRPRLRLGQVHQRRVDLKIVVHRQIKGNVHGFDEHAA AVGIARKIGF AHARDDVPDT					
	70	80	90	100	110	120
	130	140	150	160	170	
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGV-----VHQGIVRNLPHQAVVEYGLF					
	:: ::					
g261	LPFGKNGGVKQEKRVTPVHKGIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAVIEYGLT					
	130	140	150	160	170	180
	180	190	200	210	220	230
m261.pep	DAQILRNPAFTQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGLLVX					
	: : : ::					
g261	DTQILRDPLCAFQLDGMALPVSEGDLDFVAPVGLDCLNQAGGRILTAREDDQGFLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1   ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGC GCGT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAAG
201 TTTGCGCCTT GGTCAGATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGAGA AGTCGGTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGT TGTTCGACGC CCAAATCTG CGCAATCCAG
551 CGGCGACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTG GATTGCCTGA ATCAGGCAGG
651 TGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1   MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPSLRL GQIHQRRVDL KIIVHRQIKG NVHGFDKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAQV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAPVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQRAH					
	10	20	30	40	50	60
m261.pep	FVRQRPRRLRGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAGVIAGEVGFHAHARDDVPYP					
a261	FVRQRPSLRLRGQIHQRRVDLKIIVHRQIKGNVHGFDKHVTAVGIAGEVGFHAHARDDVPYP					
	70	80	90	100	110	120
m261.pep	FVRQRPRRLRGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAGVIAGEVGFHAHARDDVPYP					
a261	FVRQRPSLRLRGQIHQRRVDLKIIVHRQIKGNVHGFDKHVTAVGIAGEVGFHAHARDDVPYP					
	70	80	90	100	110	120
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAQVEYGLFDAQIL					
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAQVEYGLFDAQIL					
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAQVEYGLFDAQIL					
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAQVEYGLFDAQIL					
	130	140	150	160	170	180
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGFVLX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1   atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgcca
51  accgcgcgta gaggcgtac ccaaaaaaa cggctttatc cccaacctca
101 tcggcgattt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgccgcaa cagcctgacc gccggcgaag tcgaagtgat
201 ccggatcatc gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acaccaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgcccgcg ctttggcggc aggtaaatct gacgatgcca aactcggcgc
351 gcttgccgcc ttcaccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

g263.pep

1	MARLTVHTLE	TAPEAAKPRV	EAVPKNNGFI	PNLIGVLANA	PEALAFYQEV
51	GKLNAANSLT	AGEVEVIRII	AVTRNQCSFC	VAGHTKLATL	KKLLSEQSLN
101	AARALAAGKS	DDAKLGALAA	FQTQVMACKG	AVSDDELNAF	LEAGYNRQQA
151	VEVVMGVALA	TLCNYANNLA	QTEINPKLQA	YA*	

```
m263.seq (partial)
1 ..GCAGCAGGCG AATTTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC
51 CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101 CATTTTTCGA TCGCGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG
151 GGCCT.AsyC TtGCAACCCT GTGCAACTAC GTCAACAACC TCGGACAAAC
201 CGAAATCAAC CCGAATTGC AGGCTTACGC CTGA
```

```
m263.pep (partial)
1 ..GCAGCAGGCG AATTTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC
51 CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101 CATTTTTCGA TCGCGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG
151 GCGGT.AsyC TgGCAACCTT GTGCAACTAC GTCAACAACC TCGGACAAAC
201 CGAAATCAAC CCGGAATTGC AGGCTTACGC CTGA
```

ORF 263 shows 85.7% identity over a 77 aa overlap with a predicted ORF (ORF 263.ng) from *N. gonorrhoeae*:

m263/g263

m263.pep
AAGEFDDAKLGALAAFTQAVMAKKGAVSDE
|||:|||||

g263
QCSFCVAGHTKLATLKKLLSEQSLNAARALAAGKSDDAKLGALAAFTQAVMAKKGAVSDD
80 90 100 110 120 130

m263.pep
ELKAFFDAGYNQQQAVEVVMGVXLATLCNYVNNLGQTEINPELQAYAX
||:|||||

g263
ELNAFLEAGYNRQQAVEVVMGVALATLCNYANNLAQTEINPKLQAYAX
140 150 160 170 180

a263.seq

1	ATGGCACGTT	TAACCGTACA	CACCCTCGAA	ACCGCCCCCG	AAGCCGCCAA
51	AGCGCGCGTC	GAGGCGGTAC	TTCAAAACAA	CGGCTTTATC	CCCAACCTTA
101	TCGGCGTATT	ATCAAACGCG	CCCGAAGCCT	TGGCGTTTTA	CCAAGAAGTC
151	GGCAAGTCA	ACGCCGCCAA	CAGCCTGACC	CGCGCGCAAG	TCGAAGTAAT
201	CCAGATTATT	GCCGCGCCGA	CCAACCAATG	CGGCTTCTGC	TGGCAGGGC
251	ACACCAAAC	CGCAACCCTG	AAAAAACTCC	TTTCCGAACA	ATCCGTCAAA
301	GCCGCGCGCG	CTTTGGCGGC	AGGCGAATTT	GACGATGCTA	AACTCGGCGC
351	GCTCGCCGCC	TTTACCCAAG	CCGTAATGGC	AAAAAAAGGC	GCGGTATCCG
401	ACGAGGAAC	CAAGCATTT	TTTGTATGCG	GCTACAACCA	GCAGCAGGCA
451	GTCGAAGTCG	TGATGGCGCT	AGCCTTGGCA	ACTTTGTGCA	ACTACGTCAA
501	CAACCTCGGA	CAAACCGAAA	TCAACCCCGA	ATTGCAGGCT	TACGCCTGA

a263.pep

1	MARLTVHTLE	TAPEAAKARV	EAVLQNNGFI	PNLIGVLSNA	PEALAFYQEV
51	GKLNAANSLT	AGEVEVIQII	AARTNQCGFI	VAGHTKLATL	KKLLSEQSVK
101	AARALAAGEF	DDAKLGALAA	FTQAVMAKKG	AVSDEELKAF	FDAGYNQQQA
151	VEVVMGVALA	TLCNYVNNLG	OTEINPELOA	YA*	

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m263/a263 97.4% identity in 77 aa overlap

					10	20	30
m263.pep					AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
a263	QCGFCVAGHTKLATLKKLLSEQSVKAARALAAAGEFDDAKLGALAAFTQAVMAKKGAVSDE						
	80	90	100	110	120	130*	
		40	50	60	70		
m263.pep	ELKAFFDAGYNQQQAVEVVMGXLLATLCNYYVNNLGQTEINPELQAYAX						
a263	ELKAFFDAGYNQQQAVEVVMGVALATLCNYYVNNLGQTEINPELQAYAX						
	140	150	160	170	180		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

g264.seq

1	ttgactttaa	cccgaataaac	ccttttcttc	ctcaccgccc	cgttcggcac
51	acactccctt	cagacggcat	ccgcccgcgc	agtgggtcaag	ccggaataaac
101	tgcacgcctc	cgccaaccgc	agctacaaag	tcgccgaatt	cacgcaaac
151	ggcaacgcct	cgtggtacgg	cggcagggtt	cacgggacga	aaacttccgg
201	cggagaccgc	tacgatatga	acgcctttac	cgccgcccac	aaaaccctgc
251	ccatccccag	ccatgtgcgc	gtaaccaaca	ccaaaaacgg	caaaagcgtc
301	atcgctccgc	tcaacgaccg	cgcccccttc	cacggcaacc	gcacatcaga
351	cgtatccaaa	gccgcccgcg	aaaaattggg	ctttgtcagc	caaggacgg
401	cacacgtcaa	aatcgaaaca	atcgctccgc	gccaatccgc	accggttgcc
451	gaaaacaaag	acatctttat	cgacttgaaa	tctttcggtg	cggaacacga
501	agcacaagcc	tatctgaacc	aagccgcccc	aaatttcgcc	gcttcgcat
551	caagcccga	cctctcggtt	gaaaaacgcc	gttacgaata	cgttgtcaaa
601	atgggcccgt	ttgcctcgca	ggaacgcgcc	gccgaagccg	aagcgcaggc
651	acgcggtatg	gttcgggcgg	tactgacctc	cggttgga	

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

g264.pep

1	<u>LTLTRKTLFL</u>	<u>LTAAFGTHSL</u>	<u>QTASADAVVK</u>	PEKLHASANR	SYKVAEFTQT
51	GNASWYGGRF	HGRKTSGGDR	YDMNAFTA AH	KTLPPIPSHVR	VTNTKNGKSV
101	IVRVNDRGPF	HGNRIIDVSK	AAAQKLGFVS	QGTAVHKIEQ	IVPGQSAPVA
151	ENKIDIFIDLK	SFGTEHEAQA	YLNQAAQNFA	ASSSSPNLSV	EKRREYEVVK
201	MGPFSQERA	AEAEAQARGM	VRAVLTS*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

m264.seq

1	TTGACTTTAA	CCCAGAAAAC	CCTTTTCCTT	CTCACC GCCG	CATTCCGGCAC
51	ACACTCCCTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAAG	GCAGAAAAC
101	TGCACGCCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGAAG	ACGCTACACG
151	CCGAAAAC	AAGTCGCCGA	ATTACGCAA	ACCGGCAACG	CCTCGTGGTA
201	CGCGGCAGG	TTTCACGGGC	GCAAACTTC	CGCGGAGAA	CGATACGATA
251	TGAACGCCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTATCGTCC	CGGTCAACGA
351	CCGCCGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCCG
401	CGCAAAAT	GGGCTTTGTC	AACCAAGGGA	CGGCACACGT	CAAAATCGAA
451	CAAATCGTCC	CGGGCCAATC	CGCACCGGTT	GCCGAAAACA	AAGACATCTT
501	TATCGACTTG	AAATCTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAACTTC	GCCGTTTCGT	CATCGGGTAC	GAACCTCTCG
601	GTTGAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTACCTC
651	GCAGGAACGC	GCCGCCGAAG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTGAC	CGCCGGCTGA			

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

1	<u>LTLTRKTLFL</u>	<u>LTAAFGTHSL</u>	<u>QTASADAVVK</u>	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTS GGE	RYDMNAFTA A	HKTLPPIPSYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAAQKLGFV	NQGTAVHKIE
151	QIVPGQSAPV	AENKIDIFIDL	KSFGEHEAQ	AYLNQAAQNF	AVSSSGTNLS
201	VEKRREYEVV	KMGPFSQER	AAEAEQAARG	MVRAVLTA*	

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTS GGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHGRKTS GGDYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFGEHEAQ					
g264	FHGNRIIDVSKAAQKLG FVSQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFGEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGT NLSVEKRRYEYVVKMGPF TSQERAAEAE AQARGMVR AVLTAGX					
g264	AYLNQAAQNFAASSSP NLSVEKRRYEYVVKMGPF ASQERAAEAE AQARGMVR AVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

1	TTGACTTTAA	CCCGAAAAAC	CCTTTTCCTC	CTCACC GCG	CATTCCGCAT
51	ACATTCCTTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAGG	GCAGAAAAAC
101	TGCACGCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGA	ACGCTACACG
151	CCGAAAAACC	AAGTCGCCGA	ATTCACGCAA	ACCGGCAACG	CCTCGTGGTA
201	CGGCGGCAGG	TTCACGGGC	GCAAACTTC	CGGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTCATCGTCC	GCGTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCCG
401	CGCAAAAATT	GGGCTTTGTC	AACCAAGGGA	CGGCGCACGT	CAAAATCGAA
451	CAAATCGTCC	CGGGCCAATC	CGCACC GGTT	GCCGAAAACA	AAGACATCTT
501	CATCGACTTG	AAATCTTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAAACCTG	GCTTCATCGG	CATCAAACCC	GAACCTCTCG
601	GTTGAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTGCCTC
651	GCAGGAACGC	GCCGCCGAGG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTAAC	CGCCGGTTGA			

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

1	LTLTRKTLFL	LTAAFGIHSF	QTASADAVVR	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTS GGE	RYDMNAFTA	AHKTLPISYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAQKLG FV	NQGT AHVKIE
151	QIVPGQSAPV	AENKDIFIDL	KSFGTEHEAQ	AYLNQAAQNL	ASSASNP NLS
201	VEKRRYEYVV	KMGPFASQER	AAEAE AQARG	MVRAVLTAG*	

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAAQKLGFVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ					
a264	FHGNRIIDVSKAAAQKLGFVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPFTSQERAAEAEAQARGMVRVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPFASQERAAEAEAQARGMVRVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```

m265 . seq
  1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
 51  GGCGCGGCTG ATGATTTTGT CTTGTTTGTT GTGTTGGTGT GCGGCGTGTC
101  CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151  ATGCTCAGCA GTGCGGTTGC GCGCGAGGTC AAGAGAAGGT GTTTGATGTT
201  CATAT.TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251  AGGTATCAAA TAACCGTCAG CCGCGCGTCA ATACCGCCCG AACCATACCG
301  CGCGCCTGAG CTTCGGCTTC GGCGGCGCGT TCCTGCGAGG TAAACGGTCC
351  CATTTTGACG ACGTATTCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```

m265 . pep
  1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
 51  MLSSAVAAEV KRRCLMFI XF AFVNRGLENV DINKVSNRQ PAVNTARTIP
101  RAXASASAAR SCEVNGPILT TYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGA EMLSSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGA EMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFAFVNRGLENVDINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

m265/a265 79.7% identity in 123 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

```
m266.seq
1  ATGCCGTTCC  GCAACGCGtT  cAGACGGCAT  CGCCGCCGAC  AACGCCTAAA
51  CAGAAAGCCC  ACCATGACCG  CATCCATGTA  CATCCTTTTG  GTCTTGGCAC
101 TCATCTTTGC  CAACGCGCCC  TTCCTACAGA  CCAGACTGTT  CGCGGTGGCC
151 rCACTCAAGC  GCAAACATTT  CGGACACCAC  ATGATCGAGC  TGGCGGCAGG
201 TTTTCGCGTG  ACCGCCGTTT  TTGCCTACAT  CCTsGAATCC  CGTGCAGGAT
251 CGGTACACGA  TCAGGGTTGG  GAGTTTTATG  CCACAGTCGT  CTGCCTGTAC
301 CTGATTTTTG  CGTTTCCATG  TTTTGTGTGG  CGGTATTTTT  GGCACACCGG
351 CAACAGGGA  TAG
```

611

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

```
m266/g266

      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||
g266      MQFRRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
          10      20      30      40      50

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          :|||
g266      LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          60      70      80      90      100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCCT
101  TGATTTTTGC CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTCGAATCC CGTGCGGGAG
251  CGGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTG CGTTCCCTG TTTCTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```
      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||
a266      MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTLKLGIVPLKRKHFGHH
          10      20      30      40      50      60

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          :|||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          70      80      90      100     110     120

m266.pep  X
          |
a266      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

```
g267.seq
```

612

```

1  atgcaagtcg ccttttttct cgccgtggta ttcaaaaata tgggtttcca
51  caatcgcatc ggtcgggcag gcctcttcgc agaaaccgca gaagatgcac
101 ttggtcaggt cgatgtcgta acgcttgggtg cggcgggtgc cgtcttcgcg
151 ttcttccgat tcgatgttga tcgccattgc cggacacacc gcctcgaca
201 atttacacgc gatgcagcgt tcctctccgt tcggaaaacg gcgttgcgcg
251 tgcagaccgc ggaaacgcac ggattgcggc gttttctctt cgggaaaata
301 aattgtgtct ttgcgggcaa aaaagttttt gagcgttacg cccatgcctt
351 tgaccagttc gccaaagcaga aaggttttta ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1076; ORF 267.ng>:

g267.pep

```

1  MQVAFFLAVV FKNMGFHNRI GRAGLFAETA EDALGQVDVV TLGAAGAVFA
51  FFRFDVDRHC RTHRLAQFTR DAAFLSVRKT ALRVQTAETH GLRRFLFGKI
101 NCVFAGKKVF ERYAHAFDQF AKQKGFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1077>:

m267.seq

```

1  GTGCAAGTCG CCTTTTTTCT CGCCGTGGTA TTCAAAAATA TGGGTTTCCA
51  CAATCGCATC AGTCGGGCAT GCCTCTTCGC AGAAACCGCA GAAGATGCAC
101 TTGGTCAGGT CGATGTCGTA ACGCTTGGTG CGGCGCGTAC CGTCTTCACG
151 TTCTCCGAT TCGATGTTAA TCGCCATTGC CGGACACACT GCCTCACACA
201 ACTTACACGC GATACACCGC TCTTCGCCGT TCGGATACCG CcGCTGCGCG
251 TGCAGACCGC GGAAACGCAC GGATTGCGGC GTTTTCTCTT CGGGGAAATA
301 AATTGTGTCT TTGCGGGCGA AAAAGTTTTT GAGCGTTACG CCCATACCTT
351 TTACCAATTC GCCAAGCAGA AAGGTTTTTA CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1078; ORF 267>:

m267.pep

```

1  VQVAFFLAVV FKNMGFHNRI SRACLFAETA EDALGQVDVV TLGAARTVFT
51  FFRFDVNRHC RTHCLTQLTR DTPLFAVRIP PLRVQTAETH GLRRFLFGEI
101 NCVFAGEKVF ERYAHTFYQF AKQKGFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 267 shows 82.7% identity over a 127 aa overlap with a predicted ORF (ORF 267.ng) from *N. gonorrhoeae*:

m267/g267

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI SRACLFAETAEDALGQVDVVTLGAARTVFTFFRFDVNRHC					
	: : : : : : : : : :					
g267	MQVAFFLAVVFKNMGFHNRI GRAGLFAETAEDALGQVDVVTLGAAGAVFAFFRFDVDRHC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPLFAVRIPPLRVQTAETHGLRRFLFGEINCVFAGEKVFERYAHTFYQF					
	: :					
g267	RTHRLAQFTRDAAFLSVRKTALRVQTAETHGLRRFLFGKINCVFAGKKVFERYAHAFDQF					
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
g267	AKQKGFYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1079>:

a267.seq

```

1  GTGCAAGTCG CCTTTTTTCT CGCCGTGGTA TTCAAAAATA TGGGTTTCCA
51  CAATCGCATC GGTcgggcag GCTTCTTCGC AGAAACCGCA GAAGATGCAC
101 TTGGTCAGGT CGATGTCGTA ACGCTTGGTG CGGCGCGTGC CGTCTTCGCG
151 TTCTCCGAT TCGATGTTGA TCGCCATTGC GGGGCAAACG GCTTCACACA
201 ATTTACACGC GATGCAGCGT TCCTCGCCGT TTGGATAACG GCGTTGCGCG
251 TGCAGACCGC GGAAACGCAC GGATTGCGGC GTTTTCTCTT CGGGAAAATA
301 AATCGTGTCT TTGCGGGCAA AAAAGTTTTT GAGCGTTACG CCCATACCTT
351 TTACCAATTC GCCAAGCAGA AAGGTTTTTA CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLF	FAETAEDALGQVDVV	TLGAARTV	FTFFRFDVNRHC	
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFA	FFRFDVDRHC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTP	FAVRIPPLRVQTAETH	GLRRFLFGEIN	CVFAGEKVFERYAHTFYQF		
a267	GANGFTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFLFGKINRV	FAGKKVFERYAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaatatt
101 cctgcggaag cgaagagact aaagagattt tgggtcaaact ggtccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251 gtttggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccgcacga
351 tgttgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaaagccc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaaagcaa
501 aatctttgccc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctggtgtc tatggcactg attaaagagc cgttggacaa agcgaaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgaggga
651 ggcagaagaa gcggcggcgc aggaggcatt gggctcgggag caggaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctgcgagaaa acatggaaaa gcggtatgga caagatctgt gccacaatg
851 cgaaaagccga aggtgaaacg ccaaacggca taaaagttag tgagttggcg
901 tgtaaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLGINPFSG KEISCGSEET KEILVKLVRD
51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101 SSKLKCEAAL KLDVPDDVD YAVAANQSIG NSHKKTPDF EPYRKEGAY
151 YVKTISYSVQ PTDDSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAAEA TAQAREAE EAAAQALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLQASQK TWKSGMDKIC ANNAKAEGT PNGIKVSELA
301 CKTAETEARL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGGACAAA GTGAAACAAA GGAACGAAGA
```

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```

51   ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101  AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTGCGCG
151  AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201  GCTGCAACcN TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251  CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCAGC
301  GAACTGGCAT GCAAAACGGC GAAAACCGAA GCACGCTTGG AAGAGCTGCA
351  CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401  AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1   .MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAARVS EWEERYKLSR
51  XQFEQFWKGL PQTVQNKLP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

                                10      20
m268.pep                      MALIKEPLDKVKQRNEELEAAE-----
                                |||:|||:|||:|||:|||:|||:|||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
          160      170      180      190      200      210

                                30      40      50      60      70      80
m268.pep  --EAAAQEALGREQEAARVSEWEERYKLSRSQFEQFWKGLPQTVQNKLPQSQKTWKSMD
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      AEEAAAQEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQNKLPQASQKTWKSMD
          220      230      240      250      260      270

                                90      100     110     120     130     140
m268.pep  KICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      KICANNAKAEGETPNIGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

a268.seq

```

1   ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTGCGCG
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GGAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

a268.pep

```

1   MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTVQNKLP SQKTWKSMD KICANNAKAE GETPNIGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

                                10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAAEEAAAQEALGREQEAARVSEWEERYKLSRXQFEQFWKGL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a268      MALIKEPLDKAKQRNEELEAAEEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

615

	10	20	30	40	50	60
	70	80	90	100	110	120
m268.pep	PQTVQNKLQPSQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
	: : : : : : : : : : : : : : : :					
a268	PQTVQNKLQASQKTWKSMDKICANNAKAEGETPNGIKFSELACKTAETEARLEELHNRK					
	70	80	90	100	110	120
	130	140				
m268.pep	KALIDEMKREADKKELSKRLX					
	:					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAAGCTG ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.pep

```

1  VQSRDGLHK FKHICSAAMA LIKEPLDKVK QRNEELEAAE EAAAEALGR
51  EQEAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLQASQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

		10	20	30	
m268-1.pep		VQSRDGLHKFKHICSAAMALIKEPLDKVKQRNE			
		: : : : : : : : : : : : : : : : :			
g268	KEGAYVVKTISYSVQPTDDKSKIFAELSQAHDIIHPLSELVS--MALIKEPLDKAKQRNE				
	150	160	170	180	190
	200				
	40	50	60	70	80
m268-1.pep	ELEAAE-----EAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
	: : : : : : : : : : : : : : : : :				
g268	KLEAAEATAQEAREAEAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
	210	220	230	240	250
	260				
	90	100	110	120	130
m268-1.pep	KLQASQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDE				
	: : : : : : : : : : : : : : : :				
g268	KLQASQKTWKSMDKICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDE				
	270	280	290	300	310
	320				
	150	159			
m268-1.pep	MAREADKKELSKRLX				
	:				
g268	MVREEDKKELPKRLX				
	330				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAAGCTG ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAC CGAAGCACGC TTGGAAGAGC

```

401 TGCACAACCG TAAAAAGCC CTTCTCGACG AAATGGCCAG GGAAGCGGAC
 451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep

1 VQSRDGLHK FKHICSAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR
 51 EQEVDVSEW EERYKLSRSE FEQFWKGLPQ TVQNKQASQ KTWKSGMDKI
 101 CANNAKAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LLEDEMAREAD
 151 KKELPKRL*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHICSAAMALIKEPLDKAKQRNEELEAAE	EAEEAAAEALGREQ	EQEVDVSEW			
m268-1	VQSRDGLHKFKHICSAAMALIKEPLDKVQRNEELEAAE	EAEEAAAEALGREQ	EAARVSEW			
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKQASQKTWKSMDKICANNAKAEGE	TPNGIKFSEL				
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKQASQKTWKSMDKICANNAKAEGK	TPNGIKFSEL				
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKAL	LLEDEMAREAD	KKELPKRLX			
m268-1	ACKTAKTEARLEELHNRKKAL	LLEDEMAREAD	KKELSKRLX			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq

1 atggttttggc gtgtgaattg cgcggcaacg gcggcgctga ttttttcgct
 51 cagcccttgg atttgggcgg tgggtgtgggt gtggtcgcgg tcggcttttt
 101 cctgcaaac ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttggcg
 151 gtttcgccgt gggactttat ccggaacacg gtttcgccca aggtgtcggc
 201 ggctttgatg cacagtttta aaaccagggc tttggggcgg ttttctgcgc
 251 cgcccggttg cattttgtctg tccaatcgcg ggggttaaaaa accgttgcgc
 301 ttaagtgcg cgtccgtcca agtcgatacg agcgcgcttc tttgccttcc
 351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep

1 MWVRVNCAAT AALIFSSSPW IWAVVWWSR SAFSCKPCAS LDASSAPALA
 51 VSPWDFIRNT ASPKVSALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS
 101 FKSPSVQVDT SALLCLSLRS S*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq

1 ATGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
 51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGTCTCGG TCGGCTTTGT
 101 CTTGCAAAACC TTGCGCcaCG TGCCCGCGTC CAGCGCCTGC GTTGATGGTT
 151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTCGGCGGC
 201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCGCCGC
 251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTCGTTT
 301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT
 351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep

1 MWVRVNCAAT AVLIFSSSPW IWAIVWWSR SALSCKPCAT CPRPAPALMV
 51 SPWDFIQNTA SPKVSALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF
 101 KFSSVQVDT SALLCLSLRS *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

```

m269.pep  MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT  59
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g269      MVWRVNCAATAALIFSSSPWIWAVVWVWSRSASFCKPCASLDASSAPALAVSPWDFIRNT  60

m269.pep  ASPKVSAAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT SALLCLSLRS 119
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g269      ASPKVSAAALMHSFKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDT SALLCLSLRS 120

m269.pep  SX 121
          ||
g269      SX 122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269.seq
1   ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51  CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCCGCGT CCAGCGCGCC GCGGTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTAA AAACCAGGGC TTTGGGGCGG TTTTCGTCGC
251 CGCCTGTGCG CATTGTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTTGTGCG
301 TTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269.pep
1   MVWRVNCAAT AVLIFSSSPW IWAAVWVWAR SALSWRFCAS VPASSAPALT
51  VSPWDFIQNT ASPKVSAAALM HSFKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

          10      20      30      40      50      59
m269.pep  MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a269      MVWRVNCAATAVLIFSSSPWIWAAVWVWARSALSWRFCASVPASSAPALTVSPWDFIQNT
          10      20      30      40      50      60

          60      70      80      90      100     110     119
m269.pep  ASPKVSAAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT SALLCLSLRS
          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a269      ASPKVSAAALMHSFKTRALGRFSSPPVAILLSGRGVKKPLSFKFSSVQVDT SALLCLSLWS
          70      80      90      100     110     120

          120
m269.pep  SX
          ||
a269      SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270.seq
1   atgaataaaa accgcaaatt actgcttgcc gcactgetgc tgactgcctt
51  tgccgccttc aagctcgttt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg agggttgcac gctgccggac
151 ggaagccgtg tccgcgccgc cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgccgc ccggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcata cgctgcccgc tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

g270.pep

```

1  MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG Ca. CAGCCGC
101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCGGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTC
401 AGACGGCATT TACCGCCGAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep

```

1  MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRKLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
g270	MNKNRKLLLAALLLTAFAAFKLVLQWWQAQQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARIRLPVCVEGRR					
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG CAGCAGCCGC
101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCCGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTC
401 AGACGGCATT TACCGCCGAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep

```

1  MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
```

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRLLLLAALLLIAFAAVKLVLQWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAS					
a270	MNKNRLLLLAALLLIAFAAVKLVLQWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAS					
	10	20	30	40	50	60
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
a270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
a270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
	70	80	90	100	110	120
m270.pep	DFTADITIGSRTFQTAFTAE					
a270	DFTADITIGSRTFQTAFTAE					
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAE					
a270	DFTADITIGSRTFQTAFTAE					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

1	atgttcagtt	cgcggtatggc	gaggatttgg	gcgacggggg	taacgtttgtg
51	tatggtcagt	ccgtgtccgg	cggtgacgac	caagcccaaa	tcgcccgcga
101	aatgcgcgcc	gttttgatg	cgctcgaaact	gcctgatttg	ttcggcggtg
151	ctttgtgcgt	cgccatatgc	gccggtgtgc	agctcgacaa	cgggcgcgcc
201	gacatcacgg	gcggcttga	tttgccgtgc	gtcggcatcg	ataaacaagg
251	acacgcgat	gcccgcgtcg	gtcaggattt	tggcgaattc	ggcgattttt
301	tcctgttgcg	ccaatacgtc	caaaccgcct	tcggtcgtga	tttcctgccc
351	tttttcaggc	acgatgcaca	cgtcttccgg	catcacttta	agcgcgtttt
401	cgagcatttc	ttccgtcaac	gccatttcaa	ggttcaggcg	cgtgcggatg
451	gcgtttttga	cggcaatac	atccgcgtct	ttgatgtggc	ggcggtcttc
501	gcgcaggtgc	atggtaatca	ggtctgcacc	gtgcgtttcg	gcaaccagtg
551	ccgcctccac	ggggctggga	taa		

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

1	MFSSRMARIW	ATGVTLCMVS	PCPALTTKPK	SPAKCAPFWM	RSNCLICSAW
51	LCASAYAPVC	SSTTGAPTSR	AAWICLSSAS	INKDTRMPAS	VRILANSAIF
101	SCCANTSKPP	SVVISCRFSG	TMHTSSGITL	SAFSSISSVN	AISRFRVRM
151	AFLTANTSAS	LMWRRSSRRC	MVIRSAPCVS	ATSAASTGLG*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

1	AwGTTcagTT	CGCGGATGGC	GAGGATTtGG	GCGATGGGGG	TAACGTTGTG
51	TATGGTCAGT	CCGTGTCCGG	CGTTGACGAC	CAAGCCCAAA	TCGCGGCGGA
101	AATGCGCGCC	GTTTTGGATG	CGCTCGAACT	GCCTGATTtG	TTcGGCGTGG
151	CTGCGCGCGT	CGGCATACGC	GCCTGTGTGC	AGCTCGACAA	CGGGCGCGCC
201	GACATCACGG	GCGGCTTGA	TTTGCCTGTC	GTCGGCATCG	ATAAACAAAG
251	ACACGCGTAT	GCCTGCGTCG	GTCAGGATTt	TGGTGAACCC	GGCGATTtTT
301	TCCTGTTGCG	CCAATACGTC	CAAACCGCCT	TCGTCGTGA	TTTCCTGACG
351	TTTTTCAGGC	ACGATGCACA	CGTCTTCCGG	CATCACTtTC	AAAGCGTtTT
401	CCAACATTTC	TTCCGTCAAC	GCCATTtCAA	GGTTcAGGCG	CGTGCgGATG
451	GCGTTTTTGA	CGGCAACAC	GTCCGCGTCT	TTGATGTGGC	GGCGGTCTTC
501	GCGCAGGTGC	ATGGTAATCA	AATCCGCACC	GTGCGTtTCG	GCAACcAGTG
551	CCGCTCCAC	GGGCTGGGA	TAA		

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

1	XFSSRMARIW	AMGVTLCMVS	PCPALTTKPK	SPAKCAPFWM	RSNCLICSAW
51	LRASAYAPVC	SSTTGAPTSR	AAWICLSSAS	INKDTRMPAS	VRILVNPAIF
101	SCCANTSKPP	SVVISXRFSG	TMHTSSGITF	KAFSNISSVN	AISRFRVRM
151	AFLTANTSAS	LMWRRSSRRC	MVIKSAPCVS	ATSAASTGLG *	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLCASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSAIFSCCANTSKPPSVVISCRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITLFAFSNISVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAAPCVS					
g271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271.seq

1	ATGTT	CAGTT	CGCGG	ATGGC	GAGGA	TTTGG	GCGAT	GGGGG	TAACG	TTGTG
51	TATGG	TCACT	CCGTG	TCCGG	CGTTG	ACGAC	CAAGC	CCCAA	TCGCT	GGCAA
101	AATGC	GCGCC	GTTTG	GATG	CGCTC	GAACT	GCCTG	ATTG	TTCGG	CGTGG
151	CTGCG	CGCGT	CGGCA	TACGC	GCCTG	TGTC	AGCTC	GACAA	CGGGC	GCGCC
201	GACAT	CACGG	GCGGC	TTGGA	TTTGC	CTGTC	GTCGG	CATCG	ATAAA	CAAGG
251	ACACG	CGTAT	GCCCG	CGTCG	GTCAG	GATTT	TGGTG	AATTC	GGCAAT	TTTG
301	TCTTG	TTGCG	CCAAT	ACGTC	CAAGC	CGCCT	TCGGT	CGTGA	TTTCT	GACG
351	TTTTT	CCGGC	ACGAT	GCACA	CGTCT	TCCGG	CATCA	CTTTA	AGCGC	GTTTT
401	CGAGC	ATTTC	TTCCG	TCAAC	GCCAT	TTCAA	GGTTC	CAGGC	CGTGC	GGATG
451	GCGTT	TTTGA	CAGCA	AACAC	GTCCG	CGTCT	TTGAT	GTGGC	GGCGG	TCTTC
501	GCGCA	GGTGC	ATGGA	TATCA	GGTCG	GCACC	GTGCG	TTTCG	GCAAC	CAGTG
551	CCGCT	CCAC	GGGCT	GGGA	TAA					

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271.pep

1	MFSSRMARIW	AMGVTL	CMVS	PCPAL	TTKPK	SLAKCAP	FWM	RSNCLICSAW
51	LRASAYAPVC	SSTTGAPT	SR	AAWICL	SSAS	INKDTRMP	PAS	VRILVNSAIL
101	SCCANTSKPP	SVVIS*	RFSG	TMHTSSGITL	SAFSSISSVN	AISRFRVR	RM	
151	AFLTANTSAS	LMWRRSS	RRRC	MVIRSA	PCVS	ATSAASTGLG	*	

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTSKPPSVVISXRFSG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIKSAPCVS					
a271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1   atgactgcaa aggaagaact gttcgcattg ctgcgccata tgaacaaaaa
51  caaagggttcc gacctgtttg tgacgaccca tttcccgccc gctatgaagc
101 tggacggcaa aatcacccgc atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgctttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcattcgacc aacgagtgca atttcgccat cagcctgccg gacaccagcc
251 gcttccgcgt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccttgaag gatgttgccg tgaaaaaacg cgggctggtt atttttgtcg
401 gcggcaccgg ctcgggcaaa tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcadc accatcgaag atccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgcg gaggtcggcg
551 tggacacgga aaactggatg gcggcggtga aaaatacgct gcgtcaggcg
601 ccggaatgta tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctcgaccgca tcatcaactt cttccccgag
751 gagcggcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatttcgcaa cgctcgttc cgcgagacgg cggcaaggcg aggggtggcg
851 cagtgcagggt gctgctcaat tcgccccgta tttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggaatgcctt gaaatgccc attccgcaca tgatttgctg
1051 ttggcggtac agttgcgcag ccgcagggca caaagttccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1   MTAKEELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESLNLPALK DVALKKRGLV IFVGGTGSOK STSLASLIDY
151 RNENSGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMDT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1   ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCG GACCTGTTTC TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GCGGAAAAAA
151 TGTATGGAAA TCGCTTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAaaaaaac CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTTCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG

```

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```

551 TGGATACGGA AAACCTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATTG GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTGA TTTGGAGTT GATTACAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAATGCCG ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CAaAGTTyCA GCCCCGATT
1101 GGnACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272 . pep

```

1  MTAKEELFAW LRHMxQNKGs DLFVTTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAM IORGATALVF
101 RTITSKIPKF ESLNLPVLK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAlA FAETGHLcMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLyQLYE KGDISLQEAL KNADSAHDLR
351 LAVQLRSRRA QSXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

m272 . pep	10	20	30	40	50	60
	MTAKEELFAWLRHMxQNKGsDLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
g272	MTAKEELFAWLRHMKNKNKGsDLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
m272 . pep	70	80	90	100	110	120
	AKQAEFSSTNECNFAISLPDTSRFRVNAMIORGATALVFRTITSKIPKFESLNLPPVLK					
g272	AKQAEFSSTNECNFAISLPDTSRFRVNAMIORGATALVFRAITSKIPKFESLNLPPALK					
	70	80	90	100	110	120
m272 . pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
g272	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180
m272 . pep	190	200	210	220	230	240
	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAlAFAETGHLcMATLHANSTNQA					
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAlAFAETGHLcMATLHANSTNQA					
	190	200	210	220	230	240
m272 . pep	250	260	270	280	290	300
	LDRIINFFPEERREQLLTDLSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
g272	LDRIINFFPEERREQLLTDLSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
m272 . pep	310	320	330	340	350	360
	GNIHEIKEVMKKSTTLGMQTFDQHLyQLYEKGDISLQEALKNADSAHDLRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGMQTFDQHLyQLYEKGEISLQDALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360

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```

          370
m272.pep  QSXSPDLXLLX
          || :||| |||
g272      QSSDPDLELLX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272.seq
1   ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCG TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GCGGAAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTTCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AAAGTGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGGAG
751 GAGCGGCGCG AACCAATTGCT GACGGATTTC TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGCA GGATGCCTTG AAAAAATGCC ATTCCGCACA CGATTTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTCCG GTCCCGATTT
1101 GGAAGTGTCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272.pep
1   MTAKEELFAW LRHMNKNKGS DLFVTHFPF AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTGSGK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHLMA TLHANSTNQA LDRIINFFPE
251 ERREQLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

          10      20      30      40      50      60
m272.pep  MTAKEELFAWLRHMNKNKGS DLFVTHFPFAMKLDGKITRITDEPLTAEKCM EIAFSIMS
          ||||| :|||||
a272      MTAKEELFAWLRHMNKNKGS DLFVTHFPFAMKLDGKITRITDEPLTAEKCM EIAFSIMS
          10      20      30      40      50      60

          70      80      90     100     110     120
m272.pep  AKQAEFFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRITITSKIPKFESLNLPVVK
          ||||| :|||||
a272      AKQAEFFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRITITSKIPKFESLNLPVVK
          70      80      90     100     110     120

          130     140     150     160     170     180
m272.pep  DVALKKRGLVIFVGGTGSGKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
          ||||| :|||||
a272      DVALKKRGLVIFVGGTGSGKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
          130     140     150     160     170     180

```

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	190	200	210	220	230	240
m272 . pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272						
	190	200	210	220	230	240
	250	260	270	280	290	300
m272 . pep	LDRIINFFPEERREQLLDLSNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFFPEERREQLLDLSNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272 . pep	GNIHEIKEVMKKSTTLGMQTFDQHLQLYEKGDISLQEALKNADSAHDLRLAVQLRSRRA					
a272	GNIHEIKEVMKKSTTLGMQTFDQHLQLYEKGEISLQDALKNADSAHDLRLAVQLRSRQA					
	310	320	330	340	350	360
	370					
m272 . pep	QXSPDLXLLX					
	:					
a272	QSSGPDLELLX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

g273 . seq

```

1  atgagtccttc aggcgggtatt tatatacccc ccaagccgta ccgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcaccg ttttcctgcc gttcttctgt gcttttgaaa taaaggatga
201 tgccggcaag cagcgcggca gccgcgcccgc acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aacccgcccgc gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcggggcgc gtgcccgtga aatcaaggcg
351 gtttgagaag tgtttccnac gcgcccgcgc tatgtgccga aatattatct
401 tgcgctcacc tgcaaaatcg ccaagaacgc gctttgcgga atttcacgt
451 tgcccacttg tttcatacgg cgtttgccctg cttttgttt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

g273 . pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHTDRR QDIGVFEAGT
51  PFTVFLPFLV AFEIKDDAGK QRGSRRARWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRREFK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

m273 . seq

```

1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCCCG TTTTCCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT TGTGTTCATT
251 GTTGTTCCTT AATGCTTAAA AACCCGCTG TCCGTGCAAC CGTTTTAAGG
301 CGGCAAATTG CAAAATTGT TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTCCCGAC GCGCCGCCCT GTGTGCCGGA GTTATTGTGTC
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACCTGTTT CATACGGCGT TTACCTGCCT TTTGtKtWTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

m273 . pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHADRC QDIGVFKAGT
51  PFPVFLPLL V AFEIKDDAGK QRGSRRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRRAALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSY A*

```

Computer analysis of this amino acid sequence gave the following results:

m273/g273

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

m273/a273 80.1% identity in 171 aa overlap

		10	20	30	40	50	60						
m273.pep		MSLQAVFIYPPSR	TAQYNE	NQENG	GKAHKQ	QSGKHADRC	QDIGVF	KAGT	PPFVFL	PLL	V		
a273		MSLQAVFVYPPSR	TAQYNE	NQENG	GKAHKQ	QSGKHADRR	QDIGVF	QTGT	PFTVFL	PLF	V		
		10	20	30	40	50	60						
		70	80	90	100	110	119						
m273.pep		AFEIKDDAGK	QGRS	RARHXH	CVHCCS	MLKNPP	VRATVL	-RRQIA	KFVCG	RVPLK	SGRFE		
a273		AFEIKDDAGK	QGRS	RARHXH	NVHCCS	LTVKNPP	VRATV	FKRRX	ITKFV	GGRALL	QSGRFK		
		70	80	90	100	110	120						
		120	130	140	150	160	170						
m273.pep		GCSRRAAL	CAGVIC	RS	PAKSP	TRTFAE	FP	HCPLV	SYG	VYLF	VFVQAV	FSYAX	
			:	:	:								
a273		GHDALPRV	-PDI	ICRS	PAKL	PRTRF	AGF	P	HCPLV	SYG	VCLLF	VVFQAV	FSYAX
		130	140	150	160	170							

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

```
g274.seq
  1  ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTTTTTGT
 51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101  GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151  CATATCGGGG TGCAGGTCCT CATTCTCCG GATATGAATG CGGCAAAAGT
201  GTTTGTCCGgc ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251  TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301  GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTgt tcaaAACCT
351  TCCGCCGCC AACCCTGGT ATGTGCGCGT GGAggacgCG GCAGGCGTGT
401  GGCgcGTCGA GAACAAATGG ATTACCAGCC AGGGCAATGC GGTGATTTG
451  ACCCCGATGG ACAAACTTTT CAATAATGCA GGAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

```
g274.pep
  1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
 51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101  GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVWRVENKW ITSQGNVAVL
151  TPMDKLFNNA GSK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

```
m274.seq
  1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
 51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101  GCAAACATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151  CATATCGGGG TGCAGGTTCT CATTCCCCC GATATGAATG CGGCAAAAGT
201  GTTTGTCCGgc GCGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251  TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301  GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAAACCCT
351  TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401  GCGCGCTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGATTTG
451  ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

```
m274.pep
  1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
 51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101  GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQGNVAVL
151  TPMDKLFNNT ESK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

```
g274/m274

      10      20      30      40      50      60
g274.pep  MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP
          |||
m274      MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP
          |||

      10      20      30      40      50      60
g274.pep  DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA
          |||
m274      DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSP
          |||

      70      80      90     100     110     120
g274.pep  DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA
          |||
m274      DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSP
          |||

      70      80      90     100     110     120
g274.pep  DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA
          |||
m274      DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSP
          |||

      130     140     150     160
g274.pep  NHWYVRVEDAAGVWRVENKWITSQGNVAVLTPMDKLFNNAGSKX
          |||
m274      NHWYVRVEDAAGVWRVENKWITSQGNVAVLTPMDKLFNNNTESKX
          |||

      130     140     150     160
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1   ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCCCC GATATGAATG CGGCAAAAGT
201 GTTGTGTCGGC GCGCAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAACCCT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTCGATTG
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1   MAGPIFVIA SVAMFFVAQQ HATDLVTDDY YKDGHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQ LHRDEEAVRRHIGVQVLISP					
a274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQ LHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m274.pep	DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
a274	DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
m274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1   atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tgggcgacga tgatgccggt gcggttttcc atcaggcgtt
101 cgagcgcttg ttggacgagg cgttcggtt cgttgtccaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgtct ttcaaaatgg cgcgggcgat
201 ggcgacgcgt tgcgctgtc cgccggataa gttgctgccg ttcgatccga
251 tgggctggtg cagtccgagc ggggatgcgt cgatcaggct ttgcagggtg
301 gcggtctgga gggcgacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcggagc ttttcaaaca ggggtgtcgtc aaacaggaat acgtcttggtg
401 agacgaggcg gaattggcg cgaggcagt cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcgggg
501 cagaagggtg acgacggtg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgcttg atgtcgaggt tgaagttgtc gagggctttg
601 atgctgcttg aacggtattc gacatcgacg ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcggcgaga gcgtgccttt gtcctgttcg ggcggggtgt
701 cgagaaatgc acatacgccg tcggcgggca ggaacatcgt ctgcataggg
751 atgctgatgt tggcaaggct tttgatgggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgccgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

m276.seq

1	ATGATTTTGC	CGTCGTCCAT	CACGATGATG	CGGTCGGCCC	CTTCGATGGT
51	GGTCAGGCGG	TGGGCGACGA	TGATGCCGGT	GCGGTTTTCC	ATCAGGCGTT
101	CGAGCGCCTG	TTGGACGAGG	CGTTCGGATT	CGTTGTCTAA	TGCGCTGGTG
151	GCTTCGTCCA	ATAATAATAT	CGGCGCGTCT	TTCAAAATGG	CGCGGGGCAAT
201	GGCCAGCGGT	TGCCGTGTGC	GCGCCGATAA	GTTGTGTCGG	TTCCGATCCGA
251	TGGGCTGGTG	CAGTCCGAGC	GGGGAGCTGT	CAATCAGGCT	TTGCAGGTTG
301	GCGGTTTGGG	GGGCGAACAG	GACTTCGGCT	TCGCCC CGGT	CGGGACGGCT
351	GTATCGGACG	TTTTCAAACA	GGGTGTCGTC	AAACAGGAAT	ACGTCTGGG
401	AGACGAGGGC	GAATTGGGGC	CGCAGCGCAT	CGAGTTTGAT	GTCCGCCGATG
451	TCGATACCGT	CTATGCAGAT	GTTGCCGGCA	GACGGTTCGA	CAAGCGGGGG
501	CAGCAGGTTG	ACGACGGTGG	ATTTGCCGCT	GCCGGAACGT	CCGACCAGGG
551	CGACCGGTTT	GCCTTGCTCG	ATGTCGAGGT	TGAAGTTGTC	GAGGGCTTTG
601	ATGCCGCTCG	AACGGTATTC	GACATCGACG	TTGCGGAAGC	TGATGCGCCC
651	TTCGACACGC	TGCGGTGCGA	GCGTGCCCTT	GTCTGTTCG	GGCGGGGTGT
701	CGAGAAATCG	ACATACACCG	TCGCGCGCGA	GGAACATCGT	CTGCATAGGG
751	ATGCTGATGT	TGGCAAGGCT	TTTGATGGGG	GCGTACATTT	GCAGCATCGC
801	GACGATGAAT	GCCATAAAAT	CGCCGATGGT	GGTGTAG	

m276 . pep

1	MILPSSITMM	RSAPSMVVR	WATMPVRFS	IRRSSACWTR	RSDSLSNALV
51	ASSNNNIGAS	FKMARAMATR	CRCPPDKLLP	FDPMGWCSPS	GELSIRLCRL
101	AVWRANRTSA	SPASGLYRT	FSNRVSSNRN	TSWETRANWA	RRQSSILMSAM
151	SIPSMQMLPA	DGSTKRGSR	TTVDLPLPER	PTRATRSPCL	MSRLKLSRAL
201	MPSERYSTST	LRKLMPRST	CGASVPLSCS	GGVSRNAHTP	SAARNIVCIG
251	MLMLRLALMG	AYICSIATMN	AINSMPVV*		

Homology with a predicted ORF from *N.gonorrhoeae*

m276/q276

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRRWATMMPVRF	SIRSSACWTRRSDSLSNALVASSNNNIGAS				
g276	MILPPSMTMMRSADSTVVRRWATMMPVRF	SIRSSACWTRRSDSLSNALVASSNNNIGAS				
	10	20	30	40	50	60
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSP	SGELSIRLCRLAVWRANRTSASPASGRLYRT				
g276	FKMARAMATRCRCPPDKLLPFDPMGWCSP	GDASIRLCRLAAWRADRTSASPASGRLYRT				
	70	80	90	100	110	120
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLSAMS	IPSMQMLPADGSTKGRSRLTTVDLPLPER				
g276	FSNRVSSNRNTSWETRANWARRQSSLSAMS	IPSMQMLPADGSTKGRRLTTVDLPLPER				
	130	140	150	160	170	180
m276.pep	PTRATRSPCLMSRLKLSRALMPSE	RYSTSLRKLMPSTRCGASVPLSCSGGVSRNAHTP				
g276	PTRATRSPCLMSRLKLSRALMPSE	RYSTSLRKLMPSTRCGASVPLSCSGGVSRNAHTP				
	190	200	210	220	230	240

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

```
a276.seq
1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGT CAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGGTGTGCTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGGTGCGA GCGTGCCTTT GTCCTGTTCG GGCGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATTG GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

```
a276.pep
1  MILPSSITMM RSAPSMVVRW WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKGRSRL TTVDLPLPER PTRATRSPLC MSRLKPSRAL
201 MPSEYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*
```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSIKRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSIKRLAARADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIIPSMQMLPADGSTKGRSRLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIIPSMQMLPADGSTKGRSRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPLCMSRLKPSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPLCMSRLKPSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

g277.seq (partial)

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

Computer analysis of this amino acid sequence gave the following results:

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277.pep

10 20 30

MVHVAVAYGIAVRRFCPNEVIDVFHALQVH

631

```

m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVHVAVGDGVAVERFCPNEVVDVFYTLQVH
           30      40      50      60      70      80

g277.pep   40      50      60      70      80      90
RQAFDAVGNFAEYGRAIDTADLLEIGKLGYPHAEVPDFPAQTPRTEGGVFPVVFDAKADV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAEVPDFPAQTPRAEGGVFPVVFDAKADV
           90     100     110     120     130     140

g277.pep   100     110     120     130     140     150
DFGIDAQFAQGVEIEVLDIGGGGFEGLDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPRL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      DFGIDAQFAQVEIEVLDIGGSGLEGLDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPRL
           150     160     170     180     190     200

g277.pep   160     170     180     190     200
GAERAQAGGGMGCAGTDFHVEGLDDGAAFVCPPEGLQFEDDLLEGKHGLL
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAFVCPPECLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1  ATGCCCCGCT TTAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51 TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGTTT
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTGACAAA GCGGATGTCG TGCACTTTGG GGTGATGCC
451 CAATTGCGCG AGGGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGGCGAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCAGA ATGTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DEVLVVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VGDFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVFPVVFDA ADVVHFGVDA
151 QFAQGVEIEV LDIGGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCPPECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

m277.pep   10      20      30      40      50      60
MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPIGIAVFEVVGGLLDFVLVHVAV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a277      MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPIGIAVFEVVGGLLDFVLVHVAV
           10      20      30      40      50      60

m277.pep   70      80      90      100     110     120
GDGVAVERFCPNEVVDVFYTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAEV
:  ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a277      SYCITVQRFCPNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP
           70      80      90      100     110     120

           130     140     150     160     170     180

```

632

```

m277.pep      DFPAQTPRAEGGVFPVVFDDKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQA
a277          DFPAQTPRAEGGVFPVVFDDKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQA
              130      140      150      160      170      180

              190      200      210      220      230      240
m277.pep      VGVVAVAAVFGAAAGLDVGGKPRLLGAECAQAGGGMGCGAGTDFHVEGLDDGAAAFVCPCECLQ
a277          VGVVAVATVFGAAAGLDVGGKPRLLGAECAQTGGGMCAGTDFHVEGLDDGAAAFVCPCECLQ
              190      200      210      220      230      240

              250
m277.pep      FEDDLLEGKHGLX
a277          FEDDLLEGKHGLX
              250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1   ttgctgtcaa tcacgcccgg tgcgattttt tcgacagggg cgggtcaaagt
51  tgtattaatc ggacctttgc cgtcgatagg cggacccaat gcatcgacga
101 cgcgtccgac caattcgcgt ccgaccggca cttctaaaat acggccggta
151 caggtaacgg tgtcgccttc tttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gagtgcgctt ccaggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcattg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcatTTACA gacagatttt cgatcttggc tttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgcctt gtacagacaa atccaaaacc tgatcaccga
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1   LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1   TTGCGCGCAA TCACGCCCGG TCGATTTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCTGTA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTGTATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1   LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VQVRTSFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRDFD DRDFQLAVET LIQHLHQLAD
201 LFVGQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

q278/m27.8

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278.seq

1	TTGCGCGCAA	TCACGCCCGG	TGCGATTTTT	TCGATAGGGG	CGGTCAAAGT
51	TGTATTAATC	GGGCCCTTGC	CGTCGATAGG	CCGACCCAAT	GCATCAACGA
101	CGCGTCCGAC	CAGTTCGCGT	CCGACCGGCA	CTTCCAAGAT	ACGACCGGTA
151	CAGGTAACCG	TGTCGCCTTC	TTTAATATGT	TCGTGCTCGC	CCAACACTAC
201	GGCGCCGACG	GAGTCGCGCT	CCAGGTTCAT	CGCCAAGCCG	AAAGTGTTAC
251	CCGGGAATTC	GAGCATCTCA	CCTTGCATTG	CATCTGACAA	ACCATGGATG
301	CGAACGAATC	CGTCAGTTAC	CGAAATCACC	GTACCAACGG	TACGCATCTC
351	GGCATTTTACA	GACAGATTTT	CGATCTTGCG	TTTAATCAAA	TCGCTAATTT
401	CAGCAGGATT	AAGCTGCATG	AAAACCTCTC	TAATTTCGTC	TAGTCGTGTA
451	CAAGGCACTC	AATTTGCCCT	GTACAGACAA	ATCCAAAACC	TGATCACCCT
501	CTTCAACTTT	TATGCCGCCA	ATCAGCTCCG	GTTTCGATTTC	GACAGAGATT
551	TTCAGCTCGC	TGTCGAAACG	CTTATTCAGC	ATTTGCGCCA	ACTCGCCGAC
601	CTGTTTGTGC	GTCAACGGAT	AGGCACTGTA	AATGACGGCA	GATTTGATAT
651	GGTTGAATGA				

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

1	<u>LRAITPGAIF</u>	<u>SIGAVKVVLI</u>	GPLPSIGRPN	ASTTRPTSSR	PTGTSKIRPV
51	QVTVSPSLIC	SCSPNTTAPT	ESRSRFIAKP	KVLPGNSSIS	PCIASDKPWM
101	RTIPSVTEIT	VPRVRTSAFT	<u>DRFSILALIK</u>	<u>SLISAGLSCM</u>	KTLLIRHSRV
151	QGTQFALYRQ	IQNLITHFNF	YAANQLRFDF	DRDFQLAVET	LIQHRLQLAD
201	LFVGGRIGTV	NDGRFDMVE*			

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVVLLIGPLPSIGRPNASTTRPTSSSRPTGTSKIRPVQVTVSPSLMC					
a278						
	10	20	30	40	50	60
	LRAITPGAIFSIGAVKVVLLIGPLPSIGRPNASTTRPTSSSRPTGTSKIRPVQVTVSPSLIC					
	70	80	90	100	110	120
m278.pep	SYPNTTAPTESRSRFIAKPKVLPGNSSISPCIASDKPMMRTIPSVTEITVPQVRTSAFT					
a278						
	70	80	90	100	110	120
	SCSPNTTAPTESRSRFIAKPKVLPGNSSISPCIASDKPMMRTIPSVTEITVPRVRTSAFT					

634

	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
a278	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHLHQLADLFVQGRIQTVNDGRFDMVEX					
a278	DRDFQLAVETLIQHLHQLADLFVQGRIQTVNDGRFDMVEX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279.seq

```

1  atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgtcg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 cggcagcggc cagggcgctg ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcgcgggc gttgcctgca atcacgactt gtccgggcca
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcattc tccaaaccca aaatggccgc cattgcgcct
301 acgccttgag gtacggcgga ctgcattcag tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaaat ccaatgcttc ggcgggcaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgcccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSK SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

```

1  ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTCT GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGCAGCCGG CAGGCGCGCT TTGGCACC GGCTTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCTGCA ATCACGATT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACCTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GCGGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTCGCCGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTTT GCCGCCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

a279.seq

1	ATGACNCNGA	TTTGC GGCTG	CTTGATTTC A	ACGGTTTNN A	GGGCTTCGG C
51	GAGTTTGTC G	GCGGCGGGT T	TCATGAGGCT	GCAATGGGA A	GGTACNGACA
101	CNNGCAGCGG	CAGGCGCGCT	TTGGCGCCGG	CTTCTTTGG C	GGCAAGCATA
151	GCGCGCTCGA	GCGGCGCGGC	ATTGCGTGCA	ATCACGACTT	GTCCGGGCGA
201	GTTGAAGTTG	ACGGCTTCAA	CCACTTCATC	CTGTGCGGAT	TCGGCGCAAA
251	TTTGTTTTAC	CTGTTCATCT	TCCAAGCCGA	GAATCGCCGC	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	NGCGCACGAG
351	TTTGACCGCG	TCGGCAAAAT	CCAATGCGCC	GGCGGCAACN	AGTGCGGTGT
401	ATTCGCCGAN	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCCGAATAG				

a279.pep

1	<u>MTXICGCLIS</u>	<u>TVXRASASLS</u>	<u>AAGFMRLQWE</u>	<u>GTDTGSGRAR</u>	<u>LAPASLAASI</u>
51	ARSTAAALPA	ITTCPGELKL	TASTTSSCAD	SAQICFTCSS	SKPRIAAIAP
101	TPCGTADCIS	SARXRSLTA	SAKSNAPEAT	SAVYSPXLCP	ATAAGVLPPA
151	SE*				

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	:					
a279	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
a279	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPASKX					
a279	SAKSNAPAATSAVYSPXLCPPATAAGVLPASEX					
	130	140	150			

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttccgg ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggg gagcgcgtag ccgtacaaag cctcgtcggg
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgccgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat caccgaccag atcatgacca cgaaggacac caccacgacc
401 acggcggaata tgaccccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccata acgtcgtctga aacctgata aaggccgatc ccgaaggcaa
501 agttttattat caacaacgct tgggcaacta ccaaattgcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcattttaatg ccgtccctgc cgccaaacgc
601 aaagtctctga ccgggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtgag cagcgaagcc gagccgtccg
701 ccaaaacaagt cgccgccatc atccggcaaa tcaaacgcga aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtg accgcatcgc
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgacagacac tacatcggca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAKQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADIQRAV KQSKVSYAEA
101 TKGIQPLKAE EGGHHHDH HDHDHDEGH HHDHGEYDPH VWNDFVLMSD
151 YAQNVAETLI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQ AAFNAVPAKR
201 KVLTHGDAFS YMGNRYNISF IAPQVSSEA EPSAKQVA AI IRQIKREGIK
251 AVFTENIKDT RMDRIAKET GVNVSGLYS DALGNAPADT YIGMYRHNE
301 ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAATCAC CTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTCAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAACTCG TCCTGTCAA CCGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCAAGAT CATGACCACG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCTTA TGCCCAAAAC
451 GTTGCCAAAG CCTGATAAAA GGCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCAGCATG CCTTTCCTA TATGGGCAA CATTACCATA TCGAATTCAT
651 CGCCCCGCAA GCGGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTACC
751 GAAACATCA AGGACACCCG TATGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACGCGCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADVQRAV KQSKVSYTEA
101 TKGIQPLKAE EGGHHHDH HDHGHHDH GEYDPHVWND PVLMSAYAQN
151 VAKALIKADP EGKVYYQQL GNYQMLKKL HSDAQAAFNA VPAKRKVL

```

Homology with a predicted ORF from *N.gonorrhoeae*

m280/q280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

1	ATGAAACACC	CCAAACTCAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
51	AAC TGCCGCGC	CCCCTGCCGG	TTGTAAACAG	CTTCAGCAAT	TTAGGCGACG
101	TAGCCAAACA	AATCGGCGGA	GAGCGCGTAT	CCACAGCAAG	TTTGGTCGGA
151	GGCAACCAAG	ATACGCACGC	CTATCATATG	CCATAGCGCG	ACATTAATAAA
201	AATCCGCGAGT	GCAAAACTCG	TCCTGATTAA	CGGCTTAGGA	CTTGAAGCTG
251	CGGACATCCA	ACGTGCCGTC	AAACAGAGCA	AAGTATCTCA	TGCCGAAGCG
301	ACCAAAAGGCA	TCCAACCCCT	CAAAGCCGAA	GAAGAAGCGG	GACACCATCA
351	GACCAACGAT	CATGACACAG	ACCATGACCA	CGAAGGACAC	CACCAACGAC
401	ACGGCGAATA	TGACCCCCAC	GTCTGGAACG	ACCCCGTCCT	TATGTCGCGC
451	TATGCCCAAA	ACGTGCGCGA	AGCCCTGATA	AAGCGATGAC	CCGAAGGCCAA
501	AGTTTATTAT	CAACAACGCT	TGGGCAACTA	CCCAATGCAG	CTCAAAAAAC
551	TGCACAGTGA	CGCACAAGCC	GCATTTAATG	CCGTCCCTGC	CGCCAAACGC
601	AAAGTCCTGA	CCGGGCACGA	TGCCTTTTCC	TATATGGGCA	AACGTTACCA
651	TATCGAAATC	ATCGCCCCAC	AAGTGTGTAG	CAGCGAAGCC	GAGCCTTCAG
701	CCAAACAAGT	CGCGCCCATC	ATCCGACAAA	TCAAACGCGA	AGGCATCAAA
751	CCGTATTTTA	CCGAAAATAT	CAAGGACACC	CGCATGGTTG	ACCGCATCGG

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801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep
 1 MKHPKLTLIA ALLTTAATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
 51 ANQDTHAYHM TSGDIKKIRS AKLVLLINGLG LEAADIQRAV KQSKVSYAEA
 101 TKGIQPLKAE EEGGHHHDHD HDHDHDHEGH HHDHGEYDPH VWNDPVLMSA
 151 YAQNVAEALI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQA AFNAVPAAKR
 201 KVLTGHDFAFS YMGKRYHIEF IAPQGVSSSEA EPSAKQVAAI IRQIKREGIK
 251 AVFTENIKDT RMVDRIAKET GVNVSGLKLYS DALGNAPADT YIGMYRHNK
 301 ALTNAMKQ*

m280/a280 96.4% identity in 308 aa overlap

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVTFSISILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
a280	MKHPKLTLIAALLTTAATAAPLPVVTFSISILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
	10	20	30	40	50	60
m280.pep	70	80	90	100	110	120
a280	TSGDIKKIRSAKLVLLINGLGLEAADVQRAVKQSKVSYEATKGIQPLKAE EGGHHHDHD					
	70	80	90	100	110	120
m280.pep	TSGDIKKIRSAKLVLLINGLGLEAADVQRAVKQSKVSYEATKGIQPLKAE EGGHHHDHD					
a280	TSGDIKKIRSAKLVLLINGLGLEAADVQRAVKQSKVSYEATKGIQPLKAE EGGHHHDHD					
	130	140	150	160	170	
m280.pep	HDH----EGHHHDHGEYDPHVWNPVLMSAYAQNVAKALIKADPEGKVYYQQRLGNYQMQ					
a280	HDHDHDHEGHHHDHGEYDPHVWNPVLMSAYAQNVAEALIKADPEGKVYYQQRLGNYQMQ					
	130	140	150	160	170	180
m280.pep	180	190	200	210	220	230
a280	LKKLHSDAQA AFNAVPAAKRKVLTGHDFAFSYMGKRYHIEFIAPQGVSSSEA EPSAKQVAAI					
	190	200	210	220	230	240
m280.pep	LKKLHSDAQA AFNAVPAAKRKVLTGHDFAFSYMGKRYHIEFIAPQGVSSSEA EPSAKQVAAI					
a280	LKKLHSDAQA AFNAVPAAKRKVLTGHDFAFSYMGKRYHIEFIAPQGVSSSEA EPSAKQVAAI					
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
a280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	250	260	270	280	290	300
m280.pep	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq
 1 atgcactacg ccctcgcatc cgtcttctgc ctgtccctca ggcgcgcacc
 51 cgctcgcgta ttcctcgta tgcgcggtat gagcctgata ggcgacgcat
 101 tgagccacgc cgtcctgccc ggtgcccgcg tcggctacat gtttgccggc
 151 ttgagcctgc ccgctatggg tgtgggcggg tttgcccgcg gtatgctgat
 201 ggcgctgctt gccggactcg tcagccgctt taccaccctg aaagaagatg
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc
 351 tgtgcttgcc gtcgatattc ccgcactgca actcatcgcc gccgctccg
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa
 451 agcatagacc cccttttctt caagtccgct aacggcaaa ggcgggctttg

g281.pep

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

1	ATGCGCTACG	CCCTCGCATC	CGTCTTCTGC	CTGTCCCTCA	GTGCCGCACC
51	CGTCGGCGTA	TTCCTCGTCA	TGCGCCGTAT	GAGCCTGATA	GGCGACGCAT
101	TGAGCCACGC	CGTCCTGCCC	GGTGCCGCCG	TCGGGTACAT	GTTTGCCTGGC
151	TTGAGCCTGC	CCGCCATGGG	TTTGGGCGCG	GTAGCCGCAG	CGATGCTGTAI
201	GGCACTGCTT	GCCGGATCTG	TCAGCGCCTT	CACCACCTGT	AAAGAAGATG
251	CCAACTTTGC	CGCCTTTTAT	CTCAGCAGCT	TCGCCATCGG	CGTAGTCCTC
301	GTCAGCAAAA	ACGGGAGCAG	CGTCGATTTG	CTCCACCTCC	TTTTCGGCTC
351	TGTACTTGCC	GTCGATATTC	CTGCCCTGCA	GCTCATCGCC	GCCGTCTCCA
401	GCCTCACGCT	CATTACCCTT	GCCGTCACTA	ACCGCCCGCT	CGTACTCGAA
451	AGCATCGACC	CCCTGTTTCT	CAAAATCCGT	GGCGGCCAAAG	GCGGGCTTTTG
501	GCACGTCTCT	TTTTCTCGTC	TGGTCGTCAT	GAACCTCGTA	TCCGGCTTTC
551	AAGCCCTCGG	CACACTCATG	TCCGTCGGAC	TCATGATGCT	GCCAGCCATT
601	ACCGCCCGCC	TGTGGGCGAA	GCATATGGGC	GCATCATCC	TCCTATCCGT
651	TCTGACAGCT	CTGCTGTGCG	GCTTGAAGCG	ACTGCTCATC	TCCTACCACA
701	TCGAAAATTCC	TTCGGTCTCC	GCCATCATCC	TCTGTTGCAG	CGTCTCTTAT
751	CTCTTTTTCG	TCATACTCGG	CAAGAAGGC	GGCATCTCTGA	CC...

m281.pep (partial)

1 MRYLASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAGVGYMFAG
 51 LSLPAMGLGG VAAGMLMALL AGLVSRTTTL KEDANFAAFY LSSLAIGVVL
 101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTLITL AVIYRPLVLE
 151 SIDPLFLKSV GGKGGWLHV FLVLVVMNLV SGFQALGTL SVGLMMLPAI
 201 TARLWAKHMG ALILSVLTA LLCGLSGLLI SYHIEIPSGP AIILCCSVLY
 251 LFSVILKEG GILT..

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

m281/g281

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSLSAAPVGVLVMMRMSLIGDALSHAVLPGAAVGYMFAGLSLPAMGLGG					
g281	: :					
	10	20	30	40	50	60
	MHYALASVFCLSLSAAPVGVLVMMRMSLIGDALSHAVLPGAAVGYMFAGLSLPAMGVGG					
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA					
g281	: :					
	70	80	90	100	110	120
	FAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVILISKNGSSVDLLHLLFGSVLA					
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAVSSSLTLITLAVIYRPLVLESIDPLFLKSVGGKGGGLWHVFLVLVVMNL					

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```

|||||:|||||:|||||:|||||:|||||:|||||:
g281  VDIPALQLIAAVSGLTLITLAVIYRPLVLESIDPLFLKSVNGKGLWHVIFLILVVMNLV
      130      140      150      160      170      180

      190      200      210      220      230      240
m281.ppep SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP
|||||:|||||:|||||:|||||:|||||:|||||:
g281  SGFQALGILMSVGIMMLPAITARLWARNMGTLLLSVLIALFCGLIGLLISYHIEIPSGP
      190      200      210      220      230      240

      250      260
m281.ppep AIILCCSVLYLFSVILGKEGGILT
/ |||||:|||||:|||||:|||||:
g281  AIILCCSVLYLFSVILGKEGGILPKWFKNHRHHTTX
      250      260      270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1161>:

```

a281.seq
1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCCTCGTCA TGCGCCGTAT GAGCCTGATA GGCGACGCAT
101 TGAGCCACGC CGTCTGCCCC GGTGCCGCCG TCGGCTACAT GTTTGCCGGC
151 TTAAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCAG GTATGCTGAT
201 GGCACGTGCTT GCCGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG TGTAGTCCTC
301 GTCAGCAAAA ACGGCAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC
351 CGTACTTGCC GTCGATATTC CTGCCCTGCA ACTCATCGCC GCCGTATCCA
401 CCCTCACACT GCTTACCTT GCCGTCATCT ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCTGTC GGCGGCAAAG GCGGGCTTTC
501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TTATGATGCT GCCAGCCATT
601 ACCGCCCGCC TATGGGCGAA GCACATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCCGGTCCC GCCATCATCC TCTGTTGAG CGTCCTTTAT
751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CCAAATGGCT
801 CAAAACCAC CGCCACCACA CCACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1162; ORF 281.a>:

```

a281.ppep
1  MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSTLTLTL AVIYRPLVLE
151 SIDPLFKSV GKGGLWHVL FLVLVVMNLV SGFQALGTL SVGLMMLPAI
201 TARLWAKHMG ALILLSVLTA LLCGLSGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILTKWLKNH RHHTT*

```

m281/a281 99.2% identity in 264 aa overlap

```

      10      20      30      40      50      60
m281.ppep MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPGAAGVGYMFAGLSLPAMGLGG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a281  MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPGAAGVGYMFAGLSLPAMGLGG
      10      20      30      40      50      60

      70      80      90      100     110     120
m281.ppep VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVVLSKNGSSVDLHLLFGSVLA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a281  VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVVLSKNGSSVDLHLLFGSVLA
      70      80      90      100     110     120

      130     140     150     160     170     180
m281.ppep VDIPALQLIAAVSSSLTLITLAVIYRPLVLESIDPLFLKSVGGKGLWHVFLVLVVMNLV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a281  VDIPALQLIAAVSTLTLTLAVIYRPLVLESIDPLFLKSVGGKGLWHVFLVLVVMNLV
      130     140     150     160     170     180

```

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	190	200	210	220	230	240
m281 . pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281 . pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

```

g282 . seq
1   atgggattgg gtatggaaat cggcaagctg attgtggctc ttttggtgct
51  gatcaatccg tttagcgcgt tgctgcttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgacg ggcggtgcgc tattgaaggt
201 tttgggcata agcgtcggtt cgtttcaggt cggcggcggg attttggtgc
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggcgatt gccgtcgtgc ccatcgccat accgatcacc atcggtcagg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcgc tgattatcgc ggccggtttg gtggtcagtg cgatttggtt
501 tgccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattcccg c aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

```

g282 . pep
1   MGLGMEIGKL IVALLVLINP FSALSPLYLDL TNGHSTKERR KVARTA AVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYS
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMMLA AVS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

```

m282 . seq
1   ATGGGATTGG GCATGGAAT CCGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCGCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTGTGTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGCGCGACGG
551 GGCTGACGAT TTTAAACCGC ATTATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

```

m282 . pep
1   MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTA AVAV
51  FAVIAVFALI GTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMMLA AVS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng) from *N. gonorrhoeae*:

m282/g282

```

      10      20      30      40      50      60
m282.pep  MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI
          |||||:|||||
g282      MGLGMEIGKLIVALLVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI
          10      20      30      40      50      60

      70      80      90     100     110     120
m282.pep  GGTLLKVLGISVGSFQVGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI
          ||:|||||
g282      GGALLKVLGISVGSFQVGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI
          70      80      90     100     110     120

      130     140     150     160     170     180
m282.pep  AVVPIAIPITIGPGGISTVYIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL
          |||||:|||||
g282      AVVPIAIPITIGPGGISTVYIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRL
          130     140     150     160     170     180

      190     200     210
m282.pep  GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX
          |||||
g282      GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX
          190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282.seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51 GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCGCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGA ATTTTGGTGT
251 TGCTGATTGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GTGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTGTGTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCTGCTG GGTGCGACGG
551 GGCTGACGAT TTAAACCGT ATCATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAATG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSPLYDL TNHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ VRPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRL GATGLTILNR IMGMLAAVS
201 VEIIVSGLKM IFPQLAG*

```

m282/a282 99.1% identity in 217 aa overlap

```

      10      20      30      40      50      60
m282.pep  MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI
          |||||
a282      MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI
          10      20      30      40      50      60

```

643

	70	80	90	100	110	120
m282 . pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI					
	70	80	90	100	110	120
m282 . pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
m282 . pep	GATGLTILNRIMGMLAASVVEIIVSGLKTIFFPQLAGX					
a282	GATGLTILNRIMGMLAASVVEIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

g283 . seq

1	atgaactttg	ctttatccgt	catcacattt	accctcgcct	ctttcctgcc
51	cgtcccgccct	gccggaaccg	ccgtctttac	ttggaaagac	ggcggcgcca
101	acagctattc	ggatgtgccg	aaacagcttc	atcccgacca	gagccaaatc
151	ctcaacctgc	ggacgctcca	aaccaaaccg	gcggtcaagc	ccaaacctgc
201	cgtcgatacg	aatgcggaca	gtgcgaagga	aaacgaaaag	gatatcgccg
251	agaaaaacgg	gcagcttgag	gaagaaaaga	aaaaaatgac	cgaaaccgaa
301	cggcagaaca	aagaagaaaa	ctgccggatt	tcaaaaatga	acctgaaggc
351	ggtgggaaac	tcaaatgcga	aaaacaagga	tgatttgatc	cgtaaatata
401	ataacgccgt	aaacaaatac	tgccgttaa		

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

g283 . pep

1	MNFALSVITF	TLASFLPVPP	AGTAVFTWKD	GGGNSYSDVP	KQLHPDQSQI
51	LNLRTLQTKP	AVKPKPAVD	NADSAKENEK	DIAEKNGQLE	EEKKKIAETE
101	RQNKEENCRI	SKMNLKAVGN	SNKKNKDDLI	RKYNNAVNKY	CR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

m283 . seq

1	ATGAACTTTG	CTTTATCCGT	CATTATGTTG	ACCCTCGCCT	CTTTCCTGCC
51	CGTCCCGCCT	GCCGGAGCCG	CCGTCTTTAC	TTGGAAGGAC	GGCGGCGGCA
101	ACAGCTATTC	GGATGTACCG	AAACAGCTTC	ATCCCGACCA	AAGCCAAATC
151	TTAAACCTGC	GGACGCGCCA	AACCAAACCG	GCGGTCAAAC	CCGCCCAAGC
201	CGACGCAGGG	AAGCGCACAG	ACGGCGCGGC	ACAGGAAAAC	AATCCCGACA
251	CTGCCGAGAA	AAACCGGCAG	CTTGAGGAAG	AAAAGAAAAG	AATTGCCGAA
301	ACCGAACGGC	AGAACAAGA	AGAAACTGC	CGGATTCAA	AAATGAACCT
351	GAAGGCGGTG	GGAAATTCAA	ATGCAAAAAA	CAAGGATGAT	TTGATTCCGA
401	AATACAATAA	CGCCGTAAAC	AAATACTGCC	GTAA	

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

m283 . pep

1	MNFALSVIML	TLASFLPVPP	AGAAVFTWKD	GGGNSYSDVP	KQLHPDQSQI
51	LNLRTRQTKP	AVKPAQADAG	KRTDGAAQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERQNKEENC	RISKMNLKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283 . pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP					
	10	20	30	40	50	60

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              70      80      90      100      110      120
m283.pep      AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV
              |||| | : | :||| | |||| ||||| : ||||| ||||| ||||| |||||
g283           AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKKIAETERQNKEENCRI SKMNLKAV
              70      80      90      100      110

              130      140
m283.pep      GNSNAKNKDDLIRKYNNAVNKYCRX
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g283           GNSNAKNKDDLIRKYNNAVNKYCRX
              120      130      140

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1173>:

```
a283.seq
1  ATGAAC TTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCC GCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GC CGGGCGGCA
101 ACAGTAT TC GGATGTACCG AAACAGCTTC ATCCCCACCA AAGCCAAATC
151 TTAAACCT GC GCACGCGCCA AACCAAACCG CGGGTCAAAC CGGCCAAAGC
201 CGACGCAG GG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAG AA AAACCGCGAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACG GC AGAACAAAGA AGAAAAC TCG CGGATTTCAA AAATGAACCT
351 GAAAGCGT GC GGAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATA CGCCGTA AAC AAATACTGCC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1174; ORF 283.a>:

a283.pep

1	MNFALSVIML	TLASFLPVPP	AGAAVFTWKD	GGGNSYSDVP	KQLHPDQSQI
51	LNLRTQRTKP	AVKPAQADAG	KRTDGAAQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERQNKEENC	RISKMNLIKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*

m283/a283 100.0% identity in 144 aa overlap

		10	20	30	40	50	60
m283.pep		MNFALSVMILTLASFLVPVPPAGAAVFTWKDGGGNSYS	SDVPKQLHPDQSQILNLRTRQTKP				
a283		MNFALSVMILTLASFLVPVPPAGAAVFTWKDGGGNSYS	SDVPKQLHPDQSQILNLRTRQTKP				
		10	20	30	40	50	60
		70	80	90	100	110	120
m283.pep		AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
a283		AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
		70	80	90	100	110	120
		130	140				
m283.pep		GNSNAKNKDDLIRKYNNAVNKYCRX					
a283		GNSNAKNKDDLIRKYNNAVNKYCRX					
		130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1175>:

```
g284.seq.
1  atgccgtctg aaactcgaaa tcggtttcag acggcattgg tttacgcggc
51  aggttggggc ttagcggctc ttgtaacggc attcgccttt gcctgcaaaa
101 gagtcgccgg ctttgcgttt gcctttgaag ccttcgccgg tttttttgaa
151 actgtctttc ttaaagcctt cttcttgtaa accttcgccg cgcgttttgc
201 cgccgaagcc ttctttgccg gctttatgat gcgcgcgcgg gcgcgcggat
251 ttctatcgc ccagccgcc tttgccttcc ggcttgccgc ctgcggattt
301 gcgtttgcgg gccggctcca tgccttcgat ggtcagttcg ggcagtttgc
351 ggttaatgta tttttcgatt ttgtggactt tgacgtattc gttcacttcg
401 gcaaacgtaa tcgcaatacc cgtgcggcct gcgcggccgg tgcgcccgat
451 gcggtggacg tagtcttccg cctgtttcgg caggtcgtat tttatgacg
```

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```

501  gggtaaatggt  cggtagctca  ataccgcgtg  cggcaacgtc  ggtggcaacc
551  aaaattttgc  agcggccttt  acgcaaatac  gtcagcgtgc  ggttgcgcca
601  gccctgcggc  atatcgccgt  gcaggcagtt  ggcggcgaaa  cttttttcgt
651  acaattcatc  cgcgatgact  tcggtcacgc  ctttggtgga  cgtgaaaatc
701  acacattggt  cgatgttggc  atcgcgcagg  atgtggtcga  gcaggcggtt
751  tttgtggcgc  atatcgtcgc  agtacaacaa  ctgctcttcg  attttgcctt
801  ggcgcgtccac  gcgttcgact  tcgataattt  cagagtcttt  ggtcagtttg
851  cgcgccagtt  tgccgactgc  gccgtcccaa  gtggcggaga  acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
  1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRVAGFAF  AFEAFAGFFE
 51  TVFLKAFFLE  TFAARFAAEA  FFARFMIAAP  AAGFPIAPAA  FAFRLAACGF
101  AFAGRLHAFD  GQFGQFAVNV  FFDFVDFDVF  VHFGKRNNT  RAACAAGAPD
151  AVDVVFRFLR  QVVVYDVNG  RYVNTACGNV  GGNQNFAAAF  TQIRQRAVAP
201  ALRHIAVQAV  GGETFFVQFI  RDDFGHRRFG  RENHTLVDVG  IAQDVVEQAV
251  FVAHIVAVQQ  LLFDLALAVH  AFDFDNFRVF  GQFARQFADC  AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
  1  ATGCCGTCTG  AAACTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
 51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCCTT  GCCTGCAAAA
101  GAATCGCCGG  CTTTGCCTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTTTTGAA
151  ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTGC
201  CGCCGAAGCC  TTCTTTGCTC  GGTTTATGAT  CGCCGCGCCA  ACCGCCGGAT
251  TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301  GCGTTTGCGG  GTCGGTTCCA  TGCCTTCGAT  GGTCAGTTCG  GGCAGTTTTC
351  GGTAAATGTA  TTTTTCGATT  TTGTGACTT  TGACGTATTC  GTTCACTTCG
401  GCAAACGTAA  TCGCAATACC  CGTGCGGCC  GCGCGGCCGG  TGCGCCCGAT
451  GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501  GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACATC  GGTGGCAACC
551  AAAATTTTGC  AGCGGCCTTT  ACGCAAATCC  ATCAGCGTGC  GGTTGCGCCA
601  GCCTTGCGGC  ATATCGCGGT  GCAGGCAGTT  TGCGGCGAAA  CCTTTTTTCG
651  ACAGTTCATC  CGCAATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701  ACGCATTGAT  CGATATTGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751  TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801  GATCGTCCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTCAGTTTG
851  CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901  CTGACGGTCG  CTCGGCGTTG  CTTCCACGAT  GGTTTCGATG  TCGTCGATAA
951  AGCCCATATC  CAACATACGG  TCGGCTTCGT  CAAAATCAG  CACTTCCAAA
1001  CGTTCAAAAT  CAACTTTGCC  GCTTTGCATC  AGGTCCATCA  GACGGCCCGG
1051  CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCACGG  GTTTGGTAGC
1101  CGAAAGACGC  GCCGCCGACG  ATGCTGACGG  TGCGGAACCA  ACGCATATTT
1151  TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  GTTCGCGGGT
1201  CGGGGTCAAC  ACCAAAGCAC  GCGGGCCTTT  GCCCGGTTTT  TCGCTGCGTT
1251  TGGTCAGTTT  TTGCAAAGTC  GGTA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
  1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE
 51  TVSLKAFFLE  TFAARFAAEA  FFARFMIAAP  TAGFTIAPAA  FAFRLAACGF
101  AFAGRFHAFD  GQFGQFSVNV  FFDFVDFDVF  VHFGKRNNT  RAACAAGAPD
151  AVDVVFRFLR  QVVVDNVNG  RYVDTACGNI  GGNQNFAAAF  TQIHQRAVAP
201  ALRHIAVQAV  CGETFFVQFI  RNDFGHGFVG  RENHALIDIG  IAQDMIEQAV
251  FVAHIVAVQQ  LFFDFALIVH  AFDFDDFRVF  GQFARQFADR  AVPSGGEQQS
301  LTVARRCFHD  GFDVVDKAHI  QHTVGFVQNG  HFQTFKINFA  ALHQVHQFAR
351  RGDNDQIDRFA  QGTGLVAERR  AADDADGAEP  THIFGIRQRV  FLDLSRQFAG
401  RGQHQSTRAF  ARFFAAFGQF  LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284.pep	MPSETRNR FQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNR FQTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAAGFPIAPAAFAFRLAACGFAGRLHAFDGGQFGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDV FVHF GKRRNRNTRAACAAGAPDAVDVVFRLFRQVVVDVNGRNVDTACGNI					
g284	FFDFVDFDV FVHF GKRRNRNTRAACAAGAPDAVDVVFRLFRQVVVDVNGRNVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNF AAFTQI HQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNF AAFTQI HQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHRFGGRENHTLVDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLLDFALAVHAFDFFDFRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284.pep	LTVARRCFHDFDVVDKAHIQHTVGFVQNQHFTKINFAALHQVHQTARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284.seq
1  ATGCCGTCTG  AAACCTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101  GAATCGCCGG  CTTTGCGTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTTTTGAA
151  ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTGC
201  CGCCGAAGCC  TTCTTTGCTC  GGTTCATGAT  CGCCGCGCCA  ACCGCGCGAT
251  TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGCAATT
301  GCGTTTGCGG  GTCGGTTCCA  TGCCTTCGAT  GGTCACTTCG  GGCAGTTTTC
351  GGTAAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401  GCAAACGTAA  TCGCAATACC  CGTCGGCCTT  GCGCGGCCGG  TGCGCCCGAT
451  GCGGTGGACG  TAGTCTTCGG  CCTGTTTCGG  CAGGTCTGAT  TTGATAACGT
501  GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACGTC  GGTGGCAACC
551  AAAATTTTGC  AGCGGCCTTT  GCGCAAATCC  ATCAGCGTGC  GGTGCGCCA
601  GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  GGCGGCGAAA  CCTTTTTCGT
651  ACAATTCATC  CGCGATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701  ACGCATTGAT  CGATGTCGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751  TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801  GGTCGTCCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTCACTTTG
851  CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901  CTGACGGTCT  TCCGGCGTGG  CTTTCGACAT  GGTTCGATG  TCGTCGATAA
951  AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAATCAG  CACTTCCAAG
1001  CGGGCGAAAT  CGACTTTGCC  GCTTTGCATC  AAGTCCATCA  GACGGCCCGG
1051  CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGCGCGGG  GTTTGGTAGC
1101  CGAACGATGC  ACCACCGACG  ATGCTGACGG  TACGGAACCA  ACGCATATTT
1151  TTGGCATACG  CCAGCGGCTT  TTTCTCGACT  TGAGCCGCCA  ATTCGCGGGT
1201  CGGCGTCAAC  ACCAACGCGC  GCGGGCCTTT  GCCCGGTTTT  TCGCTGCGTT
1251  TGGTCAGTCG  CTGCAAAGTC  GGTA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284.pep
1  MPSETRNRFQ TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE

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```

FFARFMIAAP TAGFTIAPAA FAFRLAACGF
FDFVDFDVF VHFGRNRNT RAACAAGAPD
RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
RDDDFGHGFGG RENHALIDVG IAQDMIEQAV
AFDFDDFRVF GQFARQFADR AVPSGGEQQS
QHTVGFVQNQ HFQAGEIDFA ALHQVHQTAR
PTDDADGTEP THIFGIRQRV FLDLSRQFAG
LQSR*

```

24 aa overlap

```

      30      40      50      60
LAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
|||||
LAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
      30      40      50      60

      90     100     110     120
PTAGFTIAPAAFAFRLAACGFAFAGRFHAFDGGQFGQFSVNV
|||||
PTAGFTIAPAAFAFRLAACGFAFAGRFHAFDGGQFGQFSVNV
      90     100     110     120

      150     160     170     180
TRAACAAGAPDAVDVVFRLEFRQVVVDNVGNRGYVDTACGNI
|||||:
TRAACAAGAPDAVDVVFRLEFRQVVVDNVGNRGYVDTACGNV
      150     160     170     180

      210     220     230     240
PALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG
|||||:|
PALRHIAVQAVGGETFFVQFIRDDFGHGFGGRENHALIDVG
      210     220     230     240

      270     280     290     300
QLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS
|||||:|
QLFFDFALVVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS
      270     280     290     300

      330     340     350     360
LQHTVGFVQNHQHFQTFKINFAALHQVHQTARRGDNQIDRFA
|||||:|:|
LQHTVGFVQNHQHFQAGEIDFAALHQVHQTARRGDNQIDRFA
      330     340     350     360

      390     400     410     420
PTHIFGIRQRVFLDLSRQFAGRGQHQSTRAFARFFAAFGQF
|||||:|
PTHIFGIRQRVFLDLSRQFAGRRQHQRARAFARFFAAFGQS
      390     400     410     420

```

identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

cgataccgat ccgaccgaaa acggcacgcg
ccccgcccc gccggcaaaa aaacgccgcc
cactgctgt ctgtcctgat tttggcagta

```

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151  tgtttccctcg gctggatcgc cggtagcgaa gcaggtttgc gcttcgggct
201  gtaccaaatac ccgtcctgggt tcggcgtaaa catttcctcc caaaacctca
251  aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc
301  gagggggcag accttaaaat cagccgcttc cgcttcgctg ggaaaccgtc
351  cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca
401  tcgccatcgt aaccaaaccg actccgccta aagaagaacg cccgcctcaa
451  ggctgcccgc acagcataga cctgcccgcc gctgtctatc tcgaccgctt
501  cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaacgctct
551  atctcgaacg cctcaacgcg gcataccgtt acgaccgtaa agggcaccgc
601  ctcgacctga aggcgcgcga cagcccggtg agcagttcgt cggggtcagc
651  ctcggtcggc ttgaaaaaac cgtttgccct cgataccgcc atttacacca
701  aaggcggatt cgaaggcgaa accatacaca gtacggcgcg gctgagcgcg
751  agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
801  cctctcggga aaatccgtca tccaccggtt tgccgaatca ttggataaaa
851  cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901  gtgccttccc tgcccgatgc cgggctgaat ttcgacctga ccgccatccc
951  gtcgtttttca gacggcatcg cgctggaagg ctcgctcgat ttggaaaaaca
1001 ccaaagccgg ctttgccgac cgcaacggca tcccgtccg tcaggttttg
1051 ggcggttttg tcatccggca ggacggcacg gtgcatatcg gcaatacgtc
1101 cgccgccctg ctcggacggg gcggcatcag gctgtcgggc aaaatcgaca
1151 ccgaaaaaga catccttgat ttaaatatag gcatcaactc cgtcggcgcg
1201 gaagacgtgc tgcaaacgcg gttcaaaagg aggttgagcg gcagcatcgg
1251 catcggcggc acgaccgcct cgcccaaaat ctcttggaac ctcggcaccg
1301 gcacggcacg cagggacggc agcctcccca tcgcaagcga ccccgcaaac
1351 gaacagcgga aactggtgtt cgacaccgtc aacatctccg ccggggaagg
1401 cagcctgacc gcgcaaggct atctcgagct gtttaaagac cgctgtctca
1451 agctggacat ccgttccgcg gcattcgacc cttcgcgcat cgatccgcga
1501 tttccggcag gcaatatcaa cggttcgatt catcttgccg gtgaactggc
1551 aaaagagaaa tttacgggca aaatgcgttt tttgcccggt acgttcaacg
1601 gcgtgccgat tgccggcagc gccgacattg tttacgagtc ccgccacctt
1651 ccgcgcgcgc ccgtcgattt gcggttgagg cggaaacatc tcaaaacaga
1701 cggcggttcc ggcaaaaaag gcgaccggct taacctcaat atcaccgcac
1751 ccgatttatc ccgtttcggg ttcggactcg cggggtcttt aaatgtacgc
1801 ggacaccttt ccggcgattt ggacggcgcg atccgaacct ttgaaaccga
1851 cctttccggc acggcgcgca acttacacat cggcaaagcg gcagacatcc
1901 gttcgctoga tttaccctc aaaggctcac ccggcacaag ccgcccatg
1951 cgcgccgata tcaaggcgcg ccgcctttcc ctgtcgggcy gcgcggcggt
2001 tgtcgatacc gccggcctga cgctggaagg tacgggcgcg cagcaccgca
2051 tccgcacaca cgccgccatg acgctggagc gcaaaccggt caaactcgat
2101 ttggacgctt caggcgcat caacagggaa cttaccgat ggaaaggcag
2151 catcgcatc ctcgacatcg gcggcgcat caacctcaag ctgcaaaacc
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaag tcgggcaaat
2251 tggcaggcaa tgggcggcag cctcaacctg caacactttt cttgggacag
2301 gaaaaaccggc atatcggcaa aaggcgcgcg acgcggcctg cacatcgccg
2351 agttgcacaa tttcttcaaa ccgccccttcg aacacaatct ggttttaaac
2401 ggcgactggg atgtcgcta cgggcacaaac gcgcgcggct acctaatat
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt
2501 tgaacgcatt ttccctgaaa acgcgcttcc aaaacgaccg catcggaatc
2551 ctgcttgacg gcggcgcgcg tttcgacagg attaacgccg atttgggcat
2601 cggcaacgcc ttcggcgga atattggcaa tacaccgctc ggcggcagga
2651 ttacagctc ccttcccgcac ttgggcgcat tgaagccctt tctgcccgcc
2701 gccgcgcaaa acattaccgg cagcctgaat gcctccgcgc aaatcggcgg
2751 acgggtaggc tctccgtccg tcaatgcccgc cgtcaacggt agcagcaact
2801 acgggaaaat caacggcaat atcaccgtcg ggcaaagccg ctccctcgat
2851 accgcacctt tgggcggcag gctcaacctg accgttgccg atgccgaagc
2901 attccgcaac ttcctaccgg tcggacaaac cgtcaaaagg agcctgaatg
2951 ccgccgtaac cctcggcggc agcatcgccg acccgcaact gggcggcagt
3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatcatctt
3051 ggacaacggc tcgctgcgtt cgcatattgc aggcaggaaa ttggtaatcg
3101 acagcctgaa attccggcac gaaggacgg cggaactctc cggcaccggtc
3151 agcatggaaa acagcgtgcc cgatgtcgat atcggcgcgg tgttcgacaa
3201 ataccgcac ctgtcccgcc ccaaccgccg cctgacgggt tccggcaaca
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt
3301 aaaactgatc aggggctgtt cggttcgcaa aaatcctcga tgccgtccgt
3351 cggcgacgat gtcgtcgat tgggcgaagt caagaaagag gcggcgccat
3401 cgctcccgt caatatgaac ctgactttag acctcaatga cggcatccgc

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649

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3451 ttctccggct acggcgcgga cgttaccata ggccgcaaac tgaccctgac
3501 cgcgcaaccg gccggaaatg tgcgtggggt gggcacggtc cgcgtcatca
3551 aaggcggtta caaagcatac gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgtc caacgacccc aacctgaaca tccgcgccga
3651 acgcccgcctt tcccccgctg gtgcgggctg ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcgcca gcagcgcgga
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctggtg gatgatttgg gctttaccag caagcgcagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtcgctc aaactgattt accggctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccgttcg tcgggcggcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

g285.pep

```

1 MTDTTPDTD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWIAGTE AGLRFGlyQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRSLHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLDREFETG KISMGTFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGFEFE TIHSTARLSG
251 SLKDVRALTE IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGLSD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAIL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFFK RLDGSIGIG TTASPKISWQ LGTGARTDGL SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTDGGF GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLSE TARNLHIGKA ADIRSLDFTL KGSPGTSRPM
651 RADIKGGRLS LSGGAADVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKSGSIG LDIGGAFLNK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSLNL QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFENLVLN
801 GDWDVAYGHN ARGYLNISRO SGDAVLPGGQ ALGLNAFLSK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFPLA
901 AAQNITGSLN ASAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSF
951 TAPLGGRLNL TVADAEAFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGGG
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 SMENSVPDVG IGAVFDKYRI LSRPNRRLTV SGNTRLRYSF QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGVADVTI GGKLTILTAQP GGNVRGVGTG RVIKGRYKAY GQDLDTIKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SSGELTYTIR FDRFLGSDKK DSAGNGKKG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

m285.seq

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1 ATGACCGATA CCGACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51 CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCTGAT TTTGGCAGTA
151 TGTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAAAT CCGTCTTGGT TCGGCGTAAA CATTTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGACGCC TGCACATTAC CGAAATTTC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCCCTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCCGTGG AGCAGTTCGT CGGGGGCGGC
651 CTCGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

```


801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCCTTC
901 GTGCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCCG TCAGGTTTTA
1051 GCGGGCTTTG TCATCCGGCA GGACGGCACG GTGCATATCG GCAATACGTC
1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCCCAAAT CTCTTGGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTTCGACC CTTCGCGCAT CGATCCGCAA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCGGC ACGTTCAACG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTTAAACAGA
1701 CCGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC
1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGTGATTT GGACGGCGGC ATCCGAACCT TTGAAACCGA
1851 CCTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTTCG CCGACACAAG CCGCCCGATA
1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTCGGGCG GAGCGGCGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCAGA
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAAGGCAG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAAT
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAAACCGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GCGGACTGGG ATGTCGCCTA CGGGCGCAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CGGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC
2551 CTGCTTGACG GCGGCGGCGG TTTGCGGCGG ATTAACGCCG ATTTGGGCAT
2601 CGCCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
2651 TTACCGCCTC CCTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC
2701 GCCGCGCAAA ACATTACCGG CAGCCTGAAT GCCGCCGCGC AAATCGGCGG
2751 ACGGCTAGGC TCTCGTCCG TCAATGCGGC CGTCAACGGC AGCAGCAACT
2801 ACGGGAAAAT CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCCGCAAC TTCTTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGCAGC
3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC
3151 GGTATGGAAG ACAGCGGACC CGATGTCGAT ATCGGCGCGG GTTTCGACAA
3201 ATACCGCATC CTGTCCCGCG CCAACCGCCG CCTGACGGTT TCCGGCAACA
3251 CCGCCTGCG CTATTGCGCG CAAAAAGGCA TATCCGTTAC CGGGATGATT
3301 AAAACGGATC AGGGGCTGTT CGGTTTCGCA AAATCCTCGA TGCCGTCCGT
3351 CGGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
3401 CGCTCCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC
3451 TTCGCCGGT ACGGCGCGGA CGTTACCATA GCGGCGAAAC TGACCTGAC
3501 CGCCCAATCG GGCGGAAGCG TACGGGCGGT GGGCACGGTC CGCGTCATCA
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
3601 GTCTCCTTTG TCGGCCCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA
3651 ACGCCGCTT TCCCCGTCG GTGCGGCGT GGAATATTG GGCAGCCTCA
3701 ACAGCCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAAAAGAC
3751 AAGCTCTCTT GGCTCATCCT CAACCGCGCC GGCAGCGGCA GCAGCGGCGA
3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAAATCA
3851 ACGACCGCAT CGGGCTGGTG GATGATTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT
3951 CGGCAACAAA CTGACCGGCA AACTCTACAT CCGGTACGAA TACAGCATCT
4001 CAGCGCGGGA ACAGTCCGTC AAATGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTTCG TCGGCGGCG AGCTGACATA

651

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
4151 GAAACGGCAA AGGAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep
1 MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRSLHITEIS AGDIAIVTKP TPPKEERPPPL
151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRaela IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGLSD LENTKAGFAD RNgIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAfKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGSlt AQGYLELFKD RLLKLDIRSR AFDPsRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFPLG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIIKTDGGF GKKGDRLNLN ITAPDLsRFG FGLAGSLNVR
601 GHLSGDLdGG IRTFETDLsG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAAVVDt ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKGSIGI LDIGGAfNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN
801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFPLPA
901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRsFD
951 TAPLGGRNLN TVADAEVfRN FLPVGQTVKG SLNAAVTLGg SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGKLTlTAQS GGSVRGVGTv RVIKGRYKAY GQDLdITKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNAa LSAAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISsAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNGKKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	: : : : : :					
g285	MTDTPPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM					
	: : : : : :					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPSLPDSIDLPAAVYLDRFETGKISMKGAFDK					
	: : : : : :					
g285	RRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDSIDLPAAVYLDRFETGKISMKGTFDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m285.pep	QTVYLERLDASRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
	: : : : : :					
g285	QTVYLERLNAAARYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRaelaIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					

653

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g285      |||||:|||||
AAQNITGSLNASAQIGGRVGSPSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN
          910      920      930      940      950      960

m285.pep      970      980      990      1000      1010      1020
TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIAADPHLGGSINGDKLYRNTQGIILDNG
g285      |||||:|||||
TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIAADPHLGGSINGDKLYRNTQGIILDNG
          970      980      990      1000      1010      1020

m285.pep      1030      1040      1050      1060      1070      1080
SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
g285      |||||:|||||
SLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENSVPDVDIGAVFDKYRILSRPNRRLTV
          1030      1040      1050      1060      1070      1080

m285.pep      1090      1100      1110      1120      1130      1140
SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
g285      |||||:|||||
SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAASLPVNMN
          1090      1100      1110      1120      1130      1140

m285.pep      1150      1160      1170      1180      1190      1200
LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSRVGVGTVRVIKGRYKAYGQDLDTKGT
g285      |||||:|||||
LTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVRGVGTVRVIKGRYKAYGQDLDTKGT
          1150      1160      1170      1180      1190      1200

m285.pep      1210      1220      1230      1240      1250      1260
VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
g285      |||||:|||||
VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
          1210      1220      1230      1240      1250      1260

m285.pep      1270      1280      1290      1300      1310      1320
GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
g285      |||||:|||||
GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
          1270      1280      1290      1300      1310      1320

m285.pep      1330      1340      1350      1360      1370      1380
LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
g285      |||||:|||||
LTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFLFGSDKK
          1330      1340      1350      1360      1370      1380

m285.pep      1390
DSAGNGKGKX
g285      |||||
DSAGNGKGKX

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1185>:

```

a285.seq
1   ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTGCTGTA GCTGTCGGCG GCACTGCTGT CTGTTCTGAT TTTGGCAGTA
151 TGTTCCTCG GCTGGCTCGC CGGCACGGAA GCGGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAATGATG CGCCGACGCC TGCACATTAC CGAAATTTC GCCCGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTCGACCTGA AGGCTGCCGA CACGCCGTGG AGCAGTTCGT CGGGGTCAGC

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651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG
801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGCCTTC
901 GTGCCTTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGGAACACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGTCCG TCAGTTTTA
1051 GGCAGCTTTG TCATCCGGCA GGACGGCAGG GTGCATATCG GCAATACGTC
1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGG AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCCAGAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTGACG CTTCGCGCAT CGATCCGCA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACACAGA
1701 CCGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCACG
1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CCGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA
1851 CCTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTTCG CCGACACAAG CCGCCGATA
1951 CCGCGCGACA TCAAAGGCG CCGCCTTTCG CTGTCGGGCG GAGCGGAGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCAGC
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGA CTTACCCGAT GGAAAGGCG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAT
2251 TGGCAGGCAA TGGGCGGCG CCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAACCAGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GCGGACTGGG ATGTGCGCTA CCGGCGAAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC
2551 CTGCTTGACG GCGGCGCGCG TTTCCGGGCG ATTAACGCCG ATTTGGACAT
2601 CGGCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGCGGAGGA
2651 TTACCGCCTC CCTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC
2701 GCCGCGCAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGGAAAAA CAACGGCAAC ATCACCCTCG GGCAAGGCC CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTTGCCG ATGCCGAGT
2901 ATTCCGCAAC TTCCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGACG
3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC
3151 GGTATGGAAC ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTGACAAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA
3251 CCCGCTGCG CTATTGCGCG CAAAAAGGCA TATCCGTTAC CCGGATGATT
3301 AAAACGGATC AGGGGCTGTT CGGTTGCAA AAATCCTCGA TGCCGTCCGT
3351 CCGCGACGAT GTCGTCGAT TAGGCGAAGT CAAAAAGAG GCGGCGGCGC
3401 CGCTCCCGCT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC
3451 TTCGCCGGCT ACGGCGCGGA CGTTACCATA GCGGCGAAAC TGACCTGAC
3501 CGCCCAATCG GCGGAAGCG TGCGGGGCGT GGGCACGGTC CGCGTCATCA
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGACATTAC CAAAGGCACG
3601 GTCTCCTTTG TCGGCCGCT CAACGACCCC AACCTCAACA TCCGCGCCGA
3651 ACGCCGCTT TCCCCGTCG GTGCGGGCGT GGAAATATTG GGCAGCCTCA
3701 ACAGTCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAGAGAC
3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA
3801 CAATCCGCC CTGTCCGAG CCGCGGCGC GCTGTTGCC GGGCAATCA
3851 ACGACCGCAT CCGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

655

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3951 CGGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTATT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTG CCCGTATCGG CAGCCGTTG TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

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a285.pep
  1 MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
 51 CFLGWLAGE AGLRFGLYQI PSWFGVNIS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPPL
151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGLD LENTKAGFAD RNGIPVRQVL
351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGSST AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIKTGGSF GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAEVVDT ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKSGSIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENLVLN
801 GDWDVAYGRN ARGYNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFPLA
901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSF
951 TAPLGGRLNL TVADAEVFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGG
1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSMPSVGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGKLTITAQS GGSVRGVGTV RVIKGRYKAY QDLDITKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGELTYTIR FDRFSGSDDK DSAGNSKKG*

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m285/a285 99.4% identity in 1389 aa overlap

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          10      20      30      40      50      60
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          |||
a285       MTDTAPTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
          10      20      30      40      50      60

          70      80      90     100     110     120
m285.pep  AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM
          |||
a285       AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM
          70      80      90     100     110     120

          130     140     150     160     170     180
m285.pep  RRSLLHITEISAGDIAIVTKPTPPKEERPPSLPDSIDLPAAYLDRFETGKISMKGAFDK
          |||
a285       RRSLLHITEISAGDIAIVTKPTPPKEERPPSLPDSIDLPAAYLDRFETGKISMKGAFDK
          130     140     150     160     170     180

          190     200     210     220     230     240
m285.pep  QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
          |||
a285       QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK
          190     200     210     220     230     240

          250     260     270     280     290     300
m285.pep  TIHSTARLSGSLKDVRAELADGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF
          |||

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a285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPPFAESLDKTL EEVLVKGFNINPSAF
	250 260 270 280 290 300
m285.pep	310 320 330 340 350 360
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a285	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGSFVIRQDGT
	310 320 330 340 350 360
m285.pep	370 380 390 400 410 420
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
a285	VHIGNTSVALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
	370 380 390 400 410 420
m285.pep	430 440 450 460 470 480
	TTASPKISWQLGIGTARTDGLAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
a285	TTASPKISWQLGIGTARTDGLAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
	430 440 450 460 470 480
m285.pep	490 500 510 520 530 540
	RLKLDIRSFADPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
a285	RLKLDIRSFADPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	490 500 510 520 530 540
m285.pep	550 560 570 580 590 600
	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
a285	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
	550 560 570 580 590 600
m285.pep	610 620 630 640 650 660
	GHLSGDLGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
a285	GHLSGDLGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
	610 620 630 640 650 660
m285.pep	670 680 690 700 710 720
	LSGGAHVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
a285	LSGGAHVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
	670 680 690 700 710 720
m285.pep	730 740 750 760 770 780
	LDIGGA FN LKLQNRMTLEAGAERVAASAANWQAMGGS LNLQHFSWDKKTGISAKGGAHGL
a285	LDIGGA FN LKLQNRMTLEAGAERVAASAANWQAMGGS LNLQHFSWDKKTGISAKGGAHGL
	730 740 750 760 770 780
m285.pep	790 800 810 820 830 840
	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
a285	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
	790 800 810 820 830 840
m285.pep	850 860 870 880 890 900
	TRFQNDRIGI LLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
a285	TRFQNDRIGI LLDGGARFGRINADLDIGNAFGGNMANAPLGGRITASLPDLGTLKPFLPA
	850 860 870 880 890 900
m285.pep	910 920 930 940 950 960
	AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYKINGNITVGQSRSFDTAPLGGR LNL
a285	AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYKINGNITVGQSRSFDTAPLGGR LNL

657

a285	AAQNITGSLNAAAQIGGRVGS	PSVNA	AVNGSSNYGKINGNITVGQSR	SFDTAPLGGRLNL	
	910	920	930	940	950 960
m285.pep	970	980	990	1000	1010 1020
	TVADAEVFRNFLPVGQTVKGS	LNAAVTLGGS	IADPHLGGS	INGDKLYYRNQTQGI	ILDNG
a285	TVADAEVFRNFLPVGQTVKGS	LNAAVTLGGS	IADPHLGGS	INGDKLYYRNQTQGI	ILDNG
	970	980	990	1000	1010 1020
m285.pep	1030	1040	1050	1060	1070 1080
	SLRSHIAGRKWVIDSLKFR	HEGTAELSGTV	GMENSGPDVD	IGAVFDKYRILSRPN	RRLTV
a285	SLRSHIAGRKWVIDSLKFR	HEGTAELSGTV	GMENSGPDVD	IGAVFDKYRILSRPN	RRLTV
	1030	1040	1050	1060	1070 1080
m285.pep	1090	1100	1110	1120	1130 1140
	SGNTRLRYSPQKGISVTGM	IKTDQGLFGS	QKSSMP	SVGDDVVVLGEVK	KKEAAAPLPVNMN
a285	SGNTRLRYSPQKGISVTGM	IKTDQGLFGS	QKSSMP	SVGDDVVVLGEVK	KKEAAAPLPVNMN
	1090	1100	1110	1120	1130 1140
m285.pep	1150	1160	1170	1180	1190 1200
	LTLDLNDGIRFAGYGADV	TIGGKLT	LTAQSGGS	VRGVGTVRVIKGRY	KAYGQDLDTKGT
a285	LTLDLNDGIRFAGYGADV	TIGGKLT	LTAQSGGS	VRGVGTVRVIKGRY	KAYGQDLDTKGT
	1150	1160	1170	1180	1190 1200
m285.pep	1210	1220	1230	1240	1250 1260
	VSVFGPLNDPNLNIRAER	RLSPVGAGVEIL	GSLNSPRIT	LTANEP	MSEKDKLSWLILNRA
a285	VSVFGPLNDPNLNIRAER	RLSPVGAGVEIL	GSLNSPRIT	LTANEP	MSEKDKLSWLILNRA
	1210	1220	1230	1240	1250 1260
m285.pep	1270	1280	1290	1300	1310 1320
	GSGSSGDNAALSAAAGAL	LQINDRIGL	VDDLGF	TSKR	SRNAQTGELNPAEQVLT
a285	GSGSSGDNAALSAAAGAL	LQINDRIGL	VDDLGF	TSKR	SRNAQTGELNPAEQVLT
	1270	1280	1290	1300	1310 1320
m285.pep	1330	1340	1350	1360	1370 1380
	LTGKLYIGYEYSSISAEQ	SVKLIYRL	TRAIQAVARIG	SRSSGGELTYTIR	FD
a285	LTGKLYIGYEYSSISAEQ	SVKLIYRL	TRAIQAVARIG	SRSSGGELTYTIR	FD
	1330	1340	1350	1360	1370 1380
m285.pep	1390				
	DSAGNGKGKX				
a285	DSAGNSKGKX				
	1390				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

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1  CTGAAGCTGT  CGGCGGCACT  GCTGTCTGTC  CTGATTTTGG  CAGTATGTTT
51  CCTCGGCTGG  ATCGCCGGTA  CGGAAGCAGG  TTTGCGCTTC  GGGCTGTACC
101 AAATCCCGTC  CTGGTTCGGC  GTAAACATTT  CCTCCCAAAA  CCTCAAAGGC
151 ACACTGCTCG  ACGGCTTCGA  CGGCGACAAC  TGGTCGATAG  AAACCGAGGG
201 GGCAGACCTT  AAAATCAGCC  GCTTCCGCTT  CGCGTGGAAA  CCGTCCGAAC
251 TGATGCGCCG  CAGCCTGCAC  ATCACCAGCA  TCTCCGCCGG  CGACATCGCC
301 ATCGTAACCA  AACCGACTCC  GCCTAAAGAA  GAACGCCCGC  CTCAAGGCCT
351 GCCCCAGAGC  ATAGACCTGC  CCGCCGCCGT  CTATCTCGAC  CGCTTCGAGA
401 CGGGCAAAAT  CAGCATGGGC  AAAACCTTGG  ACAACAACAA  CGTCTATCTC
451 GAACGCCTCA  ACGCGGCATA  CCGTTACGAC  CGTAAAGGGC  ACCGCCTCGA
501 CCTGAAGGCC  GCCGACACGC  CGTGGAGCAG  TTCGTCGGGG  TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CCGGCCGAAC TGACGATCGA CCGCGGCAAT ATCCGCCTCT
701 CGGGAATAAT CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAAAATTG
751 GAAGAAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCG GATGCCGGGC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAAG TTTTGGGCGG
951 CTTTGTCTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTG GCGCGGAAGA
1101 CGTGCTGCAA ACCCGCTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCTCGCCC AAAATCTCTT GGCAACTCG CACCGGCACG
1201 GCACGCACGG ACGGCAGCCT cgcATCGCA AGCAGCCCCG CAAACGAACA
1251 GCGGAAACTG GTGTTGACA CCGTCAACAT CTCCGCCGGG GAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTT AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCTTCG CGCATCGATC CGCAATTTCC
1401 GGCAGGCGat atCAACGGTT CGATTCTCT TGCCGGTGA TGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTGC CCGGTACGTT CAACGGCGTG
1501 CCGATTGCCG GCAGCGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 CGCCGCCGTG GATTTGCGGT TGGGGCGGAA CATCGTCAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCCGGC GATTTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCCGTTCT
1801 CTCGATTTTA CCTCAAAGG CTCACCCGGC ACAAGCCGCC CGATGCGCGC
1851 CGATATCAAG GCGGCGCCGC TTTCCTGTG GGGCGGCGCG GCGGTTGTCT
1901 ATACCGCGCG CTGACGCTG GAAGGTACGG CCGCGCAGCA CCGCATCCCG
1951 ACACACGCCG CCATGACGCT GGACGGCAA CCGTTCAAAC TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGAACCTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGGTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGGCG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GACAGGAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACGCG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCGCGG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGCG CGCGTTTCG GACGGATTAA CGCCGATTG GGCATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAAATACAC CGCTCGGCGG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCTC CGCGCAAATC GCGGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGTAGCAG CAACTACGGG
2701 AAAATCAACG GCAATATCAC CGTCGGGCAA AGCCGCTCCT TCGATACCGC
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG GCGGCAGCAT CGCCGACCGG CACTTGGGCG GCAGTATCAA
2901 CGGCGACAAG CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGAAC
2951 ACGGCTCGCT CGGTTGCGAT ATTGCAGGCA GGAAATGGGT AATCGACAGC
3001 CTGAAATTCG GGCACGAAGG GACGGCGGAA CTCTCCGGCA CGGTCAGCAT
3051 GGAAAACAGC GTGCCCGATG TCGATATCGG CGCGGTGTTC GACAAATACC
3101 GCATCCTGTC CGGCCCAAC CGCCGCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAAAAC
3201 TGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGCGGCG GGCATCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCTC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCGC
3401 AACCGGGCGG AAATGTGCGT GGGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTACAAAG CATAACGGCA GGATTTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTTGTGCGC CGCTCAACG ACCCAAACCT GAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGC GCGGTGGAAA TATTGGGCAG CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GTGCCGGCAG CGGCAGCAGC GCGCACAATG
3701 CCGCCCTGTC CGCAGCCGCA GCGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAACC GCGCAACTCA ACCCGCGCGA ACAGGTGCTG ACCGTCCGCA
3851 AACAACGTAC CGGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACCT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTTCGCCGT ATCGGCAGCC GTTCGTGGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTCTTC GGTTCGGACA AAAAAGACTC CGCAGGAAAC
4051 GGCAAAAGGA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:
g285-1.pep

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1  LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAVYLD RFETGKISMG KTFDKQTVYL
151 ERLNAARYD RKGHRLDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSIDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGTTASP KISWQLGTGT
401 ARTDGSIAIA SDPANEQRKL VFDTVNISAG EGSILTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAG LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKGPSG TSRPMRADIK GGRSLSLGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASANWQAMG GSLNLQHFSW DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRRIT
851 ASLPDLGALK PFLPAAQNI TGSNLASAQI GGRVGSPPSVN AAVNGSSNYG
901 KLNNGITVGO SRSFDTAPLG GRNLNTVADA EAFRNFLPVG QTVKGSLNAA
951 VTLLGGSIADP HLGGSINGDK LYRNTQTQGI ILDNGLSLRH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTMGIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAASL
1101 PVMNMLTDL NDIIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIK
1151 RYKAYGQDLF ITKGTVSFVG PLNDPNLNIR AERRLSPPVA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAAEQL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL TYTIRFDRIF GSDKKDSAGN
1351 GKKG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCGC GCGCTGCAC ATTACCGAAA TTCCGCGCGC CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCGCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAAAACAAAC CGCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTTGA
501 CCTGAAGGCC GCGGACACGC CGTGGAGCAG TTCGTCGGGG GCGGCCTCGG
551 TCGGCTTGAA AAAACGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGCATCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA CGGCGAGCCT
651 GAAGGATGTG CCGCGCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGCGCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGAC TGAATTTTGA CCTGACCGCC ATCCCGTCGT
851 TTTGAGACGG CATCGCGCTG GAAGGTTTCG TCGATTTTGA AAACACCAAA
901 CGCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGCGCG
951 CTTTGTATC CCGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCGC
1001 CCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCGCGCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATT CGACCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGCGGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GAGTGCCGCA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGCGT GATTGCGGCG TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 CGTTTCGGCA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGT GATTGAGACG GCGGCATCCG AACCTTTGAA ACCGACCTT
1751 CCGCGCGGCG GCGCAACCTG CACATCGGCA AGGCGGCGAG CATCCGTTCC
1801 CTCGATTTC ACGCTCAAAG TTCGCCCAGC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTCGCTGTC GGGCGGAGCG GCGGTTGTCG
1901 ATACCGCCGA CCTGATGCTG GACGGCACGG CGGTGCAGCA CCGCATCCGC
1951 ACACACGCCG CATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGAACCTTAC CCGATGAAA GGCAGCATCG
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2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGCGG CAAATTGGCA

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660

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GGCGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTCGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GCAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAA
2401 GCATTTTCCC TGAACACGCG CTTTCAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGCG GCGCGTTTCG GCGGATTAA CGCGGATTG GGCATCGCCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAATC GCGGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
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2851 GTAACCCCTC GCGCGAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT GCGTTCGCAT ATCGCGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGTA CGGTCCGTAT
3051 GGAACACAGC GGACCCGATG TCGATATCGG CGCGGTGTTC GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCGCCTGA CGGTTTCCG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTCCGTT CGCAAAATC CTCGATGCCG TCCGTCCGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGCGGCG GGCACCGCTC
3301 CCGCTCAATA TGAACCTGAC TTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTACGG GCGGTGGGCA CGGTCCGCT CATCAAAGGG
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3501 CTTTGTCCGC CGCTCAACG ATCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGC GCGGTGGAAA TATTGGGCG CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCTTGGCTC ATCTCAACC GCGCCGGCAG CGGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC TCGAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTT ACCAGCAAGC GCAGCCGCAA
3801 CCGCGAAACC GCGGAACCTA ACCCCGCCGA ACAGGTGCTG ACCGTCCGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCGG CTGACCGCGC CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCCGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGAGCA AAAAGACTC CCGCGGAAAC
4051 GGCAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pep

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1 LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPE ERPLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLECKTIHST ARLSGSLKDV RAELAIDGDN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLSLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFLAG SLNVRGHLG DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA AVVDATDML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSNLQHFWS DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPPGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSINAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGQ SRSDTAPLG GRLNLTVADA EVFRNFLPVG QTVKGSNLAA
951 VTLLGSIADP HLGGSSINGDK LYRNTQTQGI ILDNGLSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGSEL TYTIRFDRFS GSDKDSAGN
1351 GK GK*

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g285-1/m285-1 96.5% identity in 1354 aa overlap

10 20 30 40 50 60

g285-1.pep	LKLSAALLSVLILAVCFGLGWIAGTEAGLRFLGYQIPSWFGVNISSQN	LKLTLLDGFDDGN				
m285-1	LKLSAALLSVLILAVCFGLGWLAGEAGLRFLGYQIPSWFGVNISSQN	LKLTLLDGFDDGN				
	10	20	30	40	50	60
g285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPPLSLPDS					
	70	80	90	100	110	120
g285-1.pep	IDLPAAVYLDRLFETGKISMGKTFDKQTVYLERLNAAVRYDRKGHRLLDLKAADTPWSSSSSG					
m285-1	IDLPAAVYLDRLFETGKISMGKAFDKQTVYLERLDASVRYDRKGHRLLDLKAADTPWSSSSSG					
	130	140	150	160	170	180
g285-1.pep	SASVGLKKPFALDTAIYTKGGFEGETIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	190	200	210	220	230	240
g285-1.pep	PFAESLDKTLLEEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGS	LDLENTK				
m285-1	PFAESLDKTLLEEVLVKGFNINPAAFVPSLPDAGLNFDLTAIPSFSDGIALEGS	LDLENTK				
	250	260	270	280	290	300
g285-1.pep	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILD	LNIGI				
m285-1	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILD	LNIGI				
	310	320	330	340	350	360
g285-1.pep	NSVGAEDVLQTAFFKGRDLGSGIGIGTTASPKISWQLGTGTARTDGS	LAIASDPANEQRKL				
m285-1	NSVGAEDVLQTAFFKGRDLGSGIGIGTTASPKISWQLGTGTARTDGS	LAIASDPANGQRKL				
	370	380	390	400	410	420
g285-1.pep	VFDTVNISAGEGSLTAQGYLELFKDRLLKLDIRSRADFSPRIDPQFPAGDINGS	IHLAG				
m285-1	VLDTVNIAAGQGS	LTAQGYLELFKDRLLKLDIRSRADFSPRIDPQLPAGNINGS	INLAG			
	430	440	450	460	470	480
g285-1.pep	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDRLGRNIVKTDGGFG	KKGD				
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDRLGRNIIKTDGGFG	KKGD				
	490	500	510	520	530	540
g285-1.pep	RLNLNITAPDL	SRFGFLAGSLNVRGHLSGDLDGGIRTFETDLSGTARNLHIGKAADIRS				
m285-1	RLNLNITAPDL	SRFGFLAGSLNVRGHLSGDLDGGIRTFETDLSGAARNLHIGKAADIRS				
	550	560	570	580	590	600
g285-1.pep	LDFTLKGSPGTSRPMRADIKGGRSLSLSGGA	AVVDTAGLTLEGTAQHRI	RTHAAMTLDGK			
m285-1	LDFTLKGSPDTSRPIRADIKGGRSLSLSGGA	AVVDTADMLDGTGVQHRI	RTHAAMTLDGK			
	610	620	630	640	650	660
g285-1.pep	PFKLDLDASGGINRELTRWKSGSIGILDIGGAFNLKLQNRMTLEAGA	EHVAASAANWQAMG				
m285-1	PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLQNRMTLEAGA	ERVAASAANWQAMG				
	670	680	690	700	710	720
g285-1.pep	GSLNLQHFSWDRKTGISAKGGARGLHIAELHNFFKPPFEHNLVLNGDWDV	AYGHNARGYL				
m285-1	GSLNLQHFSWDKKTGISAKGGAGHLHIAELHNFFKPPFEHNLVLNGDWDV	AYGRNARGYL				
	730	740	750	760	770	780

	730	740	750	760	770	780
	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGRITASLPDLGALKPFLPAAQNI TGSLSNAAQIGGRVGSPSVNAAVNGSSNYG					
m285-1	ANAPLGGRITASLPDLGALKPFLPAAQNI TGSLSNAAQIGGRVGSPSVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVQSRSFDTAPLGGRLNLTVADAEAFRNFLPVGQTVKGSLSNAAVTLGGS IADP					
m285-1	KINGNITVQSRSFDTAPLGGRLNLTVADAEVFRNFLPVGQTVKGSLSNAAVTLGGS IADP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVIDGAVFDKYRILSRPNRRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVIDGAVFDKYRILSRPNRRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVTIGGKLTLT AQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTLT AQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGK GK					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGK GKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTT CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGCA CGGAAGCGGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCCGC GTAAACATT CCTCCCAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGAAA CCGTCCGAAC
251 TGATGCGCGG CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCGT CTATCTCGA CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG CCAAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTTCAGACG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTCTAT CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
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1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGTATATCT GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
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1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
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1851 CGACATCAAA GGCAGCCGCC TTTCTGTGTG GGGCGGAGCG GAGGTTGTCTG
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2001 CGCTTCAGG GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCTCTGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA
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2201 CCGGCATATC GGCAAAAGGC GGGCACACAG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
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2351 GGCAAAGCGC CGATGCCGTA TTGCCCGCGG GGCAGGCTTT GGGTTTGAAC
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2451 TGACGGCGGC GCGCGTTTCG GCGGATTAA CCGCGATTTC GACATCGGCA
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2551 GCCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTCTGCG CCGCCGCCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAATC GCGGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCGCCGTCG ACGGCAGCAG CAACTACGGG
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2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTC ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTTCG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTTATTACC GCAACCAAC CCAAGGCATC ATCTTGGAAC
2951 ACGGCTCGCT GCGTTCGCAT ATCGCGGGCA GGAAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTCCGTAT
3051 GGAATAACAG GGAACCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCTGTA CGGTTTCCGG CAACACCGGC
3151 CTGCGCTATC CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTCCGTT CGCAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGTTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGCAG GCGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGC CCGCTCAACG ACCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCGTTTCCCC CGTCGGTGGG GCGTGGAAA TATTGGGCA CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCTTGGCTC ATCTCAACC GCGCCGGCAG TGGCAGCAGC GGCACAAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGTC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAACC GCGGAACCTA ACCCCGCCGA ACAGGTGCTG ACCGTCGGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTACCAG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCCGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCTG CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 AGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

a285-1.pep

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1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAVYLD RFETGKISMV KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLGRGG IRLSGKIDTE
351 KDILDNLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASAAWQAMG GSLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPPGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGNM ANAPLGGRIT
851 ASLPDLGTLK PFLPAAQNI TGSLNAAQI GGRVGSPPSVN AAVNGSSNYG
901 KINGNITVQV SRSFDTAPLG GRNLTLVADA EVFRNFLPVG QTVKGSLNAA
951 VTLLGSIADP HLGGSSINGDK LYRNRQTQGI ILDNGLSLRH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDDVVVLG EVKKEAAAPL
1101 PVMNMLTDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDL ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 SKGK*

```

a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	10	20	30	40	50	60
a285-1.pep	70 WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS	80	90	100	110	120
m285-1	70 WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS	80	90	100	110	120
	130	140	150	160	170	180
a285-1.pep	130 IDLPAAVYLDREFETGKISMVKAFFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG	140	150	160	170	180
m285-1	130 IDLPAAVYLDREFETGKISMVKAFFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG	140	150	160	170	180
	190	200	210	220	230	240
a285-1.pep	190 SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH	200	210	220	230	240
m285-1	190 AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH	200	210	220	230	240
	250	260	270	280	290	300
a285-1.pep	250 PFAESLDKTL EEVLVKGFNI NPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK	260	270	280	290	300
m285-1	250 PFAESLDKTL EEVLVKGFNI NPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK	260	270	280	290	300
	310	320	330	340	350	360
a285-1.pep	310 AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDNLNIGI	320	330	340	350	360
m285-1	310 AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDNLNIGI	320	330	340	350	360
	370	380	390	400	410	420
a285-1.pep	370 NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGLSLAIASDPANGQRKL	380	390	400	410	420
m285-1	370 NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGLSLAIASDPANGQRKL	380	390	400	410	420
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGS	SLTAQGYLELFKDRLLKLD	IRSFADPSRIDPQLPAGNINGS	INLAGE	
m285-1	VLDTVNIAAGQGS	SLTAQGYLELFKDRLLKLD	IRSFADPSRIDPQLPAGNINGS	INLAGE	
	430	440	450	460	470 480
a285-1.pep		490	500	510	520 530 540
a285-1.pep	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDRLGRNIIKTDGGFGKKGD				
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDRLGRNIIKTDGGFGKKGD				
	490	500	510	520	530 540
a285-1.pep		550	560	570	580 590 600
a285-1.pep	RLNLNITAPDLSRFGFLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS				
m285-1	RLNLNITAPDLSRFGFLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS				
	550	560	570	580	590 600
a285-1.pep		610	620	630	640 650 660
a285-1.pep	LDFTLKGPSPTSRPIRADIKGSRLSLSGGAEVVDATDMLDGTGVQHRIRTHAAMTLDGK				
m285-1	LDFTLKGPSPTSRPIRADIKGSRLSLSGGAEVVDATDMLDGTGVQHRIRTHAAMTLDGK				
	610	620	630	640	650 660
a285-1.pep		670	680	690	700 710 720
a285-1.pep	PFKFDLDASGGINRELTRWKGSIGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG				
m285-1	PFKFDLDASGGINRELTRWKGSIGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG				
	670	680	690	700	710 720
a285-1.pep		730	740	750	760 770 780
a285-1.pep	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
m285-1	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
	730	740	750	760	770 780
a285-1.pep		790	800	810	820 830 840
a285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
	790	800	810	820	830 840
a285-1.pep		850	860	870	880 890 900
a285-1.pep	ANAPLGGRITASLPDLGTLKPFLPAAAQNTGSLNAAAQIGGRVGSPSVNAAVNGSSNYG				
m285-1	ANAPLGGRITASLPDLGTLKPFLPAAAQNTGSLNAAAQIGGRVGSPSVNAAVNGSSNYG				
	850	860	870	880	890 900
a285-1.pep		910	920	930	940 950 960
a285-1.pep	KINGNITVQSRSFDTAPLGGRLNLTVAEVRNFLPVGQTVKGSLNAAVTLGGSIAADP				
m285-1	KINGNITVQSRSFDTAPLGGRLNLTVAEVRNFLPVGQTVKGSLNAAVTLGGSIAADP				
	910	920	930	940	950 960
a285-1.pep		970	980	990	1000 1010 1020
a285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS				
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS				
	970	980	990	1000	1010 1020
a285-1.pep		1030	1040	1050	1060 1070 1080
a285-1.pep	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP				
m285-1	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP				
	1030	1040	1050	1060	1070 1080
a285-1.pep		1090	1100	1110	1120 1130 1140
a285-1.pep	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR				
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR				
	1090	1100	1110	1120	1130 1140
a285-1.pep		1150	1160	1170	1180 1190 1200
a285-1.pep	GVGTVRVIKGRYKAYGQDLITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS				
m285-1	GVGTVRVIKGRYKAYGQDLITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS				

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	1150	1160	1170	1180	1190	1200
a285-1.pep	1210	1220	1230	1240	1250	1260
	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	1210	1220	1230	1240	1250	1260
	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
a285-1.pep	1270	1280	1290	1300	1310	1320
	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
m285-1	1270	1280	1290	1300	1310	1320
	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
a285-1.pep	1330	1340	1350			
	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNSKGKX					
m285-1	1330	1340	1350			
	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKGKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

g286.seq

```

1   atgcagaaca ccggtaccat gatgatcaaa ccgaccgccc tgctcctgcc
51  ggctttatth ttctttccgc acgcatacgc gcctgccgcc gacctttccg
101 aaaacaaggc ggcgggtttc gcattgttca aaagcaaaag ccccgacacc
151 gaatcagtc aattaaacc caaattcccc gtccgcatcg acacgcagga
201 cagtgaatc aaagatatgg tcgaagaaca cctgccgctc atcacgcagc
251 agcaggaaga ggttttgat aaggaacaga cgggattcct tgccgaagaa
301 gcaccggaca acgttaaaac aatgctccgc agcaaaaggct atttcagcag
351 caaggtcagc ctgacggaaa aagacggagc ttatacggtg cacatcacac
401 cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcggcgac
451 atcctttcag acggcaacct cgccgaatac taccgcaacg cgctggaaaa
501 ctggcagcag ccggtaggca gcgatttoga tcaggacagt tgggaaaaaca
551 gcaaaacttc cgtcctcggc gcggtaacgc gcaaaggcta cccgcttgcc
601 aagctcggca acaccggggc ggccgtcaac cccgataccg ccaccgccga
651 ttgaaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701 aaatcacccg cacacagcgt taccgccaac aaaccgtctc cggcctggcg
751 cgcttccaac cgggcacgcc ctacgacctc gacctgctgc tcgacttcca
801 acaggcgctc gaacaaaacg ggcattatth cggcgcgctc gtacaagccg
851 acttcgaccg cctcccaagg ggaccgcgtc cccgtcaaag tcagcgtaac
901 cgagggtcaaa cgccaaaac tcgaaaccgg catccgcctc gattcgggat
951 acggtttggg cggcaaaatc gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gtcggtcgt ctgggatag gacaaatacg aaaccacgct
1051 tgccgccggc atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaaacgcgcc
1151 ttctccggcg gcatctggta tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctggggggc gaatttctcg cagaaggccg gaaaatcccc ggctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaaacgc
1301 cagctgctca acaactgtct gcaccccgaa aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtcctccacc gcgctaattc
1401 gcacctctgc ccgcgcaggt tatttcttca cgcccgaata caaaaaactc
1451 ggcacgttca tcatacgcgg acaagcgggt tacaccgttg cagcgacaaa
1501 tgccgatgtc ccctcggggc tgatgttccg cagcggcggc gcgtcttccg
1551 tgcgcgggta cgaacttga

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This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

g286.pep

```

1   MQNTGTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKSKSPDT
51  ESVKIKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAIV HITPGPRTKI ANVGVAIGLD
151 ILSDGNLAIE YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201 KLGNTAAVN PDTATADLV VDSGRPIAF GDFEITGTQR YPEQTVSGLA
251 RFQPGTPYDL DLLLDFQQAL EQNGHYS GAS VQADFRLPR GPRPRQSQRN
301 RGQTPQTRNR HPPRFGIRFG RQNRRLRLQ LQORLYRLGR LYGQIRNHA
351 CRRHQPAQAL SGQLLDKQRF LQPFDPKPR KTRLLRRHLV CARPRGHRQC
401 AGGGISRRRP ENPRLGCREG QQPRHADRL LETPAAQQR A PRKRPLPRR

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451 QNRDDFGHIP VLHRANPHLC PRRLFLHARK QKTRHVHHTR TSGLHRCTRQ
501 CRCPLGADVP QRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq
1 ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
51 GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GGCGGGTTTC GCATTGTTCA AAAACAAAAG CCCCGACACC
151 GAATCAGTCA AATTA AAAACC CAAATTCCCC GTCCTCATCG ACACGCAGGA
201 CAGTGAAATC AAAGATATGG TCGAAGACA CCTGCCGCTC ATCACGCAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCGCCGGACA ACGTTAAAA GATGCTCCGC AGCAAAGGCT ATTTTCAGCAG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA
501 CTGGCAGCAG CCGGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAACA
551 GCAAAACTTC CGTCCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
601 AAGCTCGGCA ATACGCAGGC GGCCGTC AAC CCGGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GGCGACTTTG
701 AAATCACCGG CACACAGCGT TACCCGAAC AAATCGTCTC CGGCCTTGCG
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAACT CGAAACCGGC ATCCGCCTCG ATTCGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT
1051 GCCGCGGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCAACCA AAACCTCGAA AAACGCGCCT
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
1201 CTGGGGGCGG AATTCTCGC AGAAGCGCGG AAAATCCCG GCTCGGCTGT
1251 CGATTGTGGC AACAGCCACG CCACGATGCT GACCGCCTCT TGGAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCGAAA ACGGCCATTA CCTCGACGGC
1351 AAAATCGGTA CGACTTTGGG CACATTCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTCAC GCCGAAAAC AAAAACTCG
1451 GCACGTTTCAT CATACGCGGA CAAGCGGGT ACACCGTTGC CCGCGACAAT
1501 GCCGACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTCCGG CGCGGTGTT CACGATATGG GCGATGCCGC
1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTTCCGGA CTGGGCGTGC
1751 GCTGGTTTCAG CCCGCTTGCG CCGTTTTCCT TCGACATCGC CTACGGGCAC
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep
1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLKPKFP VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAE
101 APDNVKTMLR SKGYFSSKVS LTKDGAYTV HITPGPRTKI ANVGVAIGD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGMPYDL DLLLDFQQAL EQNGHYS GAS VQADFDR LQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYIGSVV WMDMKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNL KRAFSGGVWY VRDRAGIDAR
401 LGAEFLAAGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGTFL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRLTSGAVF HMDGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

668

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP					
g286	MONTGTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKSKSPDTESVKLPKFP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
g286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m286.pep	LTEKDGAYTVHITPGPRTKIANVGVAI LGDILSDGNLA EYYRNALENWQQPVGSDFDQDS					
g286	LTEKDGAYTVHITPGPRTKIANVGVAI LGDILSDGNLA EYYRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDTATADLN VVDSGRPIAFGDFEITGTQR					
g286	WENSKTSVLGAVTRKGYPLAKLGNTRAAVNPDTATADLN VVDSGRPIAFGDFEITGTQR					
	190	200	210	220	230	240
	250	260	270	280	290	299
m286.pep	YPEQIVSGLARFQPGMPYDL DLLDFQQA LEQNGHYS GASVQADFDR L-QGDRVPVKVSV					
g286	YPEQTVSGLARFQPGTPYDL DLLDFQQA LEQNGHYS GASVQADFDR LPRGPRPRQSQRN					
	250	260	270	280	290	300
	300	310	320	330	340	359
m286.pep	TEVKRHKLETGIRLDSEYGLGGKIAYDYNNLFNKGYIGSVVWMDKYETTLAAGISQPRN					
g286	RGQTPQTRNRHPPRFGIRFGRQNRLRL LQPLQORLYRLGRLGYGQIRNHACRRHQPA AQL					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1197>:

a286.seq

1	ATGCACGACA	CCCGTACCAT	GATGATTAAA	CCGACCGCCC	TGCTCCTGCC
51	GGCTTTATTT	TTCTTTCCGC	ACGCATACGC	GCCTGCCGCC	GACCTTTCCG
101	AAAACAAGGC	GGCGGGTTTC	GCATTGTTCA	AAAACAAAAG	CCCCGACACC
151	GAATCAGTTA	AAT'AAAACC	CAAATTCCCC	GTCCGCATCG	ACACGCAGGA
201	TAGTGAAATC	AAAGATATGG	TCGAAGAACA	CCTGCCGCTC	ATCACGCAGC
251	AGCAGGAAGA	AGTATTGGAC	AAGGAACAGA	CGGGCTTCCT	CGCCGAAGAA
301	GCACCGGACA	ACGTTAAAAC	AATGCTCCGC	AGCAAAGGCT	ATTTCAGCAG
351	CAAAGTCAGC	CTGACGGAAA	AAGACGGAGC	TTATACGGTA	CACATCACAC
401	CGGGCCCGCG	CACCAAAATC	GCCAACGTCG	GCGTCGCCAT	CCTCGGCGAC
451	ATCCTTTCAG	ACGGCAACCT	CGCCGAATAC	TACCGCAACG	CGCTGGAAAA
501	CTGGCAGCAG	CCGGTAGGCA	GTGATTTCGA	TCAGGACAGT	TGGGAAAACA
551	GCAAAACTTC	CGTCCTCGGC	GCGGTAACGC	GCAAAGCCTA	CCCGCTTGCC
601	AAGCTCGGCA	ACACCCGGGC	GGCCGTCAAC	CCCGATACCG	CCACCGCCGA
651	TTTGAACGTC	GTCGTGGACA	GCGGCCGCCC	CATCGCCTTC	GGCGACTTTG
701	AAATTACCGG	CACGCAGCGT	TACCCCGAAC	AAATCGTCTC	CGGCTTGGCG
751	CGCTTCCAAC	CGGGCACGCC	CTACGACCTC	GACCTGCTGC	TCGACTTCCA
801	ACAGGCGCTC	GAACAAAACG	GGCATTATTC	CGGCGCGTCC	GTACAAGCCG
851	ACTTCGACCG	CCTCCAAGGC	GACCGCGTCC	CCGTCAAAGT	CAGCGTAACC
901	GAGGTCAAAC	GCCACAAGCT	CGAAACCGGC	ATCCGCCTCG	ATTCGGAATA
951	CGGTTTGGGC	GGCAAAATCG	CCTACGACTA	TTACAACCTC	TTCAACAAAG
1001	GCTATATCGG	TTCGGTCGTC	TGGGATATGG	ACAAATACGA	AACCACGCTT
1051	GCCGCGGCA	TCAGCCAGCC	GCGCAACTAT	CGGGGCAACT	ACTGGACAAG
1101	CAACGTTTCC	TACAACCGTT	CGACCACCCA	AAACCTCGAA	AAACGCGCCT
1151	TCTCCGGCGG	CATCTGGTAT	GTGCGCGACC	GCGCGGGCAT	CGATGCCAGG
1201	CTGGGGGCGG	AGTTTCTCGC	AGAAGGCCGG	AAAATCCCCG	GCTCGGATAT
1251	CGATTTGGGC	AACAGCCACG	CCACGATGCT	GACCGCCTCT	TGGAAACGCC
1301	AGCTGCTCAA	CAACGTGCTG	CATCCCGAAA	ACGGCCATTA	CCTCGACGGC

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1351 AAAATCGGTA CGACTTTGGG CGCATTCTTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAAACTCG
1451 GCACGTTTAT CATAACGCGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCG ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTC CACGATATGG GCGACGCCGC
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTCTGGG CTGGGCGTGC
1751 GCTGGTTTCA CCCGCTCGCG CCGTTTTCTT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

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This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

```

a286.pep
  1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
 51 ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLLAE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAITV HITPGPRTKI ANVGVAIGLD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTAAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLDFQQAL EQNGHYS GASVQADFDRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYIGSVV WMDMKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTTQNL KRAFSGGIWY VRDRAGIDAR
401 LGAEFLAAGR KIPGSDIDL NSHATMLTAS WKRLNNNL HPENGYLDG
451 KIGTTLGAFL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NSVLPERAL LVGSLEYQLP
551 FTRTSLGAVF HDMGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDDKIRWHIS LGTRF*

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m286/a286 98.7% identity in 615 aa overlap

m286.pep	10	20	30	40	50	60
	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPKFP					
a286	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPKFP					
	10	20	30	40	50	60
m286.pep	70	80	90	100	110	120
	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLLAEAPDNVKTMLRSKGYFSSKVS					
a286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLLAEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
m286.pep	130	140	150	160	170	180
	LTEKDGAITVHITPGPRTKIANVGVAIGLDILSDGNLAAYRNALENWQQPVGSDFDQDS					
a286	LTEKDGAITVHITPGPRTKIANVGVAIGLDILSDGNLAAYRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
m286.pep	190	200	210	220	230	240
	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDTATADLNVVDSGRPIAFGDFEITGTQR					
a286	WENSKTSVLGAVTRKAYPLAKLGNTAAVNPDTATADLNVVDSGRPIAFGDFEITGTQR					
	190	200	210	220	230	240
m286.pep	250	260	270	280	290	300
	YPEQIVSGLARFQPGMPYDLDLLDFQQALEQNGHYS GASVQADFDRLQGDRVPVKVSVT					
a286	YPEQIVSGLARFQPGTPYDLDLLDFQQALEQNGHYS GASVQADFDRLQGDRVPVKVSVT					
	250	260	270	280	290	300
m286.pep	310	320	330	340	350	360
	EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKGYIGSVVWMDMKYETTLAAGISQPRNY					
a286	EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKGYIGSVVWMDMKYETTLAAGISQPRNY					
	310	320	330	340	350	360
	370	380	390	400	410	420

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m286.pep  RGNYWTSNVSYNRSTTQNLEKRAFSGGVWYVRDRAGIDARLGAEFLAEGRKIPGSAVDLG
a286      RGNYWTSNVSYNRSTTQNLEKRAFSGGIWYVRDRAGIDARLGAEFLAEGRKIPGSDIDLG
           370      380      390      400      410      420

           430      440      450      460      470      480
m286.pep  NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286      NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
           430      440      450      460      470      480

           490      500      510      520      530      540
m286.pep  KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
a286      KKLGTFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
           490      500      510      520      530      540

           550      560      570      580      590      600
m286.pep  LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPPLAPFSFDIAYGH
a286      LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPPLAPFSFDIAYGH
           550      560      570      580      590      600

           610
m286.pep  SDKKIRWHISLGRFX
a286      SDKKIRWHISLGRFX
           610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

```

g287.seq
1  atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51  ctgtgggggc ggcgtggtgc gatcgcccga tgtcaagtcg gcggacacgc
101 cgtcaaaaacc ggccgcccc cgtgtgtgtg aaaatgccgg ggaaggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcgtg cgccgcaagc
201 cgatacgtag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 tttcggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaa atgccgccga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 ccccgcgctc aaaccctgcc cctgcgaatg gcggtagcga ttttgaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtgcg aaaaataaac
501 gttgaccac tgtaaaggcg attcttgtaa tgggtgataat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaaagcat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaaacc acctactcgt tctgcacggc cgaggaggtc gcttcgggc
751 gagattccgc tgattcccgt caatcaggcc gatacgtgta ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcggtatc
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttgttgg
951 cacggccgtg tacaacggcg aagtgtgca tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatggaaa cggctttaag gggacttga
1151 cggaaaatgg cggcggggat gtttcgggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaagg
1251 cggattccgc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

```

g287.pep
1  MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV
51  LPKEKKDEEA AGGAPQADTQ DATAGEGSQD MAAVSAENTG NGGAATDNPN
101 KNEDAGAQN DMPQNAESAN QTGNQNPAGS SDSAPASNPA PANGGSDFGR

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```

151  TNVGNVSVVID  GPSQNITLTH  CKGDSCNGDN  LLDEEAPSKS  EFEKLSDEEK
201  IKRYKKDEQR   ENFVGLVADR  VKKDGTNKYI  IFYTDKPPTR  SARSRRSLPA
251  EIPLIPVNQA   DTLIVDGEAV  SLTGHSGNIF  APEGNYRYLT  YGAEKLPGGS
301  YALRVQGEPA   KGEMLVGTAV  YNGEVLHFHM  ENGRPYPSGG  RFAAKVDFGS
351  KSVDMIIDSG   DDLHMGTKF  KAAIDGNFK  GTWTENGGGD  VSGRFYGPAG
401  EEVAGKYSYR   PTDAEKGFG  VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1   ATGTTTAAAC  GCAGCGTAAT  CGCAATGGCT  TGTATTTTGT  CCCTTTCAGC
51  CTGCGGGGCG  GGCGGTGGCG  GATCGCCCGA  TGTCAAGTCG  GCGGACACGC
101 TGTCAAAACC  TGCCGCCCTT  GTTGTCTTCT  AAAAAGAGAC  AGAGGCAAAG
151 GAAGATGCGC  CACAGGCAGG  TTCTCAAGGA  CAGGGCGCGC  CATCCGCACA
201 AGGCAGTCAA  GATATGGCGG  CGGTTTTCGA  AGAAAATACA  GGCAATGGCG
251 GTGCGGTAAC  AGCGGATAAT  CCCAAAAATG  AAGACGAGGT  GGCACAAAAT
301 GATATGCCGC  AAAATGCCGC  CGGTACAGAT  AGTTCGACAC  CGAATCACAC
351 CCCGATCCG  AATATGCTTG  CCGGAAATAT  GGAAATCAA  GCAACGGATG
401 CCGGGGAATC  GTCTCAGCCG  GCAAACCAAC  CGGATATGGC  AAATGCGGCG
451 GACGGAATGC  AGGGGGACGA  TCCGTCGGCA  GGCGGGCAAA  ATGCCGGCAA
501 TACGGCTGCC  CAAGGTGCAA  ATCAAGCCGG  AAACAATCAA  GCCGCCGGTT
551 CTTCAGATCC  CATCCCCGCG  TCAAACCCTG  CACCTGCGAA  TGGCGGTAGC
601 AATTTTGGAA  GGGTTGATT  GGCTAATGGC  GTTTTGATTG  ACGGGCCGTC
651 GCAAAATATA  ACGTTGACCC  ACTGTAAAGG  CGATTCTTGT  AGTGGCAATA
701 ATTTCTTGA  TGAAGAAGTA  CAGCTAAAT  CAGAATTTGA  AAAATTAAGT
751 GATGCAGACA  AAATAAGTAA  TTACAAGAAA  GATGGGAAGA  ATGATAAATT
801 TGTCGGTTTG  GTTGCCGATA  GTGTGCAGAT  GAAGGGAATC  AATCAATATA
851 TTATCTTTA  TAAACCTAAA  CCCACTTCAT  TTGCGCGATT  TAGGCGTTCT
901 GCACGGTCGA  GGCGGTGCGT  TCCGGCCGAG  ATGCCGCTGA  TTCCCGTCAA
951 TCAGGCGGAT  ACGCTGATTG  TCGATGGGGA  AGCGGTCAGC  CTGACGGGGC
1001 ATCCCGCAA  TATCTTCGCG  CCCGAAGGGA  ATTACCGGTA  TCTGACTTAC
1051 GGGCGGAAA  AATTGCCCCG  CGGATCGTAT  GCCCTTCGTG  TTCAAGGCGA
1101 ACCGGCAAAA  GGCGAAATGC  TTGCGGGCGC  GGCCGTGTAC  AACGGCGAAG
1151 TACTGCATTT  CCATACGGAA  AACGGCCGTC  CGTACCCGAC  CAGGGGCAGG
1201 TTTGCCGCAA  AAGTCGATTT  CGGCAGCAAA  TCTGTGGACG  GCATTATCGA
1251 CAGCGCGCAT  GATTTGCATA  TGGGTACGCA  AAAATTCAA  GCCGCCATCG
1301 ATGGAACCG  CTTTAAGGGG  ACTTGACGG  AAAATGGCAG  CGGGGATGTT
1351 TCCGGAAAGT  TTTACGGCCC  GGCCGGCGAG  GAAGTGCGG  GAAAATACAG
1401 CTATCGCCCG  ACAGATGCGG  AAAAGGGCG  ATTCGGCGTG  TTTGCCGGCA
1451 AAAAAGAGCA  GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1   MFKRSVIAMA  CIFALSACGG  GGGGSPDVKS  ADTLSKPAAP  VVSEKETEAK
51  EDAPQAGSQG  QGAPSAQGSQ  DMAAVSEENT  GNGGAVTADN  PKNEDEVAQN
101 DMPQNAAGTD  SSTPNHTPDF  NMLAGNMENQ  ATDAGESSQP  ANQPDMANAA
151 DGMQGDPSA  GGQNAGNTAA  QGANQAGNNQ  AAGSSDPIPA  SNPAPANGGS
201 NFRVLDLANG  VLIDGPSQNI  TLTHCKGDSC  SGNNFLDEEV  QLKSEFEKLS
251 DADKISNYKK  DGKNDKFVGL  VADSVQMKGI  NQYIIFYKPK  PTSFARFRRS
301 ARSRRSLPAE  MPLIPVNQAD  TLIVDGEAVS  LTGHSGNIFA  PEGNYRYLTY
351 GAEKLPGGSY  ALRVQGEPAK  GEMLAGAAVY  NGEVLHFHTE  NGRPYPTRGR
401 FAAKVDFGSK  SVDGIIDSGD  DLHMGTKFK  AAIDGNFGK  TWTENGSGDV
451 SGKFYGPAGE  EVAGKYSYRP  TDAEKGFGV  FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

              10      20      30      40      49
m287.pep      MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETEA
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287           MFKRSVIAMACIFLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA
              10      20      30      40      50      60

```

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m287.pep	50	60	70	80	90	100	109
	KEDAPQAGSQGQGAPSAQGSQDMAAVSEENTGNNGAVTADNPKNEDEVAQNMPQNAAGT						
g287	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNNGAATTDNPKNEDAGAQNMPQNA--						
	70	80	90	100	110		
m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDDPSAGGQNAGNTA						
g287	-----						
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQAAGSSDPIASNPAANGGSNFGRLVLANGVLIDGPSQNTITLTHCKGDS						
g287	-ESANQTGNNQPAGSSDSAPASNPAANGGSDFGRNTVGNVSVVIDGPSQNTITLTHCKGDS						
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP						
g287	CNGDNLLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKDGTNKYIIFYTD						
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
	KPTSFAFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNRYLT						
g287	KPPT-----RSARSRRSLPAEIPLPVNQADTLIVDGEAVSLTGHSNIFAPEGNRYLT						
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGS						
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFPAKVDGFS						
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
	KSVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYR						
g287	KSVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYR						
	360	370	380	390	400	410	
m287.pep	470	480	489				
	PTDAEKGGFVGFAGKKEQDX						
g287	PTDAEKGGFVGFAGKKDRDX						
	420	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1203>:

a287.seq

1	ATGTTTAAAC	GCAGTGTGAT	TGCAATGGCT	TGTATTGTTG	CCCTTTCAGC
51	CTGTGGGGGC	GGCGGTGGCG	GATCGCCCGA	TGTTAAGTCG	GCGGACACGC
101	TGTCAAACCC	TGCCGCCCT	GTTGTTACTG	AAGATGTCGG	GGAAGAGGTG
151	CTGCCGAAAG	AAAAGAAAGA	TGAGGAGGCG	GTGAGTGGTG	CGCCGCAAGC
201	CGATACGCAG	GACGCAACCG	CCGGAAAAGG	CGGTCAAGAT	ATGGCGGCAG
251	TTTCGGCAGA	AAATACAGGC	AATGGCGGTG	CGGCAACAAC	GGATAATCCC
301	GAAAATAAAG	ACGAGGGACC	GCAAATGAT	ATGCCGCAA	ATGCCGCCGA
351	TACAGATAGT	TCGACACCGA	ATCACACCCC	TGCACCGAAT	ATGCCAACCA
401	GAGATATGGG	AAACCAAGCA	CCGGATGCCG	GGGAATCGCG	ACAACCGGCA
451	AACCAACCGG	ATATGGCAAA	TGCGCGGAC	GGAAATGCAGG	GGGACGATCC
501	GTCGGCAGGG	GAAAATGCCG	GCAATACGGC	AGATCAAGCT	GCAAATCAAG
551	CTGAAAACAA	TCAAGTCGGC	GGCTCTCAAA	ATCCTGCCTC	TTCAACCAAT
601	CCTAACGCCA	CGAATGGCGG	CAGCGATTTT	GGAAGGATAA	ATGTAGCTAA
651	TGGCATCAAG	CTTGACAGCG	GTTCGGAAAA	TGTAACGTTG	ACACATTGTA
701	AAGACAAAGT	ATGCGATAGA	GATTTCCTAG	ATGAAGAAGC	ACCACCAAAA
751	TCAGAATTTG	AAAAATTAAG	TGATGAAGAA	AAAATTAATA	AATATAAAAA

a287.pep

1	MFKRSVIAMA	CIVALSACGG	GGGGSPDVK	ADTLSKPAAP	VVTEDVGEEV
51	LPKEKKDEEA	VSGAPQADTQ	DATAGKGGQD	MAAVSAENTG	NGGAATTDNP
101	ENKDEGPQND	MPQNAADTDS	STPNHPTAPN	MPTRDMGNQA	PDAGESAQPA
151	NQPDMANAAD	GMQGDTPSAG	ENAGNTADQA	ANQAEENNQV	GSQNPASSTN
201	PNATENGGSDF	GRINVANGIK	LDSGSENVTL	THCKDKVCDR	DFLDEEAPPK
251	SEFEKLSDEE	KINKYKKDEQ	RENFVGLVAD	RVEKNGTNKY	VIIYKDKSAS
301	SSSARFRRSA	RSRRSLPAEM	FLIPVNQADT	LIVDGEAVSL	TGHSNGIFAP
351	EGNYRYLTYG	AEKLSGGSYA	LSVQGEPAGK	EMLAGTAVYN	GEVLHFHFMK
401	GRPSPSGGRF	AAKVDFGSKS	VDGIIDSGDD	LHMGTQKFKA	VIDNGFGKGT
451	WTENGSGDVS	GRFYGPAGEE	VAGKYSYRPT	DAEKGFGFVF	AGKKEOD*

```

              10      20      30      40      49
m287.pep    MFKRSVIAMACIFALSACGGGGGSPDVKSADTL SKPAAPV VSE-----KETEA
             ||||| | | | | | | | | | | | | | | | | | : |
a287        MFKRSVIAMACIVALSACGGGGGSPDVKSADTL SKPAAPVV TEDVGEEVL PKEKKDEEA
              10      20      30      40      50      60

```

```

50          60          70          80          90          100          109
m287.pep    KEDAPQAGSQGGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNDMFPQNAAGT
             ||||:| |:::||| |||||:|:|:|:|:| |||||
a287        VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNFENKDEGPQNDMFPQNAADT
             70          80          90          100          110

```

```

      110      120      130      140      150      160      169
m287.pep  DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDDPSAGGQNAGNTA
          ||||| : : ||| : ||||| : ||||| : ||||| : |||||
a287      DSSTPNHTPAPNMPTRDMGNQAPDAGESAQFANQPDMANAADGMQGGDDPSAG-ENAGNTA
          120      130      140      150      160      170

```

```

170      180      190      200      210      220      229
m287.pep  AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRGVDLANGVLIDGPSQNITLTHCKGDS
           |:||| |:|:| |:|:| :||| :|||:| |:|:| |:|:| |:|:| |:|:|
a287      DQAAQAEENNQVGGSQNPASSTNPATNGGSDFGFRINVANGIKLDSGSENVTLTHCKDKV
           180      190      200      210      220      230

```

```

      230      240      250      260      270      280      289
m287.pép  CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIIFYKP
           | :  :| | | | |  | | | | | | | : | : | | | |  : : | | | : | |
a287      CD-RDFLDEEAPPKSEFEKLSDEEEKINKYKKDEQRFVGLVADRVKNGTNGYVIIYKD
           240      250      260      270      280      290

```

```

290      300      310      320      330      340
m287.pep  KP--TSFARFRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY
          |  :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287      KSASSSSARFRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY
          300      310      320      330      340      350

```


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	350	360	370	380	390	400
m287 . pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287 . pep	GSKSVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSQKFGYPAGEEVAGKYS					
a287	GSKSVDGIIDSGDDLHMGTKQFKAVIDGNGFKGTWTENGSGDVSQKFGYPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287 . pep	YRPTDAEKGFGVFAGKKEQDX					
a287	YRPTDAEKGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288 . seq
1   atgcacaccg gacaggcggg aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgtcaag caacctacc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcgggtg cgcccttacc gcaccttttc
201 acccttgccg gtgctgccaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccgccg ttaaccggca ttctaccctg
301 cggagcccgg actttcctcc ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgcgg cgcggattat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacagggt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgtc caagtcgccc tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288 . pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288 . seq
1   ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTGTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTG CTTTCTGTTC
251 CACTTTCCTG CCGCTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288 . pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
	: : : : : : : : : :					
g288	PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	:					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTGCCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCTT GTGCTGCCAA AGCAGCCATC GCGGTTTTTG CTTTCTGTTC
251 CACTTTCGGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TAAAGCCGTC CAAGTCGCCG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGTCTTT AATGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

```

a288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHA
151 LFQAGFDKAV QVAVQYGFV ADFVACAQVF NA*

```

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
	: : : : : : : :					

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```

a288      PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADFEVACAQVF
           130      140      150      160      170      180

m288.pep   DTX
           ::
a288      NAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

```

g290.seq
1  atggcaaaaa tgatgaaatg ggcggtgtt gcggcggtcg cggcggcagc
51  ggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
151 ggcgagattt cgcggtccaa cctggtatcg gtcggcgcg caggcttcggg
201 gcagattaaa aagctttatg tcaaactcgg gcaacaggtc aaaaagggcg
251 atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg
301 gaaaaatcca aattggaaac gtatcaggcg aagctgggtg ccgcacagat
351 tgcattgggc agcgcgga aaatataa gcgtcaggcg gcgttgtgga
401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt
451 gccgcccga aagccaatgt tgccgagttg aaggctttaa tcagacagag
501 caaaatttcc atcaataccg ccgagtcgga ttggggtac acgcgcatta
551 ccgcgacgat ggacggcacg gtggtggcga ttcccgaggc agaggggcag
601 actgtgaacg cggcgcgagc tacgcccagc attgtccaat tggcgaatct
651 ggatatgatg ttgaacaaaa tgcagattgc cgagggcgat attaccaagg
701 tgaaggcggg gcaggatatt tcgtttacga tttgtccga accggatacg
751 ccgattaagg cgaagctcga cagcgtcgac cccgggctga ccacgatgtc
801 gtcgggcccg tacaacagca gtacggatac ggcttccaat gcggtctatt
851 attatgcccg ttcgtttgtg ccgaatccgg acggcaaaact cgccacgggg
901 atgacgacgc agaatacggg tgaaatcgac ggtgtgaaaa atgtgttgc
951 tattccgctc ctgaccgtga aaaatcgcg cggcaaggcg ttcgtacgcg
1001 tgttgggtgc ggacggcaag gcagtggaac gcgaaatccg gaccggtatg
1051 aaagacagta tgaataccga agtgaaaagc gggttgaaag agggggacaa
1101 agtggtcatc tccgaaataa ccgcccgcga gcagcaggaa agcggcgaa
1151 gcgccctagg cggcccgcgc cggcgataa

```

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

```

g290.pep
1  MAKMMKWA AV AAVAAAVWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDLIAEIN STTQNTIDM
101 ESKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATSK EDLESAQDAL
151 AAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPD
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYARSFV PNPDGKLTATG
301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
351 KDSMNTEVKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

```

m290.seq (partial)
1  ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
51  ACTCGGGCAA CAGGTTAAAA AGGGCGATTT GATTGCGGAA ATCAATTCGA
101 CCTCGCAGAC CAATACGCTC AATACGAAA AATCCAAGTT GGAAACGTAT
151 CAGGCGAAGC TGGTGTCTGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
251 ATTTGGAAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
301 GAGCTGAAGG CTTTAATCAG ACAGAGCAA ATTTCCATCA ATACCGCCGA
351 GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG
401 TGGCGATTCT CGTGGAAGAG GGGCAGACTG TGAACGCGGC GCAGTCTACG
451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA
501 GATTGCCGAG GGCGATATTA CCAAGGTGAA GGCGGGGCAG GATATTTTCG
551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC
601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GCGGTTTACA ACAGCAGTAC
651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCGTTTCG TTTGTGCCGA

```

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```

701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGAATAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TGCGCGTGTT GGGTGGCGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
  1 ..VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
 51 QAKLVSAQIA LGSAEKKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQUIAE GDITKVKGAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYNSSTDSTA SNAVYYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLLI PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

m290.pep                                10      20      30
                                VSVGAQASGQIKILYVKLGQVKKGDLIAE
                                |||
g290      PQAAYTEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQVKKGDLIAE
      30      40      50      60      70      80

m290.pep                                40      50      60      70      80      90
INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
|||:||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g290      INSTTQTNTIDMEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATSKEDLESAQD
      90      100     110     120     130     140

m290.pep                                100     110     120     130     140     150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g290      ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPEEGQTVNAAQST
      150     160     170     180     190     200

m290.pep                                160     170     180     190     200     210
PTIVQLANLDMMLNKMQUIAEGDITKVKGAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g290      PTIVQLANLDMMLNKMQUIAEGDITKVKGAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
      210     220     230     240     250     260

m290.pep                                220     230     240     250     260     270
GGYNSSTDSTASNAVYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g290      GGYNSSTDSTASNAVYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
      270     280     290     300     310     320

m290.pep                                280     290     300     310     320     330
KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g290      KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
      330     340     350     360     370     380

m290.pep      PPRRX
              ||||
g290          PPRRX
              390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1  ATGGCAAAAA TGATGAAATG GCGGGCTGTT GCGGCGGTCG CGGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAAC GGTCAGGCGC GGCGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAACCTTATG TCAAACTCGG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCAATTGGG AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTGGA AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATTA
551 CCGAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTTGTG CCGAATCCGG ACGGCAAACT CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAATCGAC GGTGTGAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCG CGGCAGGGCG TTTGTGCGCG
1001 TGTGGGTGTC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1  MAKMMKWAIV AAVAAAAVWG GWSYLPPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDLIAEIN STSQTNTLNT
101 ESKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSG YNSSTDASN AVYYARSFV PNPDKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTVEKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

m290/a290 98.2% identity in 334 aa overlap

m290.pep
10 20 30
VSVQAQASGQIKILYVKLGQOVKKGDLIAE
|||||
a290
PQAAYITETVRRGDISRTVSATGEISPSNLVSQAQASGQIKKLYVKLGQOVKKGDLIAE
30 40 50 60 70 80

m290.pep
40 50 60 70 80 90
INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
|||||
a290
INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATAKEDLESAQD
90 100 110 120 130 140

m290.pep
100 110 120 130 140 150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||
a290
ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
150 160 170 180 190 200

m290.pep
160 170 180 190 200 210
PTIVQLANLDMMLNKMQUIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
|||||
a290
PTIVQLANLDMMLNKMQUIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
210 220 230 240 250 260

220 230 240 250 260 270
```

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```

m290.pep      GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
a290          GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               270      280      290      300      310      320

               280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
               :||||||||||||||||||||||||||||||||||||||||||||||||||
a290          RAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
               330      340      350      360      370      380

m290.pep      PPRRX
               ||||
a290          PPRRX
               390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggccttg gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttgacaaa agccatcaaa gaagtacgcy
401 gcaacggcaa gctgaaagtc gccgtcttct cgcaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaatctt atggtgtcag cccgaccgtg ccaaagcgtg gacggatttg
601 atgcgtaaa gcaaattccc ggtcggcggc agcatctgcg acaatcccg
651 cgcggaacc acttccttgg gcgaacagtt cggttcaac ggcacgccga
701 cccttcgtct tccccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaac cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLP LLAC GQTPVSNANA ESAVKAESAG KSAASLKR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTD AEG GYMFV GELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHPQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAaaaaa CCTATTCCGC CCAAGATTG AAAGTGTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCCTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGACAAA AGCCATCAAA GAAGTGCGCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCCTGCA CCCCATGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTGAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATCCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC

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751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence <SEQ ID 1220; ORF 292>:

```

m292.pep
  1 MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLKR
 51 LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m292/g292 98.7% identity in 238 aa overlap

      10      20      30      40      50      60
m292.pep MKTKLIKILTPFTVLPLLACGQTPVSNANAEPAPVKAESAGKSVASLKRLEKTYSAQDL
          |||||
g292      MKTKLIKILTPFTVLPLLACGQTPVSNANAESAVKAESAGKSVASLKRLEKTYSAQDL
          |||||

      70      80      90     100     110     120
m292.pep KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
          |||||
g292      KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
          |||||

     130     140     150     160     170     180
m292.pep ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
          |||||
g292      ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
          |||||

     190     200     210     220     230     240
m292.pep ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNPTLVFPNG
          |||||
g292      ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNPTLRLPQR
          |||||

     250     260
m292.pep RSQSGYSPMPQLEEIIRKNQX
g292      AHPKRLQPDAPTGGNHPQKPAVNPOX
          250     260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1 ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51 GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGC GCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCTGCA CCCCAGTGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATTTCC GGTCGCGCGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC
751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAASLKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAGG GYMFVGGELIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLV AVFSDPDCPF
151  CKRLEHEFEK MTDVTYSEFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251  QLEEIIRKNQ *

m292/a292    100.0% identity in 260 aa overlap

      10      20      30      40      50      60
m292.pep    MKTKLIKILTPFTVLPLLACGQTPVSNANAEPAPVKAESAGKSVAAASLKARLEKTYSAQDL
a292         MKTKLIKILTPFTVLPLLACGQTPVSNANAEPAPVKAESAGKSVAAASLKARLEKTYSAQDL
      10      20      30      40      50      60

      70      80      90     100     110     120
m292.pep    KVLVSSETPVKGIYEVVVSQRQIIYTDAGGGMFVGGELINIDTRKNLTEERAADLNKIDF
a292         KVLVSSETPVKGIYEVVVSQRQIIYTDAGGGMFVGGELINIDTRKNLTEERAADLNKIDF
      70      80      90     100     110     120

      130     140     150     160     170     180
m292.pep    ASLPLDKAIKEVRGNGKLVAVFSDPDCPFCKRLEHEFEKMTDVTYSEFMPIAGLHPDA
a292         ASLPLDKAIKEVRGNGKLVAVFSDPDCPFCKRLEHEFEKMTDVTYSEFMPIAGLHPDA
      130     140     150     160     170     180

      190     200     210     220     230     240
m292.pep    ARKAQILWCQPDRAKAWTDWMRKGFVGGGICDNPVAETTSLSGEQFGFNGTPTLVFPNG
a292         ARKAQILWCQPDRAKAWTDWMRKGFVGGGICDNPVAETTSLSGEQFGFNGTPTLVFPNG
      190     200     210     220     230     240

      250     260
m292.pep    RSQSGYSPMPQLEEIIRKNQX
a292         RSQSGYSPMPQLEEIIRKNQX
      250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
  1  atgcgtatta cctgtgccc gatgtcgctt ttgtcggcgg cagtctggtc
 51  gggttcgggct gtcagaacat catcgaaccg ctttcctcgc gcgttacgac
101  gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151  tggcatcggg tgcggcgggt caagtcgaat cggcggacgc gtggcgtgaa
201  gccgttgaaa aaaccttata tggcgagggg ggcggaatgc agatgcaggc
251  gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301  ccgaggcggg gcgggaagcg gtatgcggac atcgggggcg atagtgtatc
351  aatccgtatc cgagttttcc ggttgaggca tcgtatgagt atttatgccg
401  tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcgtg
451  ttttttgaag tgctggtttt gtcctgctcg catacgggac ggggtgtcgcg
501  cgaggcgcgg cgcgagtggt aaaaggcaat gtcttaccgc gccgtcaggg
551  tgatgccgtt tgcggtcgga ctgctgttcg ccagggaac tctagagtcg
601  actgcagcag catgccctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
  1  MRITCAPMSL LSAAVWSVRA VRTSSNRFFA ALRRYSAPFR TIFPKPAGTP
 51  WHRVRRFKSN RRTRGVKPLK KPYLARGAEC RCRRRAWTALS HNIAERARES
101  PRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151  FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVPFAVG LLFARGTLES
201  TAAACP....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

m294.seq

```

1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTCGGGTT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
151 TGGCATCGGG TCGGCGGTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
201 GCCGTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG
451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CACACGGGAC GGGTGTCGCG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTCG CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCCG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
701 TCGCCATCGC CGTCGTCAA ATGGCGCGT CCACACTGAC GGTCCGTTGG
751 TCGAAATACA TACAGCCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
801 TTTGGCAAAA GCGATGTTT ATATCAGCTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep

```

1  MRITCAPMSL LSAAVWSIRV VRTSSNRFP AFRYSAFQ TIFPKPADTP
51  WHRVRRFKSN RRMGGKPLK KPYRPRGGC RCRRWTALS HNIAERARES
101 PRRCGKRYAD IGGSDTIRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV
151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
201 ANRYSILGE PFATSFGMTL TLKILLAFSV LAHFAIAVVK MARSTLTVGW
251 SKYIHAVVFT HMLLIVFLAK AMFYISW*

```

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSA	AVWSVRVAVRTSSNR	FPAALRRYS	AFRPTIFPK	PAGTPWHRV	RRFKSN
m294	MRITCAPMSLLSA	AVWSIRVVRTSSNR	FPAFRYS	AFQPTIFPK	PADTPWHRV	RRFKSN
	10	20	30	40	50	60
	70	80	90	100	110	120
g294.pep	RRTRGVKPLKPY	LARGAECRCRR	WTALSHNIAER	ARESPRRCG	KRYADIGG	SDTIRI
m294	RRMRGGKPLKPY	RPRGGRCRR	WTALSHNIAER	ARESPRRCG	KRYADIGG	SDTIRI
	70	80	90	100	110	120
	130	140	150	160	170	180
g294.pep	RVFRLEHRMSIY	AVAHIIHLYCAT	AFVGGVFFEV	LVLSVLHTGR	VSREARREVE	KAMSYR
m294	RVFRLEHRMSIY	AVAHIVHLYCA	IAFVGGVFFEV	LVLSVLHTGR	VSREARREVE	KAMSYR
	130	140	150	160	170	180
	190	200				
g294.pep	AVRVMFVAVGLL	FARGTLESTAA	ACP			
m294	AVRVMFVVGLL	FASGIVMAANR	YLSILGEPFAT	SFGMTLTLK	ILLAFSVLAH	FAIAVVK
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq

```

1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTCGGGCT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT
151 TGGCATCGGG TCGGCGGTT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA
201 GCCGTGAAA AAACCTTATC GTCCGAGGAG GGCGGAATGC AGATGCAGGC
251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GGTGGAGTA CCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG
451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CACACGGGAC GGGTGTCGCG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTCG CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCCG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

```

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701 TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRRYSAFRP TIFPKPAGTP
 51 WHRVRRFKSN RRTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES
 101 PRRYGKRYAD IGDDSDTIRI RVERLEYRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMPEVVG LLFASGIVMA
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFIAIVVK MARSTLTVGW
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSAAVWSIRV	VRTSSNRFPAAFRRYSAF	QPTIFPKPADTPWHRVRR	FKSN		
a294	MRITCAPMSLLSAAVWSIR	AVRTSSNRFPAAFRRYSA	FRPTIFPKPAGTPWHRVRR	FKSN		
	10	20	30	40	50	60
	70	80	90	100	110	120
m294.pep	RRMRGGKPLKPYRPRGGG	CRRAWTALSHNIAERARE	SPRRCKRYADIGGDS	DTIRI		
a294	RRTRGGKPLKTYRPRRAE	CRRTALSHNIAERARE	SPRRYGKRYADIGGDS	DTIRI		
	70	80	90	100	110	120
	130	140	150	160	170	180
m294.pep	RVERLEHRMSIYAVAHIV	HLHYCAIAFVGGVFFEVL	VLSVLHTGRVSREAR	REVEKAMSYR		
a294	RVERLEHRMSIYAVAHIV	HLHYCAIAFVGGVFFEVL	VLSVLHTGRVSCEAR	REVEKAMSYR		
	130	140	150	160	170	180
	190	200	210	220	230	240
m294.pep	AVRVMPEVVGLLFASGIV	MAANRYLSILGEPFATS	FGTMLTLKILLAFSV	LAHFIAIVVK		
a294	AVRVMPEVVGLLFASGIV	MAANRYLSILGEPFATS	FGTMLTLKILLAFSV	LAHFIAIVVK		
	190	200	210	220	230	240
	250	260	270			
m294.pep	MARSTLTVGWSKYIHAV	VFTHMLLIVFLAKAMFY	ISWX			
a294	MARSTLTVGWSKYIHTV	VFTHMLLIVFLAKAMFY	ISWX			
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq
 1 atgctcggga tggcgcggca cgacggccag cagggcatcg ccgcgatatt
 51 gttgccacgc cgccagcagt ttttcgcct cgtcttcgcc ccgataaacg
 101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaa
 151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
 201 tattgccgca cacctgcacg gatgccgcgc ccaatttcgc caaccgcgcc
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
 301 acgatcagg cgcggaactt tcagataacc gttcagcgat tttccgaca
 351 gccgcgcatt cgcaaaaac agcggcacac ccgctcgccg gcattccttc
 401 atcagatttg gccagatttc ggtttccatc aaaatgccga acatcgggcg
 451 gtgttcgcgc aaaaactgcc gtaccacagt tttttgtca tacggaagat
 501 agcggcattg cgcacggga aacagaactt gcgcgggttc ccgtcccgtc
 551 ggggtcatct cgtcatcag cagcggcgca tcgggaaaac gccgccgcaa
 601 ctgcggtatc aagggttgg cgacacgct ttctccgacc gaaacggcgt
 651 gtatccaaac cgcccggtta acgggattcg gatgcggctt gccgaaacgc
 701 tcttccctat gcgcccggtta tgcgggggca cttccggagc gtttgtccaa
 751 ataacggcgt atccatatcg gcgcaagcag ccacaataca tcataaagcc
 801 attggaacat ctttctattt cctgcaaaaac aaatgccgtc cgaacggttc
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

g295.pep

```

1  MLGMARHDDGQ OGIAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK
51  LPRQRFHVFH RHQVVFVGIAA HLHGCRAQFR QPRRIRLRLR QTARQRSRGG
101 TDQAADFQIT VQREFFRQPRI RQKQRHTRSP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPHYPR FFVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq

```

1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCGGCCGG CCTCCGATGC GTTTTCAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTCCGA CGGTATGATG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTGAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CGGCGGACTT TCAGATAACC GTTCAACGAT TTTCCGACA
351 CGCGCGCATC CGCCAAAAC AGCGGCACAC CGCGCGCGCG GCATTCCCTC
401 ATCAGGTTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGCGG
451 GTGTTGCGGC AAAAAGTCCC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATG CGCATCGGGA AACAGAACTT GCGCGGTTTC CCGCCCCGTC
551 GCGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAGAC GCCGCGCAA
601 CTGCGGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGTCCCGAT GCGCCCGATA TGCCGGGCA CTCCGGAGC GTTGTGTTAA
751 ATAACGCGGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC TGAACGGTTC
851 AGACGGCATT TCGGCAACGG AATCAAATAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pep

```

1  MLGMARHDDQ QRIAAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK
51  LPRQRFHFLR RYDVVFVGIAA HLHGCRAQFR QPRRIRLCLR QTPRQSRGGR
101 TDQAADFQIT VQREFFRQPRI RQKQRHTRAP AFPHQVGPDP GFHQNAEHRA
151 VFAQKLPHYPR FFVIRKIAAL RIGKQNLRGF PRRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV XTVQTAFRQR NQIS*

```

m295/g295 93.9% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
g295	10	20	30	40	50	60
m295.pep	70	80	90	100	110	120
g295	70	80	90	100	110	120
m295.pep	130	140	150	160	170	180
g295	130	140	150	160	170	180
m295.pep	190	200	210	220	230	240
g295	190	200	210	220	230	240
m295.pep	250	260	270	280	290	
g295	250	260	270	280	290	

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTCAAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
251 GCATCCGCCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGCGAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTTCCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCCGCG AAAAACTGCC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCGTC
551 GGGGTCTATCT GCGTCATCAG CAGCGGCGCA TCGGAAAAC GCTGCCGCA
601 CTCGCGTATC AAAGGTTGGG CGGCACGCGT TTCCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCCGATA TGCAGGGGCA CTTCCGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMARHDDQ QGIAAILLPR RQOFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRHFLFR RHQVVFGLIA HLHGCRAQFR QPRRIRLRLC QTARQSSGGR
101 TDQAADFQIT V*RRFRQPRI RQQRHTRAP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLPO
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
	MLGMARHDDQQRIAAILLPRRQOFFRLVFTPINARAAAHGNRPASDAFFKLPRQRHFLFR					
a295	MLGMARHDDQQGIAAILLPRRQOFFRLVFTPINARAAAHGNLPVSDAFFKLPRQRHFLFR					
	10	20	30	40	50	60
m295.pep	70	80	90	100	110	120
	RYDVVFGLIAHLHGCRAQFRQPRRIRLCLRQTPRQRSGGRDQAADFQITVQRFFRQPRI					
a295	RHQVVFGLIAHLHGCRAQFRQPRRIRLRLCQTARQSSGGRDQAADFQITVXRFFRQPRI					
	70	80	90	100	110	120
m295.pep	130	140	150	160	170	180
	RQQRHTRAPAFPHQVGPDFGFHQNAEHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
a295	RQQRHTRAPAFHLHQIGPDFGFHQNAEHRAVFAQKLPYPRFFVIRKIAALCIRKQNLRGF					
	130	140	150	160	170	180
m295.pep	190	200	210	220	230	240
	PPRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDRNGVYPNRAGNGIRIRLAETLVPMRPI					
a295	PSRRGHLRHQRRIGKTLPLQAYQRLGGTRFPDRNGVYPNRAGNGIRIRLAETLAPMRPI					
	190	200	210	220	230	240
m295.pep	250	260	270	280	290	
	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTVQTAFRQRNQISX					
a295	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVRTVRTAFRQRNQISX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```

```

51  GCTTGCCGTT TCGATTATTC TGGTGTcgcG GGCATACATT Gcttcgacag
101 agggggaccga gcgcgtcaga ccgcAGCGCG Tggaacaaa ACTGCCGCCG
151 CTGTCTTGGG gcggcaacgg CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgc TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGgcatt tCGGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCAGTGCG CGCGAAGTGC AGTTTTttac CGACGAAGAC GGCGAGCGCA
401 aTctGGTCCG TTTGGAaaaa AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGGCGGCA
701 CAACCCATCA GCGTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCgaG CCGCTGGTCT ATACGCGCAT TTCTTCGCGG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1051 GAAGGCATG TCGCGGCGG CGAGGTCATC GGTTTTGTG GTTCGACAGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID.1236; ORF 297.ng>:

```

g297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PQRVEQKLPP
51  LSWGGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGG EAD
101 LRHLRADQSV HVLVGGDGSA REVQFTDED GERNLVALEK KGGIWRRSAS
151 DADMKVLP TL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVAVRLLYD SLYFHGQQVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYVDEGRV LQEKGGFNIE PLVYTRISSP FGVRMHPILH TWRLHTGIDY
301 AAPQGTFPVRA SADGVITFKG RKGGYGNVAVM IRHANGVETL YAHLSAFSQA
351 GQNVVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPNVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

```

m297.seq
1  ATGGCTGTCT TCCACTTTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51  GCTTGCCGTT TCGATTATTT TGGTGTcgcG GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG Tggaacaaa TCTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCAGCGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TCGTGCCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCGAGCGCA
401 ATCTGGTCCG TTTGGAaaa AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCGG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
1051 GAAGGCATG TCGCGGCGG CGAGGTCATC GGTTTTGTG GTTCGACCGG
1101 GCGTTTCGACC GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

```

m297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERVR PQRVEQNLPP
51  LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGG EAD
101 LRHLRADQSV HVLVGGDGGA REVQFTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLP TL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

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201 EGDVRLMYD SLYFHGQQA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
 251 GNYYDEDGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
 301 AAPQGTTPVRA SADGVITFKG RGGYGNVAVM IRHANGVETL YAHLSAFSQA
 351 EGNVRGGEVI GFVSGTGRST GPHLHYEAR NGQPVNPVSV ALPTPELTQA
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIIILVSAAYIASTERTVRPQQRVEQNLPLPSWGGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIIILVSAAYIASTEGTERVRPQQRVEQKLPLPSWGGNGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA					
g297	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTDEDGERNLVALEKKGIIWRRSASEADMKVLPRLRSVVVKTSARGSLARAEPV					
g297	REVQFFTDEDGERNLVALEKKGIIWRRSASDADMKVLPRLRSVVVKTSARGSLARAEPV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRELSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQAAGDILAAEVVKGGRHQAFY					
g297	EIRELSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQQAAGDILAAEVVKGTTTQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGNYYDEDGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGNYYDEDGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTTPVRASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTTPVRASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVSGTGRSTGPHLHYEARINGQPVNPVSVLPTPELTQADKAFAAQKQKADALLARLR					
g297	GFVSGTGRSTGPHLHYEARINGQPVNPVSVLPTPELTQADKAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1 ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
 51 GCTTGCCGTT TCGATTATTT TGGTGTCCGC GGCATACATT GCTTCGACAG
 101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAAACAAA ACTGCCGCCG
 151 CTGTCTTGGG GCGGCAGCGG TGTTTCAGACG GCATATTGGG TGCAGGAGGC
 201 GGTGCAGCCA GCGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
 251 CGCGGGACGA AATTGCCCGA ATAACGGAAA AATATGGCGG CGAAGCCGAT
 301 TTGCGGCATT TCGTGCCGA CCACTCGGTT CATGTTTGG TCGGCGGCGA
 351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GCGGAGCGCA
 401 ATCTGGTTCG TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
 451 GAGGCGGATA TGAAGTTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
 501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATTCGCG

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551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTGAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TGC CGCGCGCG CGAGGTCATC GGT TTTGTCG GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GGCGCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```

a297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV R PQRVEQKLPP
51  LSWGGSGVQT AYWVQEA VQPGDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGD GGA REVQFFTD ED GERNLVALEK KGGIWRRSAS
151 EADMKVLP TL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQ QVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDEDGRV LQEKGGFNIE PLVYTRISSP FGYRMHPILH TWRLHTGIDY
301 AAPQGT PVRA SADGVITFKG RKGGYGNVAV MIRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/a297 99.3% identity in 430 aa overlap .

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              10      20      30      40      50      60
m297.pep      MAVFPLSAKH RKYALRALAVSIILVSAAYIASTERTERV R PQRVEQNL PPLSWGGSGVQT
a297           MAVFPLSAKH RKYALRALAVSIILVSAAYIASTERTERV R PQRVEQKL PPLSWGGSGVQT
              10      20      30      40      50      60
              70      80      90     100     110     120
m297.pep      AYWVQEA VQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGD GGA
a297           AYWVQEA VQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGD GGA
              70      80      90     100     110     120
              130     140     150     160     170     180
m297.pep      REVQFFTD EDGERNLVALEKKGGIWRRSASEADMKVLP TLRSVVVKTSARGSLARAEVPV
a297           REVQFFTD EDGERNLVALEKKGGIWRRSASEADMKVLP TLRSVVVKTSARGSLARAEVPV
              130     140     150     160     170     180
              190     200     210     220     230     240
m297.pep      EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSL YFHGQ QVAAGDILAAEVV KGGTRHQAFY
a297           EIRESLSGIFAGRFSLDGLKEGDAVRLIYDSL YFHGQ QVAAGDILAAEVV KGGTRHQAFY
              190     200     210     220     230     240
              250     260     270     280     290     300
m297.pep      YRSDKEGGGGN NYDEDGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY
a297           YRSDKEGGGGN NYDEDGRVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY
              250     260     270     280     290     300
              310     320     330     340     350     360
m297.pep      AAPQGT PVRASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
a297           AAPQGT PVRASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
              310     320     330     340     350     360

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          370      380      390      400      410      420
m297.pep  GFVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a297      GFVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR
          370      380      390      400      410      420

          430
m297.pep  GIPVTVSQSDX
          |||||||||||
a297      GIPVTVSQSDX
          430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

```

g298.seq
1  ATGAAAACT TTCTTCCCT TTCGCCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcgcgcac ggCTCAAGAC GGCGGTTCCG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCCGCCCC GCCGGCCGGC
301 GGAACAGAAT GGAACAAGG CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTCGCCGGAG ATTGCTGAT GCAGGCGGT GCGCCTTTCG
401 TGCAAAAAAG CCGTGAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTCGACT GGCCGAAAAAC
501 GATTGAAGAA ACCTTGAAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTCC CCGTCGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GGCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAATGCTTT CGGAACACTT GAAAGGCAA ATCATCCTGA TTCCACCCG
801 GCAAACTG AGCGCGGGA AAGgccGCTA CACCGATTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAAAAATA ATGAAAAAA TCGTTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

```

g298.pep
1  MKNFLSLFAS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51 SGAALQENAY ALSDGIKTFI SGETPPTAQD GGSADMPPEA AASEAAPPAG
101 GTEWKQGTAE AAVRSGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESANLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNPD WDFPVGKRYL
201 KFADEWAQE YLKRVDRIE AAHTRVQVW WLGI PYMKKV KLDGQMRYLD
251 KLLSEHLKGK IILPTAQT LSGGKGRYTD VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

```

m298.seq
1  ATGAAAACT TTCTTCCCT TTTCTCCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCGGAC GGCTCAAGAC GGCGGTTCCG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCC TCAAACCGGT
301 GAAACAGAAT GGAACAAGA CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTGCGCG ACTGCTGAT GCAGGCGGT GCCCCTTCG
401 TGCAAAAAAG CCGTGAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTCGACT GGCCGAAAAAC
501 GATTGAAGAA ACCCTGCAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTCC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GGCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAATGCTTT CGGAACATT GAAAGGCAA ATCATCCTGA TTCCACCCAC
801 GCACACCTG AGCGCGGGA AAGACCGCTA CACCGATTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAAAAATA ATGAAAAAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```


This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep
 1 MKNFLSLFSS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
 51 SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AASEAVPQTG
 101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS
 151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL
 201 KFASDEWAQE YLKRVDRIE AAHTRVQVV WLGIPLYMKA KLDGQMRYL
 251 KLLSEHLKGK IILPTHTL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
 301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

m298/g298 94.8% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
g298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
g298	ALSDGIKTFISGETPPTAQDGGSDMPSEAAASEAAPPAGTEWKQDTEAAAVRSGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVQKSLKQYQYIESANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWFDFPVGKLYLKFADEWAQEYLKRVDRIEAAHTRVQVVWLGIPLYMKA					
g298	LAVFLGPNDPWFDFPVGKRYLKFADEWAQEYLKRVDRIEAAHTRVQVVWLGIPLYMKV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLKLLSEHLKGKIIILPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
g298	KLDGQMRYLKLLSEHLKGKIIILPTAQTLSGGKGRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq
 1 ATGAAAACT TTCTTTCCCT TTTCGCCTCC ATACTGATGT CTGCCCTGAT
 51 TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
 101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
 151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTTCA ACGGCATCAA
 201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GGCGGTTCGG
 251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAACTGGC
 301 GAAACAGAAT GGAAACAAA CACCGAAGCC GCCGCCGTCC GAACAGGGGA
 351 CAAAGTCTTT TTCGCCGCG ACTCGCTGAT GCAGGGCGTT GCACCCTTCG
 401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
 451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAAC
 501 GATTGAAGAA ACCCTGAAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
 551 TCCTCGGTCC GAACGACCCG TGGGATTTC CCGTTGGCAA ACGCTACCTC
 601 AAATTCGCTT CCGACGAATG GGCGCAAGAA TACCTGAAAC GCGTCGACCG
 651 CATCCTTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
 701 TCCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

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751  AAACTGCTTT  CGGAATATTT  GAAAGGCAAA  ATCATCCTGA  TTCCCACCGC
801  GCACACCCTG  AGCGGCGGGA  AAGACCGCTA  CACCGACTCC  GTCAACGTCA
851  ACGGCAAACC  CGTCCGCTAC  CGCAGCAAGG  ACGGCATACA  CTTTACCGCC
901  GAAGGACAAA  AACTGCTGGC  GGCAAAAATA  ATGGAAAAAA  TCGTTTTTGA
951  ACCAAGTACG  CAACCATCAA  GTACACAGCC  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
  1  MKNFLSLFAS  ILMSALIAVW  FSQNPINAYW  QQTYHRNSPL  EPLAAYGWWR
 51  SGAALQENAY  ALSDGIKAFI  SGETPPTAQD  GGSADMPSEA  AAPETAPQTG
101  ETEWKQNTA  AAVRTGDKVF  FAGDSLMOGV  APFVQKSLKQ  QYGIESVNLS
151  KQSTGLSYPS  FFDWPKTIEE  TLKKHPEISV  LAVFLGPNDF  WDFPVGKRYL
201  KFASDEWAE  YLKRVDRIE  AAHTHYVQV  WLGIPLYMKA  KLDGQMRYLD
251  KLLSEYLGK  IILIPTAHTL  SGGKDRYTD  VNVNGKPVRY  RSKDGIHFTA
301  EGQKLLAAKI  MEKIVFEPST  QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFISGETPPTAQDGGSDMPSEAAAPETAPQTGETEWKQNTAEEAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQYQIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLMOGVAPFVQKSLKQYQIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDFWDFPVGKLYLKFADEWAEYLKRVDRIEAAHTHRVQVWLGIPLYMKA					
a298	LAVFLGPNDFWDFPVGKRYLKFADEWAEYLKRVDRIEAAHTHYVQVWLGIPLYMKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLDKLLSEHLKGKIILIPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
a298	KLDGQMRYLDKLLSEYLGKGIILIPTAHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
  1  ATGAACCCCA  AACACTTCAT  CGCATTTTCC  GCCCTGTTCC  CCGCCACGCA
 51  GGCAGAAGCC  CTGCCCCTCG  CCTCCGTCAG  CCCCGACACC  GTTACCGTTT
101  CCCCGTCCGC  CCCCTACACC  GATACAAACG  GGCTGCTGAC  CGACTACGGC
151  AACGCCGCG  CCTCGCCTTG  GATGAAAAAA  CTCCGATCCG  TCGCACAAGG
201  CAGCGGCGAG  GCCTTCCGCA  TCCTGCAAAT  CGGCGACTCG  CATACCGCCG
251  GCGACTTCTT  TACCGACGCC  CTGCGCAAAC  GCCTGCAAAA  AACATGGGGC
301  GACGGCGGCA  TAGGCTGGGT  TTACCCCGCC  AACGTCAAAG  GGCAGCGCAT
351  GGCAGCGGTC  CGTCACAGCG  GCAACTGGCA  AAGCTTCACC  AGCAGGAACA
401  ATACCGGAGA  TTTCCCGCTC  GGCAGCATCC  TCGCCCAAAC  CGGCAGCGGC
451  GGCAGCATGA  CCCTGACCGC  GTCTGACGGC  AAAACCGGCA  AACAGCGCGT

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501 TTCCCTGTTT GCCAAACCGC TGCTCGCCGA ACAAACCCTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GGCGGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGGCCAT ACAGACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTGACC CAGTGGTCTG AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCC TTCAACAACA ACATCGACAT TGCCGATACC GAACAAAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCCGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACGCGCCCC GTCTCTCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCG
1001 CCCGTCAGGG GCAGACGATG TTTTGGTCTT GGCAAAACGC AATGGGCGGC
1051 ATATGCAGCA TGAAAAACTG GCTCAACCAA GGATGGGCGG CCAAAGACGG
1101 CGTACACTTC TCCGCCAAAG GCTACGGCGC CGCGGCGGAA ATGCTTGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCGCGCGC CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1248; ORF 299.ng>:

g299.pep

```

1  MNPKHFIAFS ALFAATQAEA LPVASVSPDT VTVSPSAPYT DTNGLLTDYG
51  NAAASPWMKK LRSVAQGSGE AFRILQIGDS HTAGDFFTDA LRKRLQKTWG
101 DGGIGWVYPA NVKGQRMAAV RHSGNWQSFT SRNNTGDFPL GGILAQTSYG
151 GGMTLTASDG KTGKQRVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201 AALPLAIQTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGRTP VLLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKNWLNQ GWAADKGVHF SAQGYRRAAE MLADSLEELV RAAAIRQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1249>:

m299.seq

```

1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTTC CCGCCACGCA
51  GGCAGAAGCC CTACCTGTCT CCTCCGTCAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAA CTCCAATCCG TCGCACAAGG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAT CGGCGACTCG CATAACGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTGCAAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCGGCCGTC CGGCACAACG GTAACCTGGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCCGCTC GGCGGCATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCCTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GGCGGCGGCT GGCAGGTACT GGATACGGGC
601 CCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCTG AATGGCGTGC CGACCGTATG
751 AACGACCTCG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCT TTCAACAACA ACATCGACAT TGCCGACACC GAACAAAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCTGC CGCCGGCATC
901 CTCATCATCG GCGCACCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCG
1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC CATGGGCGGC
1051 ATATGCAGCA TGAAAAACTG GCTCAACCAA GGATGGGCGG CCAAAGACGG
1101 CGTACACTTC TCCGCCAAAG GCTACGGCGC CGCGGCGGAA ATGCTCGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCTCCGCTG CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1250; ORF 299>:

m299.pep

```

1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
51  NASASPWMKK LQSVQGSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101 DGGIGWVYPA NVKGQRMAAV RHNGNWQSLT SRNNTGDFPL GGILAHGSG
151 GSMTLTASDG IASKQRVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201 AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGRTP VRLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKNWLNQ GWAADKGVHF SAKGYRRAAE MLADSLEELV RSAAIRQ*

```

m299/g299 95.5% identity in 397 aa overlap

```

10      20      30      40      50      60
m299.pep  MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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g299	MNPKHFIAFSALFAATQAEALPVASVSPDITVTVSPSAPYTDNGLLTDYGNAAASPWMKK
	10 20 30 40 50 60
m299.pep	LQSV AQSGSETFRILQIGDSHTAGDFFDTS LRKRLQKTWGDGGIGWVYPANVKGQRMMAV
g299	LRSV AQSGGEAFRILQIGDSHTAGDFFDTS LRKRLQKTWGDGGIGWVYPANVKGQRMMAV
	70 80 90 100 110 120
m299.pep	RHNGNWQSLTSRNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
g299	RHSGNWQSFSTRNTGDFPLGGILAHTGSGGSMTLTASDGTGKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299.pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
g299	TVNGNTVSANGGGWQVLDTGAAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299.pep	LIIGAPESLKNLTGVCGTRPVRLTEVQQMQRVARQGQTMFWSWQAMGGICSMKNWLNQ
g299	LIIGAPESLKNLTGVCGTRPVLLTEVQQMQRVARQGQTMFWSWQAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.pep	GWAAKDGVHFSAGYRRAAEMLADSLEELVRSAAIRQX
g299	GWAAKDGVHFSAQGYRRAAEMLADSLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

a299.seq

1	ATGAACCCCA	AACACCTCAT	CGCATTTTCC	GCCCTATTTCG	CCGCCACGCA
51	GGCAGAAGCC	CTACCTGTCG	CCTCAGTCAG	CCTCGACACC	GTTACCGTTT
101	CCCCGTCCGC	CCCCTACACC	GATACAAACG	GGCTGCTGAC	CGACTACGGC
151	AACGCTCCG	CCTCGCCTTG	GATGAAAAAA	CTCCAATCCG	TCGCACAAGG
201	CAGCGCGAG	ACCTTCCGTA	TCCTGCAAAT	CGGCGACTCG	CATACCGCCG
251	GCGACTTCTT	TACCGACAGC	CTGCGCAAAC	GCCTACAAAA	AACTTGGGGC
301	GACGGCGGCA	TAGGCTGGGT	TTACCCCGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGCCGTC	CGGCACAAACG	GTAAC TGGA	AAGCCTCACC	AGCAGGAACA
401	ACACCGGAGA	CTTCCCCTC	GGCGGCATCC	TCGCCCACAC	CGGCAGCGGC
451	GGCAGCATGA	CCCTGACCGC	ATCGGACGGC	ATAGCAAGCA	AGCAGCGCGT
501	TTCCCTGTTT	GCCAAACCCC	TGCTTGCCGA	ACAAACCCTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCACTGC	CCCTGACCAT	ACACACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATC	GAAAAATCCC	CCGGCGGCAT	TACCGTTTCC	GCGATGGGCA
701	TCAACGCGCG	ACAATTAACC	CAGTGGTCGA	AATGGCGTGC	CGACCGTATG
751	AACGACCTTG	CCCAAACCGG	CGCCGATCTA	GTCATCCTTG	CCTACGGTAC
801	CAACGAAGCC	TTCGGCGACA	ACATCGACAT	TGCCGATACC	GAACAGAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCGCGACA	GCCTACCTGC	CGCCGGCATC
901	CTCATCATCG	GCGCGCCGA	ATCCCTGAAA	AACACGCTCG	GCGTATCGCG
951	CACACGCCCC	GTCCGCCTGA	CCGAAGTCCA	ACAGATGCAG	CGGCGCATCG
1001	CCCGTCAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAAACGC	GATGGGCGGC
1051	GTTTGCAGCA	TGAAAAACTG	GCTCAACCAC	GGATGGGCGG	CCAAAGACGG
1101	CGTACACTTT	TCCGCCAAAG	GCTACCAACG	GTCGGCGGAA	ATGCTCGCCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCTCCGCTG	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
51  NASASPWMKK LQSV AQSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101 DGGIGWVYPA NVKGQRM AAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151 GSMTLTASDG IASKQRVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201 AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRO IRDSLPAAGI
301 LIIGAPESLK NTLGVCGTRP VRLTEVQQMQ RRIARQGQTM FWSWQNAMGG
351 VCSMKNWLNH GWA AKDGVHF SAKGYQSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

```
m299.pep      10      20      30      40      50      60
MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK
|||||
a299          10      20      30      40      50      60
MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK

m299.pep      70      80      90     100     110     120
LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKGQRM AAV
|||||
a299          70      80      90     100     110     120
LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKGQRM AAV

m299.pep     130     140     150     160     170     180
RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
|||||
a299         130     140     150     160     170     180
RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL

m299.pep     190     200     210     220     230     240
TVNGNTVSANGGGWQVLDTG AALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
|||||
a299         190     200     210     220     230     240
TVNGNTVSANGGGWQVLDTG AALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT

m299.pep     250     260     270     280     290     300
QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVROIRDSLPAAGI
|||||
a299         250     260     270     280     290     300
QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIDIADTEQKWLDTVROIRDSLPAAGI

m299.pep     310     320     330     340     350     360
LIIGAPESLKNTLGVCGTRPVRLTEVQQMQRRVARQGQTMFWSWQNAMGGICSMKNWLNQ
|||||
a299         310     320     330     340     350     360
LIIGAPESLKNTLGVCGTRPVRLTEVQQMQRRRIARQGQTMFWSWQNAMGGVCSMKNWLNH

m299.pep     370     380     390
GWA AKDGVHFS AKGYRRAEMLADSLEELVRSAAIRQX
|||||
a299         370     380     390
GWA AKDGVHFS AKGYQSAEMLADSLEELVRSAAIRQX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGTCC
201 TGTGGGGCG AAAGGACGTG CCGATGACGG TTTGATTAC GTTGTCAGCC
251 TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGGCGT
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351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCGTC ATCTTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACAGG TTTTATATGG
701 CAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCGT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTTATT TTCTTGTGTG
1001 TTGCGCTGCC GGGCATTGTT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGGTTTTA TTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCTGCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTCG GGCTGATTAT GGCGACGGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATTT GGGTATTGTG
1551 TTTGGGTCTG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1  MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLGISALM RLLLTSPRK LTTFMVFTG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQAAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGAVFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPQ
451 VIQAAAYRIGD SVTNIIPTMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGTPTFY PVP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTTCATT CCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCTG
651 AGGCCCTGAA GCCAACTGGT TTTTATATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGTG ACTGAAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GGCATTCCAA
801 TGAAATCACG CCTTTGGAAT ATAAAGGATT AATTTGGGCT GGCGTGGTGT
851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGGA GCATCGTCCC TGCCGACGGT
901 ATTTTGCCTC ATCCTGAAAC AGGATTGGTT TCCGTTTCGC CGTTTTTAAA
951 ATCGATTGTT GTTTTTATTT TCTTGTGTGT TGCATGyCG GGCmTTGTTT
1001 ATGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

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1051 ATGCCGAAT CGATGAGTAC TCTGSGCTT TmTTTGswCA kcATCTTTTT
1101 TGCCGCACAG TTTGTCGCAT TTTTAAATTG GACGAATATT GGGCAATATA
1151 TTGCCGTTAA AGGGCGCAGC TTCTTAAAG AAGTCGGCTT GGGCGGCAGC
1201 GTGTTGTTTA TCGGTTTTAT TTTAATTGT GCTTTTATCA ATCTGATGAT
1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TCGCGCGATT TTCGTCCCTA
1301 TGCTGATGTT GGCCGGCTAC GCGCCCGAAG TCATTCAAGC CGCTTACCGC
1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTTCCG
1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GCGGTGGGA
1451 CGCTGATTTT TATGATGTTG CCGTATTCG CTTTCTTCTT GATTGCGTGG
1501 ATTGCCTTAT TCTGCATTG GGTATTTGTT TTGGGCCTGC CCGTCGGTCC
1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

m302.pep

```

1  MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHVPTL FIIFIVLLLI
51  ASAVGAYFGL SVPDRPVGA KGRADDGLIY IVSLLNADGF IKILHTVKN
101 FTGFAPLGTV LVSLGVGIA EKSLISALM RLLLTSPRK LTTFMVFTG
151 ILSNTASELG YVVLPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPLLACI THQAAVVGPE ANWFFMVAFT FVIALIGYFV TEKIVEPQLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVVFALSAL LAWSIVPADG
301 ILRHPETGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXIFFFAQ FVAFFNWTNI GOYIAVKGAT FLKEVGLGGS
401 VLFIGFILIC AFINLMIGSA SAQWAVTAPI FVPMLMLAGY APEVIQAYR
451 IGDVSTNIIT PMMSYFGLIM ATVIKYKKDA GVGTLISMML PYSAFFLIAW
501 IALFCIWVVFV LGLPVGPGAP TFYPAP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng) from *N. gonorrhoeae*:

m302/g302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTDTRDGRFLRTVEWLGNMLPHVPTLFIIFIVLLLIASAVGAYFGL					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNMLPHVPTLFIIFIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
m302.pep	SVPDRPVGAKGRADDGLIYIVSLLNADGFIKILHTVKNFTGFAPLGTVLVSLGVGIA					
g302	SVPDRPVGAKGRADDGLIHVSLDADGLIKILHTVKNFTGFAPLGTVLVSLGVGIA					
	70	80	90	100	110	120
m302.pep	SVPDRPVGAKGRADDGLIYIVSLLNADGFIKILHTVKNFTGFAPLGTVLVSLGVGIA					
g302	SVPDRPVGAKGRADDGLIHVSLDADGLIKILHTVKNFTGFAPLGTVLVSLGVGIA					
	70	80	90	100	110	120
m302.pep	EKSLISALMRLLLTKSPRKLTTFMVFTGILSNTASELGYVVLPLSAIIFHSLGRHPL					
g302	EKSLISALMRLLLTKSPRKLTTFMVFTGILSNTASELGYVVLPLSAVIFHSLGRHPL					
	130	140	150	160	170	180
m302.pep	EKSLISALMRLLLTKSPRKLTTFMVFTGILSNTASELGYVVLPLSAIIFHSLGRHPL					
g302	EKSLISALMRLLLTKSPRKLTTFMVFTGILSNTASELGYVVLPLSAVIFHSLGRHPL					
	130	140	150	160	170	180
m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVAFTFVI					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQIIHPDYVVGPEANWFFMAASTFVI					
	190	200	210	220	230	240
m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVAFTFVI					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQIIHPDYVVGPEANWFFMAASTFVI					
	190	200	210	220	230	240
m302.pep	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVFALSALLAW					
g302	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVFALSALLAW					
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVFALSALLAW					
g302	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVFALSALLAW					
	250	260	270	280	290	300
	300	310	320	330	340	350

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m302.pep  SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      SIVPADGILRHPETGLVAGSPFLKSIVVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLXXIFFAAQFVAFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      SMSTLGLYLVIIFFAAQFVAFNWTNIGQYIAVKGAVFLKEVGLGGSVLFIFIGFILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASAQWAVTAPIFVPMLMLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      NLMIGSASAQWAVTAPIFVPMLMLAGYAPQVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKDAGVGT LISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFFYPAPX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g302      IKYKKDAGVGT LISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGTPTFFYPVPX
          490      500      510      520      530

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCCGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251 TGCTCGATGC TGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCGGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAAT CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGCTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCTGA AGCCAACTGG TTTTATATGG
701 TAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCCGCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC TGGCGTGGTG TTTGTGCGCT TATCCGCCCT ATTGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCGT CATCCTGAAA CAGGATTGGT
951 TTCCGGTTCG CCGTTTTTAA AATCAATTGT TGTTTTATT TTCTGTGTTG
1001 TTGCACTGCC GGCATTGTT TATGGCCGGG TAACCCGAAG TTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTATAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTGTTT ATCGGTTTTA TTTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTCG GGCTGATTAT GCGACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGATTCC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATTT GGGTATTTGT
1551 TTTGGGCTG CCCGTCGGTC CCGGCGCGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQTDQTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLTKSPRK LTTFMVVF TG

```


698

```

151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQAAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIIITPM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFVLGL PVGPGAPTFY PAP*

```

m302/a302 96.1% identity in 533 aa overlap

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	TQRDGRFLRTVEWLGNM	LPHPVTLFII	FIVLLLIASAV	GAYFGL	
a302	MHSIYFFKEKQMSQTD	TQRDGRFLRTVEWLGNM	LPHPVTLFII	FIVLLLIASA	AAGAYFGL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m302.pep	SVPDPRPVGAKGRADD	GLIYIVSLLNADGFI	KILHTVKNFTGFAP	LGTVLVSL	LGVGIA	
a302	SVPDPRPVGAKGRADD	GLIHVVSLLDADGLI	KILHTVKNFTGFAP	LGTVLVSL	LGVGIA	
	70	80	90	100	110	120
	130	140	150	160	170	180
m302.pep	EKSGLISALMRLLLT	KSPRKLTFMVVFTGIL	SNTASELGYVVLIP	LSAIIFHSLGRHPL		
a302	EKSGLISALMRLLLT	KSPRKLTFMVVFTGIL	SNTASELGYVVLIP	LSAIIFHSLGRHPL		
	130	140	150	160	170	180
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYS	ANLFLSTIDPLLACI	THQAA-----	VVGPEANWFFM	VASTFVI	
a302	AGLAAAFAGVSGGYS	ANLFLGTIDPLLAGI	TQAAQIIHPDYV	VVGPEANWFFM	VASTFVI	
	190	200	210	220	230	240
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQ	LGYPQSDLSQEEKDI	RHSNEITPLEYKGLI	WAGVVFVALS	ALLAW	
a302	ALIGYFVTEKIVEPQ	LGYPQSDLSQEEKDI	RHSNEITPLEYKGLI	WAGVVFVALS	ALLAW	
	250	260	270	280	290	300
	300	310	320	330	340	350
m302.pep	SIVPADGILRHPETG	LVSGSPFLKSIVVFI	FLLFALXGXVYGRV	TRSLRGEQEV	VNAMAE	
a302	SIVPADGILRHPETG	LVSGSPFLKSIVVFI	FLLFALPGIVYGRV	TRSLRGEQEV	VNAMAE	
	310	320	330	340	350	360
	360	370	380	390	400	410
m302.pep	SMSTLXLXLXIIFFA	AQFVAFFNWTNIGQY	IAVKGATFLKEVGL	GGSVLFIFIGFI	LICAFI	
a302	SMSTLGLYLVIIFFA	AQFVAFFNWTNIGQY	IAVKGATFLKEVGL	GGSVLFIFIGFI	LICAFI	
	370	380	390	400	410	420
	420	430	440	450	460	470
m302.pep	NLMIGSASAOAVTA	PIFVPMMLAGYAPE	VIQAAYRIGDSVTN	IIITPMMSYFGL	IMATV	
a302	NLMIGSASAOAVTA	PIFVPMMLAGYAPE	VIQAAYRIGDSVTN	IIITPMMSYFGL	IMATV	
	430	440	450	460	470	480
	480	490	500	510	520	
m302.pep	IKYKKDAGVGTLI	SMMLPYSAFFLIAW	IALFCIWVFVLGL	PVGPAPTFFYP	PAPX	
a302	IKYKKDAGVGTLI	SMMLPYSAFFLIAW	IALFCIWVFVLGL	PVGPAPTFFYP	PAPX	
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

699

g305.seq

```

1  ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CGGTTTGGC GGTAGTGTT GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
301 GACAAACAAA TCAAAGAGTA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GTGTTGCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGGCCG TTCCGATGAT GGTGTCAGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTTGTGTTCC GGTGTTGGTAG
701 CGGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCCGTTT
751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGTTGTC
801 GGGCTGGATA AGTTGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLAIAP IPAAVMGLLF
101 DKQIKLEYLFN PLSVAVMLVL GGFFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
251 AYYRIVFGIV IILWLSGWI SWE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)

```

1  AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CAGTTTGGC GGTAGTGTT GAATACCGGC AACGTTTCAG
201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
301 GGCAWACAAA TCAAAGAGyA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTyTG GrCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GCGTTGCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA
551 CTGCGACAGA ATTCTCGTTT TTCTTGGCTG TGCCGATGAT GGTGCGCGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTGTTCA GGCTTGGTAG
701 CGGTAAAAGC GTTGCTGAGG TTTGTTTCGG GTAC...

```

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFSNVL HGLGKDRKAN RFVLNLAIAP IPAAVMGLLF
101 GXQIKEXLFN PLSVAVMLVL XGFXILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

```

g305.pep      10      20      30      40      50      60
               MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF
               |||
m305          10      20      30      40      50      60
               MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF

```

700

```

      70      80      90      100      110      120
g305.pep  EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL
          |||||
m305      EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL
          70      80      90      100      110      120

      130      140      150      160      170      180
g305.pep  GGFFILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTMGGMLWGI
          |||||
m305      XGFXILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTMGGMLWGI
          130      140      150      160      170      180

      190      200      210      220      230      240
g305.pep  ERKTATEFSFFLAVPMMVAATAYDVLKHRYFFTLHDVGLILIGFIAAFVSGLVAVKALLK
          |||||
m305      ERKTATEFSFFLAVPMMVAATAYDVLKHRYFFTLHDVGLILIGFIAAFVSGLVAVKALLR
          190      200      210      220      230      240

      250      260      270
g305.pep  FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX
          |||
m305      FVSG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1  ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCG
101 GCAATCTGAT TGATTTCAC AGCAATCACA AGGTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTTGGC GGTAGTGTG GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GGCAAACAAA TCAAAGAGTA TCTGTTTAA CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GGCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATATGTC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GCGTTGCCCA AGTGTTTGCA CTGGTTCAG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATT TTCTTGCCCG TTCCGATGAT GGTTCAGACA
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTTGTTC A GGCTTGGTGG
701 CGGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAI AF IPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFFILWVEK RQSRAPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHRY FFTLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

```

      10      20      30      40      50      60
m305.pep  MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF
          |||||
a305      MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHKVFEITIQLGAVLAVVF
          10      20      30      40      50      60

      70      80      90      100      110      120
m305.pep  EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL
          |||||
a305      EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFGKQIKEYLFNPLSVAVMLVL

```

701

	70	80	90	100	110	120
m305.pep	130	140	150	160	170	180
	XGFXILWVEKRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
a305	130	140	150	160	170	180
	GGFFILWVEKRSRAEPKIVDLDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
m305.pep	190	200	210	220	230	240
	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	190	200	210	220	230	240
	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAFVSGLVAVKALLR					
m305.pep	FVSG					
a305	250	260	270			
	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCGGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCCTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGGCGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAAAC  GAGAAAAAAG  CTTCAAAAAG
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAGA  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAACTGGCA  ATCTTGGGCA  TATCTTCCGA  AGTGGTCGGC  TATCAGGCGG
751 GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1  MFMNKFSQSG  KLSGFFFLGL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREPEP  GQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1  ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCgMAwAA  CCAGCyTAAG
151 GAAGACATCC  AACCTGAwCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAawGCT  GCCGACAAGC
251 AGCCCCTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGGACGG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAGCT
451 TCAAAAAGAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTCCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

702

```

601   ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
651   CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA
701   GGCGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
751   ATGCGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

```

m306.pep (partial)
  1   ..GLFFGLILAT VIIAGILFYLNQSGQNAFKI PASSKQPAET EILKPXNQXK
 51   EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
101   EREEPDGQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA
151   SKEEKKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR
201   IICKWARMPT VRARKGSVPN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP
251   MR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

```

m306/g306

          10      20      30      40
m306.pep      GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX
                |:|||||:|||||:|||||:|||||:|||||:|||||:
g306           MFMNKFSQSGKLSGFFFLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETEILK
                10      20      30      40      50      60

          50      60      70      80      90     100
m306.pep      NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPERE
                || ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| |||||
g306           NQPKEDIQPEPADQNALSEPDAEAEQSDAEXAADKQPVADKADEVEEKAGEPERE
                70      80      90     100     110     120

          110     120     130     140     150     160
m306.pep      GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAP
                ||||| ||||| ||||| ||||| : ||||| ||||| ||||| ||||| |||||
g306           GQAVRKKALTEEREQTVREKAQKKDAETVKKKAVKPSKETEKKASKEEKKAAKEKVAP
                130     140     150     160     170     180

          170     180     190     200     210     220
m306.pep      TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSVPNWQ
                ||||| ||||| ||||| ||||| : : : ||||| ||||| ||||| |||||
g306           TPEQILNSRSIEKARSAAAKEVQKMNFGQGSQRIICKWARMNPNGARKGSVPNWQ
                190     200     210     220     230     240

          230     240     250
m306.pep      YLPRWSVIRRDIKFTGCKAAICLPMRX
                ||| : ||| ||||| : ||||| |||
g306           YLPKWSAIRRDIKFTACKAAICPPMRX
                250     260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

```

a306.seq
  1   ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTTT
 51   CTTCCGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTTATC
101   TGAACCAGAG CCGTCAAAAT GCGTTCAAAA TCCCGGTTCC GTCGAAGCAG
151   CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT
201   CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA
251   AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
301   GCCGACAAAG CCGACGAGGT TGAGGAAAAG GCGGACGAGC CGGAGCGGGA
351   AAAGTCGGAC GGACAGGCAG TGCGCAAGAA AGCACTGACG GAAGAGCGTG
401   AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
451   AAACAAGCGG TAAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAAGA
501   AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCGGAAC
551   AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

```

601	GAAGTGCAGA	AAATGAAAAC	GCCGACAAGG	CGGAAGCAAC	GCATTATCTG
651	CAAATGGGCG	CGTATGCCGA	CCGCCGGAGC	GCGGAAGGGC	AGCGTGCCAA
701	ACTGGCAATC	TTGGGCATAT	CTTCCAAGGT	GGTCGGTTAT	CAGGCGGGG
751	ATAAACGCT	TTACCGGGTG	CAAAGCGGCA	ATATGTCTGC	CGATCGGGTG
801	A				

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```
a306.pep
1  MFMNKFESQSG KGLSGFFFFGL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
51  PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD GQAVRKKALT EEREQTVGEK AQKKDAETVK
151 KQAVKPSKET EKKAKSEEEK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*
```

m306/a306 93.7% identity in 252 aa overlap

		10	20	30	40	
m306.pep		GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPK				
		: :				
a306		MFMNKFSQSGKLSGFFGLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK				
	10	20	30	40	50	60
	50	60	70	80	90	100
m306.pep	NQXKEDIQXP	ADQNALSEPDA	EAEQSDAE	XAADKQPVAD	KADEVEEKAGE	PERE
a306	NQPKEDIQPE	PADQNALSEPDA	AKEAEQSDAE	KAADKQPVAD	KADEVEEKAGE	PEREKSD
	70	80	90	100	110	120
	110	120	130	140	150	160
m306.pep	GQAVRKKALTE	EEREQTVREKA	QKKDAETVKX	QAVKPSKETEK	KASKEEKKA	AKEKVAPKP
a306	GQAVRKKALTE	EEREQTVGEKA	QKKDAETVKK	QAVKPSKETEK	KASKEEKKA	EKEKVAPKP
	130	140	150	160	170	180
	170	180	190	200	210	220
m306.pep	TPEQILNSGS	IEKARSAAA	KEVQKMKTP	TRRKQRIICK	WARMPTVR	ARKGSVP
a306	TPEQILNSGS	IEKARSAAA	KEVQKMKTP	TRRKQRIICK	WARMPTAG	ARKGSVP
	190	200	210	220	230	240
	230	240	250			
m306.pep	LPRWSVIRRD	IKRTGCKAA	ICLPMRX			
a306	LPRWSVIRRD	IKRTGCKAA	ICLPMRX			
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

g307.seq	1	atgaaaac	cttcaaac	ccttcgacc	gcgtcactcg	cgctcatcct
51	cgcagcctgc	ggcgggtcaa	aagacagcgc	gcccgcagcc	tctgcgcgcg	
101	ccccctctgc	cgataacggc	gcggcgaaaa	aagaaatcgt	ctctggcagc	
151	accgtggcgc	acttcggcga	tatggtcaaa	gaacaaatcc	aatccgagct	
201	ggagaaaaaa	ggctacaccg	tcaaattggt	cgaatttacc	gactatgtgc	
251	gcccgaatct	ggcattggcg	gagggcgagt	tggacatcaa	cgtcttccaa	
301	cacaaaccc	atcttgacga	tttcaaaaa	gaacacaacc	tggacatcac	
351	cgaagccttc	caagtgcgca	ccgcgccttt	gggactgtat	cggggcaaac	
401	tgaatcgcgt	ggaagaagtc	aaagacggca	gcaccgtatc	cgcgcccaac	
451	gacccgtcca	acttcgcacg	cgcccttggtg	atgctgaacg	aactgggttg	
501	gatcaaactc	aaagacggca	tcaatccgct	gaccgcatcc	aaagccgaca	
551	tcgcggaaaa	cctgaaaaac	atcaaaatcg	tcgagcttga	agccgcacaa	
601	ctgcgcgcga	cgcgcgcgca	ctgtgatttt	gccgtcgtca	acggqaacta	
651	cgccataagc	agcggcatga	aqctgaccqa	agccctqttc	caaagaccqg	

```

701 gctttgctta tgtcaactgg tctgccgtca aaaccgccga caaagacagc
751 caatggctta aagacgtaac cgaggcctat aactccgagc cgttcaaagc
801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg
851 aaggcgcagc caaataa

```

This corresponds to the amino acid sequence <SEQ ID 1272; ORF 307.ng>:

g307.pep

1	<u>MKTFFKTLST</u>	<u>ASLALILAA</u>	GGQKDSAPAA	SAAAPSADNG	AAKKEIVFGT
51	TVGDFGDMVK	EQIQAELEKK	GYTVKLVEFT	DYVRPNLALA	EGELDINVFO
101	HKPYLDDFFK	EHNLDITEAF	QVPTAPLGLY	PGKLSLEEV	KDGSTVSAPN
151	DPSNFARALY	MLNELGWIKL	KDGINPLTAS	KADIAENLKN	IKIVELEAAQ
201	LPRSRADVDF	AVVNGNYAIS	SGMKLTEALF	QEPSFAYVNW	SAVKTADKDS
251	QWLKDVTEAY	NSDAFKAYAH	KRFEGYKYP	AWNEGAAK*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1273>:

```
m307.seq (partial)
  1  ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC
 51  CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCCTGCC GCATGGAATG
101  AAGGCGCAGC CAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1274; ORF 307>:

m307.pep (partial)
1 ..QWLKDVTEAY NSDAFKAYAH KRFEGYKSPA AWNEGAAK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 307 shows 97.4% identity over a 38 aa overlap with a predicted ORF (ORF 307.ng) from *N. gonorrhoeae*:

m307/g307

m307.pep QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA

g307 SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA

m307.pep AWNEGAAXX

g307 AWNEGAAXX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1275>:

a307.seq

```
1 ATGAAAACCT TCTTCAAAAC CCTTTCGCC GCCGCACTCG CGCTCATCCT
51 CGCCGCCTGC GCGCGTCAAA AAGATAGCGC GCCCGCCGCA TCCGCTTCTG
101 CCGCCGCCGA CAACGGCGCG GCAAAAAAAG NAATCGTCTT CGGCACGACG
151 CTCGGCGACT TCGCGGATAT GGTCAAAGAA CAAATCCAAC CCGAGCTGGA
201 GAAAAAAGGC TACACCGTCA AACTGGTCTGA GTTTACCGAC TATGTGCGCC
251 CGAATCTGCG ATTGGCTGAG GGCAGAGTNGG ACATCAACGT CTTCCAACAC
301 AAACCTTATC TTGACGACTT CAAAAAAGAA CACAATCTGG ACATACCCGA
351 AGTCTTCAA GTGCCAGCGG CGCCTTTGGG ACTGTACCCG GGCAAGCTGA
401 AATCGCTGGA AGAAGTCAA GACGGCAGCA CCGTATCCGC GCCAACGAC
451 CCGTCCAAC TCGCCCGCGT CTTGGTGATG CTCGACGAAC TGGGTTGGAT
501 CAAACTCAA GANGGCATCA ATCCGCTGAC CGCATCCAAA GCGGCAATTG
551 CCGAAAACCT GAAAAACATC AAAATCGTGC AGCTTGAAGC CGCGCAACTG
601 CCGCGTAGCC GCGCCGACGT GGATTTTGNC TCGCTCAAAG CGAANTACGC
651 CATAAGCAGC GGCATGAAGC TGACCGAAGC CCTGTTCCAA GAACCGAGCT
701 TTGCCTATGT CAACTGGTCT GCCGTCAAAA CGCCGACAA AGACAGCCAA
751 TGGCTTAAAG ACCTAACCGA GGCCTATAAC TCCGACGCGT TCAAAGCCTA
801 CGCGCACAAA CGTTTCGAGG GCTACAAATC CCCTGCCGCA TGAATGAAG
851 GCGCAGCCAA ATAA
```

This corresponds to the amino acid sequence <SEQ ID 1276; ORF 307.a>:

a307.pep
1 MKTFFKTLSA AALALILAAC GGOKDSAPAA SASAAADNGA AKKXIVEGTT

705

```

51  VGDGFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFOH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVEK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLNKI  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEGYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                                QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
          220      230      240      250      260      270

          39
m307.pep      AWNEGAAXX
          |||||
a307          AWNEGAAXX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTTCT  GTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCT  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401 CGCTTGCTC  TGTGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAG
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAGCCGCGA
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVFYRIL  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RMMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTLRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  VTEMGGVVFP  PVPAMYRKPQ
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTTCT  GTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCT  AAACGCACCT  TGTGGTATCG  AAAGGTGCCG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTC  TGTGCGCAC  GGCTTCGGCG  ACAATCTGCT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GWAACGGAAG
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGT  GCACACGCT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  gcG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

m308.pep (partial)

706

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNLMKR  XTEMGGVVFP  PVPAMYRKPQ
201 TADDIVAHSV  AHALSFLGID  TPDSA EWQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPCLSDFCFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVSKGAEMARASETDYTKDEVYALADVFHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPVPAMYRKPQTADDIVAHSAHALSLFGIDTPDSA EWQGM A					
g308	VTEMGGVVFPVPVPAMYRKPQTADDIVAHSAHTLSLFGIDTPDLA EWQGM ADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCCCT  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNLMXR  VTEMGGVVFP  PVPAMYRKPQ
201 TADDIVAHSV  AHALSFLGID  TPDSA EWQGM  AD*

```

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
a308	MLNRIFYRILGVADNLYPYLSDFCFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFVHPIGNIGACIASGTF					
a308	GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
a308	KTDGMLVAPCSMRTLASVVHGFNDLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRKQTADDIVAHSAHALSLFGIDTPDPAEWQGM					
a308	VTEMGGVVFPVPAMYRKQTADDIVAHSAHALSLFGIDTPDPAEWQGMAD					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GCGGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGACG GGATGCTGGT CGCACCCTGT TCGATGCGGA
401 CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCCTG CGATGTACCG CAAGCCGCG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFTIIA GLPLQAVLWE RMMVRRLLI
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADEVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
151 ADVVLKERRR LVLVMVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GCGGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCCTG CGATGTACCG CAAACCGCG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFTIIA GLPLQAVLWE RMMVRRLLI

```

708

```

51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVFP PVPAMYRKPO
201 TADDIVAHSV AHALSFGID TPDSA EWQGM AD*

```

m308-1/g308-1 97.0% identity in 232 aa overlap

```

      10      20      30      40      50      60
m308-1.pep MLNRVFYRILGVADNLYPRLSDFCFFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g308-1      MLNRVFYRILGVADNLYPCLSDFCFFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
          10      20      30      40      50      60

      70      80      90     100     110     120
m308-1.pep GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g308-1      GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF
          70      80      90     100     110     120

      130     140     150     160     170     180
m308-1.pep KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g308-1      KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
          130     140     150     160     170     180

      190     200     210     220     230
m308-1.pep VTEMGGVFPVPVPAMYRKPOQTADDIVAHSVAHALSFGIDTPDSA EWQGMADX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g308-1      VTEMGGVFPVPVPAMYRKPOQTADDIVAHSLAHTLSLFGIDTPDLA EWQGMADX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

```

1  ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGATTTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGTG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTGGANCT
201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
301 TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCTC GGTCTGTCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTG CGATGTACCG CAAACCGCAG
601 ACGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTCGCTGTT
651 CGGAATCGAT ACGCCGATT CCGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

```

1  MLNRIFYRIL GVADNLYPYL SDFCFFFTIIA GLPLQAVLWE RRMVRRLLI
51  GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVH GFGDNLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMXR VTEMGGVFP PVPAMYRKPO
201 TADDIVAHSV AHALSFGID TPDSA EWQGM AD*

```

a308-1/m308-1 96.1% identity in 232 aa overlap

```

      10      20      30      40      50      60
a308-1      MLNRIFYRILGVADNLYPYLSDFCFFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m308-1      MLNRVFYRILGVADNLYPRLSDFCFFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
          10      20      30      40      50      60

      70      80      90     100     110     120
a308-1      GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m308-1      GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF
          70      80      90     100     110     120

      130     140     150     160     170     180
a308-1      KTDGMLVAPCSMRTLASVHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

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m308-1      KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGMADX
              |||
m308-1      VTEMGGVVFPPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

```

g311.seq
1   atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgctgcccg gcgcgctttg ggggtgtttgg
101 gtttggaacac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcg gcattctgat tgaaacagtc agggcgggcg gtaaaacggt
201 tgccgtggtc ggtatcggca tcaatttcgt gctgcccaag gaagtggaaa
251 acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgtgtgt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgcttc
501 gcacttggaa acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tgctgttgga aggcgggaac agccggctca agtgggcgtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgcgg taccgcgatt
701 tgtcgccctt gggcgcgagg tgggcggaaa aggcggatgg aaatgtccgc
751 atcgtcggtt gcgccgtgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgccg caggctttgg
851 gcatacgcaa ccactaccgc caccgcgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgctgt
951 cagttgcggc acggcggtaa cggttgacgc gctcaccgat gacggacatt
1001 atctcggcgg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg caccggccgt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggccggcgcg cgaaagtgcg
1251 cgaagccctg ccgcctgcat ttttgccgga aaataccgtg cgcgtggcgg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

```

g311.pep
1   MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGGILIEIV RAGGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLETL LAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVLHLE TAEGEQTVVS GEISLRPDNR SVSVPKRPDS
201 ERFLLEGGN SRLKAWVEN GTFATVGSAP YRDLSPGLAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRFRS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRP AGKRYPFPTT TGNASVSGMM DAVCGSIMMM HGRLKEKNGA
401 GKPDVVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

```

m311.seq (partial)
1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTGCGCCT GTTGCGGCAG TGGCGTGTG GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCATTAAG TGGCCCAAT ATTTGGTTGT CCGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAT
351 CAGCCTGCGG TCCGACnACA GGCCGTTTC CTGnCGAAG CCGCGGGATT

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710

```

401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAC ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTCGCCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TGCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCCGACC
701 GCTGGTTCAA CGCCTTGGGC AGCCGCCGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAGTT GCGGCACGGC GGTAACGGTT GACGCGCTCA CCGATGACCG
801 ACATTATCTC GGrgGAACCA TCATGCCCAG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTTGCGGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAACCG
1001 GGGCGGGCAA GCCTGTCGAT GTCATCATTA CCGCGCGCGG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGT GCGGAAAATA CCGTGCCTGT
1101 GCGGACAAC CTCGTCATTT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGAATA TGAACAT...

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
  1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
 51 KLGILITV RTGGKTAVV GIGINFLPX EVENAASVQS LFQTASRRGN
101 ADAAVLLXXX XXXXEISLR SDXRPVSVXK RRDSEFLLL DGGNSRLKWA
151 WENGTFATV GSAPYRDLSP LGAEWAEKAD GNVRIVGCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTGNVAV ASGMMDAVCG SVMMHGRLK EKTGAGKPDV VIITGGGAAG
351 VAEALPPAFL AENTVRVADN LVIYGLLNMI AAEGREYEH...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311
      10      20      30      40      50      60
m311.pep MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILITV
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPNDLVVGRDKLGGILITV
      10      20      30      40      50      60

      70      80      90      100     110
m311.pep RTGGKTAVVVGIGINFLPXEVENAASVQSLFQTASRRGNADA AVL LXXX-----
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      RAGGKTAVVVGIGINFLPK EVENAASVQSLFQTASRRGNADA AVL LLETLLAELGAVLEQ
      70      80      90      100     110     120

m311.pep -----XXXXXXXXX
g311      YAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDGRGVLHLETAEGEQTVVS
      130     140     150     160     170     180

      120     130     140     150     160     170
m311.pep XEISLRSDXRPVSVXKRRDSEFLLLDGGNSRLKWAWENGTFATVGSAPYRDLSP LGAE
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      GEISLRPDNRSVSPKRPDSEFLLLEGGNSRLKWAWENGTFATVGSAPYRDLSP LGAE
      190     200     210     220     230     240

      180     190     200     210     220     230
m311.pep WAEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      WAEKADGNVRIVGCAVCGESKKAQVQEQLARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR
      250     260     270     280     290

```

711

```

      240      250      260      270      280      290
m311.pep  WFNALGSRRF SRNACVVVSCGTAVTVDALTDG HYLGGTIMPGF HLMKESLAVRTANLNR
          |||||
g311      WFNALGSRRF SRNACVVVSCGTAVTVDALTDG HYLGGTIMPGF HLMKESLAVRTANLNR
      300      310      320      330      340      350

      300      310      320      330      340      350
m311.pep  HAGKRYPFPTTTGNAVASGMMDAVCGSVMMMHGRLKEKTGAGKPVDV IITGGGAAKVAEA
          |||||
g311      PAGKRYPFPTTTGNAVASGMMDAVCGS IMMHGRLKEKNGAGKPVDV IITGGGAAKVAEA
      360      370      380      390      400      410

      360      370      380      389
m311.pep  LPPAFLAENTVRVADNLVIYGLLNMI AEGREYEH
          |||||
g311      LPPAFLAENTVRVADNLVIHGLLNLI AEGGESEHAX
      420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1   ATGTT CAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTTC
51  GCTGT CGCCT GTTGGCGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTG AAAAC GCAAATCAAG TGGCCAAACG ATTTGGTTCG CCGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTCGT GCTGCCCAAG GAAAGTGGAAA
251 ACGCGCTTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
301 GCCGATGCCG CCGTGTGCTG GAAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTTGCAA TATGCGCGGG ACGGATTTGC GCCTTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGGCGTTCT
501 GCACTTGGA ACGGCAGAGG GCAAACAGAC GGTCGTCAGC GCGGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTCCG TGCCGAAGCG GCGGGATTTCG
601 GAACGTTTTT TGCTGTTGGA CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAAAC GGCACGTTTC CAACCGTCGG TAGCGCGCCG TACCGGATT
701 TGTCGCCTTT GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGGTT GCGCCGTGTG CCGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAAATCG AGTGCTGCC GTCTCCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCGAAG AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGACGCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
951 CAGTTGCGGC ACGGCGGTAA CGGTTGACGC GCTCACCGAT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCCGAA CCGCCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGGCGTT TGAAAGAAAA AACCGGGCGG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GCGGCGCGG CAAAAGTTGC
1251 CGAAGCCCTG CCGCTGCAT TTTTGGCGGA AAATACCGTG CGCGTGGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCGC CGAAGGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1   MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGGIL IETV RTGGKTVA VV GIGINFVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLETL LAELDAVLLQ YARDGFAPFV AEYQAANRDH GKAVLLLRDG
151 ETVFEGTVKG VDGQGVHLHLE TAEGKQTVVS GEISLRSDDR PVSVPKRRDS
201 ERFLLLDGGN SRLKWAVVEN GTFATVGSAP YRDLSP LGAE WAEKVDGNVR
251 IVGCAVCGEF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HP EEHGSDRW
301 FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLG GTIM PGF HLMKESL
351 AVRTANLNRH AGKRYPFPTT TGNASVGMMD DAVCGSVMMH HGRLKEKTGA
401 GKPVDVIITG GGA AKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV					
a311	MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTAVVVGIGINFVLPXEVENAASVQSLFQTASRRGNADA	AVLLXXXXXXXXX----				
a311	RTGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA	AVLLETLLAELDAVLLQ				
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGV	DGGQGV	LHLETAEGKQTVVS			
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	-EISLRSDXRPVSVXKRRDSE	FLLLDGGNSRLK	WAWVENGTFATVGS	SAPYRDL	SPLGAE	
a311	GEISLRSDDRPVSVPKRRDSE	FLLLDGGNSRLK	WAWVENGTFATVGS	SAPYRDL	SPLGAE	
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQ	LARKIEWLPSSAQAL	FGIRNHYP	EEHGS	DR	
a311	WAEKVDGNVRIVGCAVCGEFKKAQVQEQ	LARKIEWLPSSAQAL	-GIRNHYP	EEHGS	DR	
	250	260	270	280	290	
	240	250	260	270	280	290
m311.pep	WFNALGSRRFSRNACVVVSCGTAVT	VDALTD	DGHYLG	GTIMPGF	HLMKESL	AVRTANLNR
a311	WFNALGSRRFSRNACVVVSCGTAVT	VDALTD	DGHYLG	GTIMPGF	HLMKESL	AVRTANLNR
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYFPPTTTGNAVASGMMDAV	CGSVMMMHGRLKEKT	GAGKPV	DV	II	TGGGA
a311	HAGKRYFPPTTTGNAVASGMMDAV	CGSVMMMHGRLKEKT	GAGKPV	DV	II	TGGGA
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPPAFLAENTVRVADNLVIYGLLN	MIAAEGREYEH				
a311	LPPAFLAENTVRVADNLVIHGLLN	LIAAEGGESEHTX				
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGCGGGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGACAA GGCACACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGCG GGCAGGGGCG GAAGTGTCG CACCGTTTGG
401 GCGAGTGCC TATGTTTCA GTTCGGCTGG CGTTTGACCG GCCGAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA CTTGCGTGCC GGCGCGCTTT
501 GGGGTGTTTG GGTTTGAAA CGCAAATCAA GTGGCCAAAC GATTTGGTCG
551 TCGGACGCGA CAAATTGGGC GGCAATCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAACACGG TTGCGGTGGT CCGTATCGGC ATCAATTTCT TGCTGCCCAA
651 GGAAGTGGA AAGCCGCTT CCGTGAGTC GCTGTTTCTG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTATTGC TGGAAACATT GCTTGGCGAA
751 CTGGGCGCGG TGTGGAACA ATATGCGGAA GAAGGGTTCG CGCCATTTTT

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801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TCGAAGGCA CGGTAAAGG CGTGGACGGA
901 CGAGGCGGTT TGCACCTGGA AACGGCAGaa ggCGAACAGa cggtcGtcag
951 cggcGaaATC AGccTGCGGc CCGaacaag gtcggtttcc GTgccgaagc
1001 gGccggatTC GgaacgttTT tTGCTgttg aagggcgga cagccggctc
1051 aAGTGGgctt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGCgCC
1101 gtaCCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGGCGCGGTG GCGGAGAATC CAAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTACCCGA
1401 TGACGGACAT TATCTCGCGG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCTTT TCCCGACCAC AACGGGCAAC GCCGTCGCAA GCGGCATGAT
1551 GGACGCGGTT TGCGGCTCGA TAATGATGAT GCACGGCGGT TTGAAAGAAA
1601 AAAACGGGCG GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1  MTLVKPSHWR VLAELADGLP QHVSQALAREA DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTKLKEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETKIKWPN DLVVGRDKLG GILIETVRAG
201 GKTAVAVGIG INFVLPKEVE NAASVQSLFO TASRRGNADA AVLLETLLE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVVDG
301 RGVHLHLETA GEQTVVSGEI SLRPDNRVS VPKRPDSERF LLEGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAAL GIRNHYRHPE EHGSDRWENA LGSRRFSRNA
451 CVVSCGTAV TVDALTDGHL YLGGTIMPGF HLMKESLAVR TANLNRPAKG
501 RYPFPTTTGN AVASGMMDAV CGSIMMHGR LKEKNGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1  ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CCGTTTGCCG CAACACGCTC CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTTCACT TTTGGCTGGG TGTTTGACCG GCCCGAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA GTGGCGTGTC GGCAGCCTT
501 GTCCGCTTTA GGTTTGGATG TGCAGATTAA GTGGCCCAAT GATTGTTGTT
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CCGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACCTGGA AACGGCAGAG GGCAACAGAG CGGTCGTCAG
951 CCGCGAAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GCGGGGATTC GGAACGTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CCGCACGTTT GCAACCGTGC GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGGCTGTGT GCGGAGAATC CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTACCCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACGG GTTGTGAAC ATGATTGCCG

```


1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence <SEQ ID 1298; ORF 311-1>:

m311-1.pep

```

1  MTVLKLSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFDPRQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILITVRTG
201 GKTVAUVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVGD
301 QGVLEHLETA GKQTVVSGEI SLRSDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQLARKI EWLPSAQAL GIRNHYRHPE EHGSDFWNA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDGHL YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

m311-1.pep	10	20	30	40	50	60
g311-1	10	20	30	40	50	60
m311-1.pep	70	80	90	100	110	120
g311-1	70	80	90	100	110	120
m311-1.pep	130	140	150	160	170	180
g311-1	130	140	150	160	170	180
m311-1.pep	190	200	210	220	230	240
g311-1	190	200	210	220	230	240
m311-1.pep	250	260	270	280	290	300
g311-1	250	260	270	280	290	300
m311-1.pep	310	320	330	340	350	360
g311-1	310	320	330	340	350	360
m311-1.pep	370	380	390	400	410	420
g311-1	370	380	390	400	410	420
m311-1.pep	430	440	450	460	470	480
g311-1	430	440	450	460	470	480
m311-1.pep	490	500	510	520	530	540
g311-1	490	500	510	520	530	540
	550	560	570	580	590	

```

m311-1.pep  VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEHIX
              |||||
g311-1      VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTTCACT TTTGGCTGGG TGTGTTGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA GTGGCGTGCC GGCGCGCCTT
501 GTCGCGTTTG GGTGTAAGAA CGCAAATCAA GTGGCCAAAC GATTGCGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCGGTGGT CCGTATCGGC ATCAATTTCC TGCTGCCCAA
651 GGAAGTGGA AAGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GGCGGGGAAA TGCCGATGCC GCGGTGTTGC TGGAAACGCT GTTGGCGGAA
751 CTTGATGCGT TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 TCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGCGC GTATTGCTGT
851 TGCGGACGCG CGAACCCTG TTCGAAGGCA CGGTTAAAGG CGTGACGCGA
901 CAAGCGCTTC TGCACTTGA AACGGCAGAG GGCAAACAGA CGGTGCTCAG
951 CGCGCAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GGCGGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCTT TGGGCGCGGA GTGGGCGGAA AAGTGGAATG
1151 GAAATGTCCG CATCGTCGGT TGCGCGGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGACAGC GCGGCTTCA GCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTGACG CGCTACCGA
1401 TGACGGACAT TATCTCGGG GAACCATCAT GCCCGGTTT CACCTGATGA
1451 AAGAAATCGT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTGCGCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGG GGGCAAGCCT GTCGATGTCA TCATTACCG CGGCGGCGCG
1651 CAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGGTGGCG GACAACCTCG TCATTACGG GCTGTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTLVKPSHWR VLAELADGLP QHVSQARMAD DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECIMFS FGWVFDPRQY
151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGRDKLG GILLETVRTG
201 GKTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVVG
301 QGVLLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAVWENGTF ATVGSAFYRD LSPLGAEWAE KVDGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSAQAAL GIRNHYRHPE EHGSDRFWNA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

```

a311-1/m311-1 98.5% identity in 591 aa overlap

```

              10      20      30      40      50      60
a311-1.pep  MTLVKPSHWRVLAELADGLPQHVSQARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR
              |||||
m311-1      MTLVKLSHWRVLAELADGLPQHVSQARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR
              10      20      30      40      50      60

              70      80      90      100     110     120
a311-1.pep  LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              |||||
m311-1      LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              70      80      90      100     110     120

```

a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECLMFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLKTQIKWPN					
m311-1	130	140	150	160	170	180
	GRGRQGRKWSHRLGECLMFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDQIKWPN					
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILIEVTRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
m311-1	190	200	210	220	230	240
	DLVVGRDKLGGILIEVTRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
m311-1	250	260	270	280	290	300
	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAWVENGTF					
m311-1	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAWVENGTF					
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPGLGAEWAEEKVDGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL					
m311-1	370	380	390	400	410	420
	ATVGSAPYRDLSPGLGAEWAEEKADGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL					
a311-1.pep	430	440	450	460	470	480
	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGF					
m311-1	430	440	450	460	470	480
	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGF					
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPFTTGNVAVSGMMDAVCGSVMMMHGRLKEKTGAGKP					
m311-1	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPFTTGNVAVSGMMDAVCGSVMMMHGRLKEKTGAGKP					
a311-1.pep	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHTX					
m311-1	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNMIAAEGREYEHIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1   atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTaccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggtcg gcaaagactT GGTGGCAacg Gcgaaacacc tTTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGTC AACCGCGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCCGCGT
651 ATCCGGTCCA GGCGTGGTCA AAGCCGCGCT GGAAAATTCT GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTGTG CGCTGGCACC GACCCCGGCC GTCGGCGACT
851 CGGTGGCGCG CATCTTGAA GAAATGGGCT TGAGCGTCTG CCGTACGCAC

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCCGTC TGCTCCGTTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

```

g312.pep
  1 MSIQSGEILE TVKMVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
 51 TTVGKDLVAT AKHLSAKYGV PIVNQIRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

```

m312.seq
  1 ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
 51 CCAGAAATTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAATC
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTC
351 CGCGTTGGTG CAAAAGGGA TGTCGCcTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACcGTc AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAAAAATTGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTWTGGCG
601 GGCGCGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCT GCGTATCCGG
651 CCCAGGTGTC GTAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAACTG CTTTCAAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTCGCCGA CCCCGCCCGT CGGCGACTCA GTGGCAGCGA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCGTTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGCTAAAA CCGTCGGCGA CAcGGTCGAG TTCGGCGGCT TGTTGGgCTA
1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

```

m312.pep
  1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
 51 TTVGKDLVTT AKYLSAKYGV PIVNQIRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCXSIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGCAKIVVFC NAVEDNPFXA
201 GAFHGSGDAV INVGVSGPGV VKAALENSDA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCGTHGTTA
301 ALALLNDAVK KGGMMASSAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLLGYPV MPVKEGSCEV FVNRGGRIPA PVQSMKN*

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718

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTGVGKDLVTT					
g312	MSIQSGEILETVKMVADRNFDVRTITIGIDLHDCISTDIDVLNQNIYNKITTGVGKDLVAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m312.pep	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSALV					
g312	AKHLSAKYGVPIVNQRISVTPIAQIAAATKADSYVSVAQTLDKAAKAIGVSFIGGFSALV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m312.pep	QKGMSPSDEVLIRSIPEAMKTTDIVCXNIGSTRAGINMDAVKLAGETVKRTAEITPEG					
g312	QKGMSPSDEVLIRSVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEG					
	130	140	150	160	170	180
	190	200	210	220	230	
m312.pep	FGCAKIVVFCNAVEDNPF XAGAFHSGS--DAVINVGVS GPGVVKAALENS DATTLTEVAE					
g312	FGCAKIVVFCNAVEDNPF MAGAFHSGSEADAVINVGVS GPGVVKAALENS DAVSLTEVAE					
	190	200	210	220	230	240
	240	250	260	270	280	290
m312.pep	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
g312	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPT PAVGDSVARILEEMGLSVCGTH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLND AVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
g312	GTTAALALLND AVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMI AVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
g312	CSVGLDMI AVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRGGRI PAPVQSMKNX					
g312	YAPVMPAKEGSCEVFVNRGGRI PAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

1	ATGAGTATCC	AATCCGGCGA	AATTTTAGAA	ACCGTCAAAA	TGTTGCCGA
51	CCAGAATTTT	GATGTCCGCA	CCATTACCAT	CGGCATTGAT	TGTCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTTGAACC	AAAAATATTTA	CAACAAAATT
151	ACCACGGTCG	GCAAAGACTT	GGTGGCGACA	GCAAAATATC	TGTCTGCCAA
201	ATACGGCGTG	CCGATTGTGA	ATCAGCGCAT	TTCTGTCACG	CCGATTGCC
251	AAATCGCGGC	GGCCACCCAT	GCTGATTCTT	ACGTCAGCGT	GGCGCAAAT

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301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTGCCTTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTTCTGC AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGCCCG GGTGTCGTAA AAGCCGCGTT GGAAAATTCG GATGCAACGA
701 CATTGACCGA AGTTGCCGAA GTTGTGAAGA AAACCGCCTT CAAAATTACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGCTG CGGTACGCAC
901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAAGCAGG CGTGCTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTCCGGTCG GCTTGGATAT
1101 GATTGCCGTT CCCGGCGACA CACCCGCGCA CACCATTTC GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATTCCGG TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCCTG TAATGCCGGT AAAAGAAGGC TCATGCCAAG
1301 TGTCGTCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

```

a312.pep
  1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
 51 TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GP VVKAALENS DATTLEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCETH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

m312/a312 96.7% identity in 451 aa overlap

```

          10      20      30      40      50      60
m312.pep  MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
          |||
a312      MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT
          10      20      30      40      50      60

          70      80      90     100     110     120
m312.pep  AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVVAQTLDKAAKAIGVSFIGGFSA
          |||
a312      AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVVAQTLDKAAKAIGVSFIGGFSA
          70      80      90     100     110     120

          130     140     150     160     170     180
m312.pep  QKGMSPSDEVLIRSIPEAMKTTDIVCX SINIGSTRAGINMDAVKLAGETVKRTAEITPEG
          |||
a312      QKGMSPSDEVLIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITLEG
          130     140     150     160     170     180

          190     200     210     220     230
m312.pep  FGCAKIVVFCNAVEDNPF XAGAFHGS G--DAVINVGVS GPVVKAALENS DATTLEVAE
          |||
a312      FGCAKIVVFCNAVEDNPF MAGAFHGS GEADAVINVGVS GPVVKAALENS DATTLEVAE
          190     200     210     220     230     240

          240     250     260     270     280     290
m312.pep  VVKKTAFKITRVGELIGREASKMLNIPFGI LDLS--PTPPVGDSVARILEEMGLSVCETH
          |||
a312      VVKKTAFKITRVGELIGREASKMLNIPFGI LDLSLAPTPAVGDSVARILEEMGLSVCETH

```

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	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

```

g313.seq
1  atggacgacc cgcgcaccta cggatcgggc aatcccggcg cgaccaatgt
51  tttagcgagc ggcaaaaaaa aggcggccgc gctgacgctc ttgggcgatg
101 cgcgcaaagg tttggttgcc gttttgcttg cacgcgtgct tcaagaaccg
151 ctcggtttat cgcacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
201 cgggcataatg tggccggtgt tttcggatt taaggcgggc aaaggcggtg
251 caacggcatt gggcgtgctt ctggcactct ctctgcaac tgccttggtc
301 tgcgcgttga tttggcttgt gatggcattc ggcttcaaag taccctccct
351 tgccgcgctg gtcgccacaa ccgcccgcct ccttgccgca ctgttttta
401 tgccgcatac ttcttggtt ttcgcaaccc tcgcaatcgc catattggtg
451 ttgctccgcc ataagagcaa catcctcaac ctgattaaag gcaaagaaaag
501 caaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

```

g313.pep
1  MDDPRTYGS NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMAF GFKVSSLAAL VATTAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNI LN LIKGKESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

```

m313.seq
1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTAGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCGCAAC TGCCTTGGTC
301 TGCGCGTTGA TTTGGCTTGT TATGGCATTG GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTCCGCCCA TCCTTCTTTA
401 TGCCGCACGT CTCGTGGGTT TGGGCGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

```

m313.pep
1  MDDPRTYGS NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMAF GFKVSSLAAL TATIAAPVAA SFFMPHVSWS WATVAIALLV
151 LFRHKSNI VK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRS GKKKAAAL TLLGDAAKGLVAVLLARVLQEPLGLSDSAIAA					
g313	MDDPRTYGSNPGATNVLRS GKKKAAAL TLLGDAAKGLVAVLLARVLQEPLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS VWVATVAIALLV LFRHKSNI VKLLEGRESKIGGSRX					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNI LNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

a313.seq

```

1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAA AGGCGGCGCG GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTGGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGCGGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCACAAC TGCCTTGCTC
301 TGCGCGTTGA TTTGGCTTGT GATGGCATTG GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCCCC CCTTGCCGCA CTGTTTTTTA
401 TGCCGCATAC TTCTTGGATT TTCGCAACCC TCGCAATCGC CATATTGGTG
451 TTGCTCCGCC ATAAGAGCAA CATCCTCAAC CTGATTAAAG GCAAAGAAAG
501 CAAAATCGGC GAAAAACGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

```

1  MDDPRTYGS NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGV LALSPTTALV
101 CALIWLVMF GFKVSSLAAL TATIAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNI LN LIKGESKIG EKR*

```

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRS GKKKAAAL TLLGDAAKGLVAVLLARVLQEPLGLSDSAIAA					
a313	MDDPRTYGSNPGATNVLRS GKKKAAAL TLLGDAAKGLVAVLLARVLQEPLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS VWVATVAIALLV LFRHKSNI VKLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNI LNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
  1  atgaaattac aacaattggc tgaagaaaaa atcggcggttc tgatttgtgtt
 51  cacgctgctt gtagtcagtg tcggtctgtt gattgaagtt gtgcccttgg
101  cctttaccaa ggcggcaaca cagccggcgc cgggcgtgaa gccttacaat
151  gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201  ctgccactct caaatgattc gtccgttccg tgcggaaacc gagcgttacg
251  gtcattactc tgttgccgga gagtcggtt acgaccatcc gttccaatgg
301  ggttccaaac gtaccgggcc tgatttggca cgtgtggcg gccgctattc
351  cgacgaatgg caccgcattc acctgctgaa tccccgtgat gtcgtgcctg
401  agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451  gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501  cagtgatgag gaaattgcga aagcgctga ggctttggca aacaaatccg
551  agctggatgc ttagtcgcc tatctgcaag gattgggtct ggctttgaaa
601  aacgtaaggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
  1  MKLQQLAEEK IGVLLIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201  NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
  1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
 51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101  CCTTTACCAA GGC GGCAACA CAGCCGGCGC CGGGCGTGAA GCCTTACAAT
151  GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTACAA
201  CTGCCACTCG CAAATGATTG GTCCGTTCCG TCGGAAACC GAGCGTTACG
251  GTCATTACTC TGTTGCCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301  GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCG GTCGCTATTC
351  CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401  AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGTC
451  GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501  CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551  AGCTGGATGC TTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601  AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
  1  MKLQQLAEEK IGVLLIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201  NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

```
m401/g401

      10      20      30      40      50      60
m401.pep  MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||
g401      MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          10      20      30      40      50      60

      70      80      90     100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVDHPFQWGSKRTGPDLARVGGRYSEW
```

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```

g401      |||||
          IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFWLNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
g401      HRIHLLNPRDVPESNMPAFWLNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
g401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1  ATGAAATTAC  AACAATTGGC  TGAAGAAAAA  ATCGGCGTTC  TGATTGTGTT
51 CACGCTGCTT  GTAGTCAGTG  TCGGTCTGTT  GATTGAAGTT  GTGCCCTTGG
101 CCTTTACCAA  GCGGCAACA  CAGCCGGCGT  CGGGCGTGAA  GCCTTACAA
151 GCCCTGCAGG  TTGCCGGACG  CGATATTTAC  ATCCGTGAGG  GCTGTACAA
201 CTGCCACTCG  CAAATGATTC  GTCCGTTCCG  TCGGAAACC  GAGCGTTACG
251 GTCATTACTC  TGTTCGCGGA  GAGTCGGTTT  ACGACCATCC  GTTCCAATGG
301 GGTTCCAAAC  GTACCGGTCC  TGATTGGCA  CGTGTGGGCG  GTCGCTATTC
351 CGACGAATGG  CACCGTATCC  ACCTGCTGAA  TCCCGTGAT  GTCGTGCCTG
401 AGTCCAATAT  GCCGGCATT  CCGTGGCTTG  CACGCAATAA  AGTCGATGTC
451 GATGCAACCG  TTGCCAAT  GAAGGCTTTG  CGTAAAGTAG  GTACTCCTTA
501 CAGTGATGAG  GAAATTGCGA  AAGCGCCTGA  GGCTTTGGCA  AACAAATCCG
551 AGCTGGATGC  TGTAGTCGCC  TATCTGCAAG  GATTGGGTCT  GGCTTTGAAA
601 AACGTAAGGT  AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1  MKLQQLAEEK  IGVLVFTLL  VSVGLLIEV  VPLAFTKAAT  QPASGVKPYN
51 ALQVAGRDIY  IREGCYNCHS  QMIRPFRAET  ERYGHYSVAG  ESVYDHPFQW
101 GSKRTGPDLA  RVGGRYSEW  HRIHLLNPRD  VVPESNMPAF  PWLNKVDV
151 DATVANMKAL  RKVGTPYSDE  EIAKAPEALA  NKSELDAVVA  YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

m401.pep      10      20      30      40      50      60
              MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
              |||||
a401           10      20      30      40      50      60
              MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
              |||||

          70      80      90      100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          |||||
a401      IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFWLNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
a401      HRIHLLNPRDVPESNMPAFWLNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
a401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

```
g402.seq
1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  ttttccttacc ggatTATTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGtttttcgTT CGCagcAcag tccgtgcctc aggCATTtTC atttattcctt
151 gcctGttttc tgACCGgtat cgcctgcgcg gCgTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTG ATATTCCctT TATCGGGCAG TgcttccttgT
251 GGGCGGGTAT TgccaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 CGtcGTCAGG GGGTTGATTT TCCCACtTG ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCGC CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttgtt
501 gTCCACCCAA CAGATttacc tgctcatCTG TTTGATTtCT GCTGctgtcc
551 cTTTGTtTTg tacaCTGtTC CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCCCTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG GCCGTCCGGA TAGGTTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGAcg agccgcAAAT CGCACCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATTCGACTT GGTACTGGCG
1101 TGCCTATTCC ACTAACCTGT TGAGTGCgGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATgctTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTcctt AATAAAGAAC
1301 TGCTCaagca aCGCCTTtcc cgGTTGATTT GGCCGGAAG CGGCAGgcac
1351 gtATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGtctctcG
1401 TATGCTGATT CGGATGACGG AacctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA
```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

```
g402.pep
1  MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPQAFSFIL
51  ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGLI MFLLPDSVFQ NIAGRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDgayNT DIFNSVNGIE RAYLLPSLKS GIRRIFFVVL STGSWARVLS
301 AIPQMqSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVVSRLMI RMTEPSAGAE VITDDNMIVE YKYGRGI*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

```
m402.seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCnTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACCCCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCGG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTcAsA sGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCGC CAmCGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TwTGATTtCT GCTGCTGTCC
551 CTTTGTtTTG TACACTGTTC CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTcYtAC TGCCGGATTC
```

m402.ppt

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/q402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPPQAFSFTLACFLTGIAVG					
	: : :					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGIEVLWVRMFSFAAQSVPPQAFSFILACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTDGNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
	:					
g402	GLIFPLVHHVGTDGNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGLMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGLMFLLPDSVFQNIAGRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVVYGANVYDGYNTDVFN SVN GIERAYLLPSLKSGIRRI FV V GLSTG SWARVLS					

726

```

g402      |||||:|||||
          HRDGDKVYVGANVYDGAYN TDI FNSVNGIERAYLLPSLKSGIRRI FVVGLSTGSWARVLS
          250      260      270      280      290      300

          310      320      330      340      350      360
m402.pep  AIPQMISMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHRPDEKFDLILM
          |||||
g402      AIPQMISMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHRPDEKFDLILM
          310      320      330      340      350      360

          370      380      390      400      410      420
m402.pep  NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          : |||||
g402      NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          370      380      390      400      410      420

          430      440      450      460      470      480
m402.pep  VGSATPVVFPNKELLKQRLSRLIWPESEGRHVFDSSTVDAAAQKVVSRLMIQMTEPSAGAE
          |||||
g402      VGSATPVVFPNKELLKQRLSRLIWPESEGRHVFDSSTVDAAAQKVVSRLIRMTGPSAGAE
          430      440      450      460      470      480

          490
m402.pep  VITDDNMIVEYKYGRGIX
          |||||
g402      VITDDNMIVEYKYGRGI
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT ATATGCTTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTTGACG
301 GGTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CTTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCCACCAA CAGATTTACC TGCTCATCTG TTTGATTTCT GCTGCTGTCC
551 CTTTGTTTTG TACACTGTTC CAAAAAGTC TCCGACTGAA TGCAGTTCG
601 GTAGCAGTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATGTG TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTCCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402.pep
1  MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL

```

727

51 ACFLTGI AVG AYFGKRICRS RFVDIPFIGQ CFWAGIADF LILGAAWLLT
 101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
 151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
 201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKV VYG
 251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRI FVVGL STGSWARVLS
 301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
 351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
 401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLQRLS RLIWPESGRH
 451 VFDSSTVDAA AQKVVSRLMI QMTEPSAGAE VITDDNMIVE YKYGRGI*

m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGLIEVLWVRMFSAFAQSVPAFSFTLACFLTGI AVG					
a402	MDIVNTKPNTSLIYMLSFLSGLLSLGLIEVLWVRMFSAFAQSVPAFSFTLACFLTGI AVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKV VYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRI FVVGLSTGSWARVLS					
a402	HRDGDKV VYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRI FVVGLSTGSWARVLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m402.pep	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
a402	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m402.pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m402.pep	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSSTVDAAAQKVVSRLMIQMTEPSAGAE					
a402	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSSTVDAAAQKVVSRLMIQMTEPSAGAE					
	430	440	450	460	470	480
	490					
m402.pep	VITDDNMIVEYKYGRGIX					
a402	VITDDNMIVEYKYGRGIX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC  GGCTGCTGAT  ACCTATTCTT  TTTTCAGTTT  TTATTTTATC
51  CGCCTGCGGG  AACTGACAG  GTATTCCATC  GCATGGCGGA  GGCAAACGCT
101  TCGCGGTCGA  ACAAGAACTT  GTGGCCGCTT  CTGCCAGAGC  TGCCGTAAAA
151  GACATGGATT  TACAGGCATT  ACACGGACGA  AAAGTTGCAT  TGTACATTGC
201  AACTATGGGC  GACCAAGGTT  CAGGCAGTTT  GACAGGGGGT  CGCTACTCCA
251  TTGATGCACT  GATTTCGCGC  GAATACATAA  ACAGCCCTGC  CGTCCGCACC
301  GATTACACCT  ATCCGCGTTA  CGAAACCACC  GCTGAAACAA  CATCAGGCGG
351  TTTGACGGGT  TTAACCACTT  CTTTATCTAC  ACTTAATGCC  CCTGCACTCT
401  CGCGCACCCA  ATCAGACGGT  AGCGGAAGTA  GGAGCAGTCT  GGGCTTAAAT
451  ATTGGCGGGA  TGGGGGATTA  TCGAAATGAA  ACCTTGACGA  CCAACCCGCG
501  CGACACTGCC  TTTCTTTCCC  ACTTGGTGCA  GACCGTATTT  TTCCTGCGCG
551  GCATAGACGT  TGTTTCTCCT  GCCAATGCCG  ATACAGATGT  GTTTATTAAC
601  ATCGACGTAT  TCGGAACGAT  ACGCAACAGA  ACCGAAATGC  ACCTATACAA
651  TGCCGAAACA  CTGAAAGCCC  AAACAAAAC  GGAATATTTT  GCAGTAGACA
701  GAACCAATAA  AAAATTGCTC  ATCAAACCCA  AAACCAATGC  GTTTGAAGCT
751  GCCTATAAAG  AAAATTACGC  ATTGTGGATG  GGGCCGTATA  AAGTAAGCAA
801  AGGAATCAAA  CCGACGGAAG  GATTGATGGT  CGATTCTCTC  GATATCCAAC
851  CATACGGCAA  TCATACGGGT  AACTCCGCCC  CATCCGTAGA  GGCTGATAAC
901  AGTCATGAGG  GGTATGGATA  CAGCGATGAA  GCAGTGCAGC  AACATAGACA
951  AGGGCAACCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL  FSVFILSACG  TLTGIPSHGG  GKRFVEQEL  VAASARAAVK
51  DMDLQALHGR  KVALYIATMG  DQSGSLTGG  RYSIDALIRG  EYINSPAVRT
101  DYTYPRYETT  AETTSGLTGG  LTTSLSTLNA  PALSRTQSDG  SGSRSSLGLN
151  IGGMGDYRNE  TLTTNPRDTA  FLSHLVQTVF  FLRGIDVVSP  ANADTDVFIN
201  IDVFGTIRNR  TEMHLYNAET  LKAQTKLEYF  AVDRTNKKLL  IKPKTNAFEA
251  AYKENYALWM  GPYKVSKEIK  PTEGLMVDFF  DIQPYGNHTG  NSAPSVEADN
301  SHEGYGYSDE  AVRQHRQGQP  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC  GGCTGCTGAT  ACCTATTCTT  TTTTCAGTTT  TTATTTTATC
51  CGCCTGCGGG  AACTGACAG  GTATTCCATC  GCATGGCGGA  GGTAACGCT
101  TTGCGGTCGA  ACAAGAACTT  GTGGCCGCTT  CTGCCAGAGC  TGCCGTAAAA
151  GACATGGATT  TACAGGCATT  ACACGGACGA  AAAGTTGCAT  TGTACATTGC
201  CACTATGGGC  GACCAAGGTT  CAGGCAGTTT  GACAGGGGGT  CGCTACTCCA
251  TTGATGCACT  GATTTCGCGC  GAATACATAA  ACAGCCCTGC  CGTCCGTACC
301  GATTACACCT  ATCCACGTTA  CGAAACCACC  GCTGAAACAA  CATCAGGCGG
351  TTTGACAGGT  TTAACCACTT  CTTTATCTAC  ACTTAATGCC  CCTGCACTCT
401  CTCGCACCCA  ATCAGACGGT  AGCGGAAGTA  AAAGCAGTCT  GGGCTTAAAT
451  ATTGGCGGGA  TGGGGGATTA  TCGAAATGAA  ACCTTGACGA  CTAACCCGCG
501  CGACACTGCC  TTTCTTTCCC  ACTTGGTACA  GACCGTATTT  TTCCTGCGCG
551  GCATAGACGT  TGTTTCTCCT  GCCAATGCCG  ATACAGATGT  GTTTATTAAC
601  ATCGACGTAT  TCGGAACGAT  ACGCAACAGA  ACCGAAATGC  ACCTATACAA
651  TGCCGAAACA  CTGAAAGCCC  AAACAAAAC  GGAATATTTT  GCAGTAGACA
701  GAACCAATAA  AAAATTGCTC  ATCAAACCAA  AAACCAATGC  GTTTGAAGCT
751  GCCTATAAAG  AAAATTACGC  ATTGTGGATG  GGGCCGTATA  AAGTAAGCAA
801  AGGAATTTAA  CCGACGGAAG  GATTAAATGG  CGATTCTCTC  GATATCCGAC
851  CATACGGCAA  TCATACGGGT  AACTCCGCCC  CATCCGTAGA  GGCTGATAAC
901  AGTCATGAGG  GGTATGGATA  CAGCGATGAA  GTAGTGCAGC  AACATAGACA
951  AGGACAACCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL  FSVFILSACG  TLTGIPSHGG  GKRFVEQEL  VAASARAAVK

```

729

```

51  DMDLQALHGR  KVALYIATMG  DQSGSLTGG  RYSIDALIRG  EYINSPAVRT
101 DYTYPRYETT  AETTSGGLTG  LTTSLSTLNA  PALSRQSDG  SGSKSSLGLN
151 IGGMGDYRNE  TLTTNPRDTA  FLSHLVQTVF  FLRGIDVVSP  ANADTDVFIN
201 IDVFGTIRNR  TEMHLYNAET  LKAQTKLEYF  AVDRTNKKLL  IKPKTNAFEA
251 AYKENYALWM  GPYKVSIGIK  PTEGLMVDFS  DIRPYGNHTG  NSAPSVEADN
301 SHEGYGYSDE  VVRQHRQGQP  *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406 . pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVK DMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVK DMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406 . pep	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
m406	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406 . pep	LTTSLSTLNAPALSRQSDGSGSRSSLGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	:					
m406	LTTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406 . pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406 . pep	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIQPYGNHTGNSAPSVEADN					
	:					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406 . pep	SHEGYGYSDEAVRQHRQGQPX					
	:					
m406	SHEGYGYSDEVVRQHRQGQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

```

a406 . seq
1   ATGCAAGCAC  GGCTGCTGAT  ACCTATTCTT  TTTTCAGTTT  TTATTTTATC
51  CGCCTGCGGG  AACTGACAG  GTATTCCATC  GCATGCGGGA  GGTAAACGCT
101 TCGCGGTCGA  ACAAGAACTT  GTGGCCGCTT  CTGCCAGAGC  TGCCGTTAAA
151 GACATGGATT  TACAGGCATT  ACACGGACGA  AAAGTTGCAT  TGTACATTGC
201 AACTATGGGC  GACCAAGGTT  CAGGCAGTTT  GACAGGGGGT  CGCTACTCCA
251 TTGATGCACT  GATTCGTGGC  GAATACATAA  ACAGCCCTGC  CGTCCGTACC
301 GATTACACCT  ATCCACGTTA  CGAAACCACC  GCTGAAACAA  CATCAGGCGG
351 TTTGACAGGT  TTAACCACTT  CTTTATCTAC  ACTTAATGCC  CCTGCACTCT
401 CGCGCACCCA  ATCAGACGGT  AGCGGAAGTA  AAAGCAGTCT  GGGCTTAAAT
451 ATTGGCGGGA  TGGGGGATTA  TCGAAATGAA  ACCTTGACGA  CTAACCCGCG

```


730

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTGT LTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
301 SHEGYGYSDE AVRRHRQGP *

```

m406/a406 98.8% identity in 320 aa overlap

	10	20	30	40	50	60
m406.pep	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAAVKDMDLQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAAVKDMDLQALHGR					
	10	20	30	40	50	60
m406.pep	KVALYIATMGDQSGSGLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGT					
a406	KVALYIATMGDQSGSGLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGT					
	70	80	90	100	110	120
m406.pep	KVALYIATMGDQSGSGLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGT					
a406	KVALYIATMGDQSGSGLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGT					
	70	80	90	100	110	120
m406.pep	LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
m406.pep	LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
m406.pep	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
m406.pep	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
m406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTEGLMVDFS DIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
m406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTEGLMVDFS DIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
m406.pep	SHEGYGYSDEVVRQHRQGPX					
a406	SHEGYGYSDEAVRRHRQGPX					
	310	320				
m406.pep	SHEGYGYSDEVVRQHRQGPX					
a406	SHEGYGYSDEAVRRHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
1  atggtcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
51  ggcaggcgga gatggcaaga tgcagcatca ctttgacggc aggggttgcgt

```

```

101  tcgtcaaacg attcggacac caagccgctg tctcgggtcga ggccgaggggt
151  cagctgggtc atgtcggttc agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcagggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggt cagacccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgcccacc
451  acggaagccc aacatcggtt tttcttcatt cggttcgat acgtgcccgc
501  cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggatgc gtaaccggcg atgcggcgga
651  taatttcgcg tttcagttcg tcgtcttggt tgtcaaattc caacaaggct
701  ttcgggtgga tgccgatttg gcggttgatg ataaattcca tacgcgcaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatcgc agttcgggat
801  tgccgacggt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taatttgtag gtccagcagg ccggcataga taaagccggt
901  atgccttcgc gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatt gccgcagccg acgacggcag gaataccagc ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgcgc cggttggtca cgatggcgga
1051 agcagctttc atcacgggtt cccaatccgc atcggtcatt tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cggagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgacaaa
1201 gacgggtttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttgga tttgacggtt tcggggcgccg cttgcaggat gtagagttag
1301 ccgtccaggg cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 ttttctgatg gtcagcgcgt agtggtgcaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatggtc ttgcgcagga tggcggttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggtgtg agccggattc
1651 ggtgctgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLTADT DIFVLLAAGG DGKMQHHFDG RFAFVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAAADQV GVFGFVGVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVFKF QGFRVDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDFDGCFWH IVQGDIGNLY VQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDGG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHALTD FLTDGTTFAQ
401 DFFAVDGV A QVAAAFFLG PDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQRVVCQ LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGF EHI KFVRVDRALY DVFAQTVRGG NKDDL VVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggctcgac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgcgt
101  tcgtcaaacg attcggatca caagccgctg tcgcgggtcga gaccgaggggt
151  cagttgggtc atgtcggttc agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcagggc cgtttttgcc gcgttccaag ccgttttctt tcagggtctt
301  gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  caacgttggg caacccatt tcatcgcgga cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgcccacc
451  acggaagccc aacatcggtt tttcttcatt cggttcgat acgttgcgcg
501  cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
651  taatttcgcg ttttaattcg tcgtcttggt tgtcaaattc caacaargct

```

732

```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca gggtggcgaa gctgaatgcg agttcgggat
801 tgccgacgtt catcatgact tttacagggt ctttaggcat attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgcccttc gcacaggata cggtaacttc ttgaccgtt ttcagcaatt
951 cgggtgcatt gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggccgcgg cggttggtaa cgatggcaga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcacg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaaagcat tttaatcagg
1151 cgacaccttg cctgaccgac tttctgaccg atggcgcgcc cttcgcataa
1201 tacgggtttt tcgccgttga tggcgaagcg gcgcaggttg cggttgccct
1251 cttcttgagg ttttacggtt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgccaa ctcagtaatt tcttcgtcgg
1401 taatggagaa gcggttgcgg tcttcctcgg ggacatcgac gttggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgttttga
1501 acccatggtt ttacgcagga tggcgggctt gcccgytttg agcgtgggtt
1551 tgaacacatr aaattcgtcc ggggtgaccg caccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
  1  MVGXALTADA DIFVLLAAGG DGKVQHFFDG RFAFVKRFGY QAAVAVETEG
 51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101  DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151  TEAQHRVFFM RFVYVAADQV GVFGFVGVGH TDDGFTRINR CGQCRHAFGD
201  FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QXXFGVDTDL AVDDKFHTRQ
251  ADAFAGQVGE AECEFGIADV HHDFYRCFRH IVXGDIGNLY VQQTGIDKAG
301  IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDGR
351  STFHHGFPIR IGHVGNFYVA GFDGIHLGSI FNQAHLLTD FLTDGAFAFX
401  YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFVQAVAS PFDIHRAAVV
451  FFDGQCVMRQ LSNFFVGNGE AVAVFLGDID VGYGFTGFCF VGKNHFDVFX
501  THGFTQDGLL ARFERGFEHX KFVRVDRPLY DVFAQTVRGG NKDDLIVXGF
551  GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

```

m501/g501
      10      20      30      40      50      60
m501.pep  MVGXALTADADI FVLLAAGGDGKVQHFFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG
          ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      MVGRTLTAADTDIFVLLAAGGDGKMQHFFDGRVAFVKRFGHQAAVSVEAEGQLGHVVRADG
          10      20      30      40      50      60

      70      80      90     100     110     120
m501.pep  EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFNDNGFGFAQSADERNHDFNVG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG
          70      80      90     100     110     120

      130     140     150     160     170     180
m501.pep  QPHFIADAFQGFQGETVFEVVGDITRRTTEAQHRVFFMRFBVYVAADQVGVFGFVGVGH
          | |||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      QTHFVTNAFQGFQGETVFEALGNITRRTTEAQHRVFFMRFBVYAAADQVGVFGFVGVGH
          130     140     150     160     170     180

      190     200     210     220     230     240
m501.pep  TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXXFGVDTDL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

733

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAA DNFRFQFVVL FVKFQQGFRVDADL
	190 200 210 220 230 240
m501.pep	250 260 270 280 290 300
	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDIGNLYVQQTGIDKAG
g501	AVDDKFHTRQADAFAGQIGEAEC EFGIADVHHDFDGC FWHIVQGDIGNLYVQQAGIDKAG
	250 260 270 280 290 300
m501.pep	310 320 330 340 350 360
	IAFGTGYGNFLT V FQQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR
g501	IAFGTGYGNFLT V FQEFGR IAAADDGRNTQFARDDGGVAGASAAVGH DGGSTFHHGFPIR
	310 320 330 340 350 360
m501.pep	370 380 390 400 410 420
	IGHVGN EYVAGFDGIHLGSI FNQ AHLALTDFLTDGA AFAXYGFVAVDGEAAQVAVALFLG
g501	IGHVGNQYVAGFDGIHLGSI FNQ AHLALTDFLTDGTTFAQDGF FAVDGVAAQVAAFFLG
	370 380 390 400 410 420
m501.pep	430 440 450 460 470 480
	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGGQCV MRQLSNFFVGNGEAVAVFLGDID
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDQQRVVCQLGDF FVGNGEAVAVFFGD F
	430 440 450 460 470 480
m501.pep	490 500 510 520 530 540
	VGYGFTGF CFVGNHFDVFXTHGFTQDGG LARFERGF EHXKFVRVDR TLYDVFAQTVRGG
g501	VGYRFAGFGFVGNHFDVFRTHGLAQDGGFACFERGF EHIKFVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	550
	NKDDLIVXGFGVEGEHHT
g501	NKDDL VVAGFGVEGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq	(partial)
1	ATGGTTCGGAC GGGCCTTGAC CGCAGATGCC GACATATTTG TTCTGCTTGC
51	GGCAGGCGGA GATGGCAAGG TGCAGCATCA CTTTGACGGC AGGGTTGCGT
101	TCGTCAAACG ATTCGGATAC CAAGCCGCTG TCGCGGTCGA GACCGAGGGT
151	CAGTTGGGTC ATGTCGTTCG AGCCGATGGA GAAGCCGTCG AAGTATTGCA
201	GGAATTGTTC CGCCAATACC GCGTTGCTCG GCAGCTCGCA CATCATAATC
251	AGGCGCAGGC CGTTTTTGCC GCGTTCCAAG CCGTTTTCTT TCAGGGCTTT
301	GACAACGGCT TCGGCTTCGC CCAAAGTGCG GACGAACGGA ATCATGATTT
351	CAACGTTGGT CAACCCCAT T CATCGCGGA CGCGTTTCAA GGCTTTGCAT
401	TCCAAGGCGA AACAGTCTTT GAAGTTGTCG GCGACATAAC GCGCCGCACC
451	ACGGAAGCCC AACATCGGGT TTTCTTCATG CGGTTCTGAT ACGTTGCCGC
501	CGACCAGGTT GGCGTATTCG TTGGATTTGA AGTCGGACAT ACGGACGATG
551	GTTTTACGCG GATAAACCGA TGCGGCCAAT GTCGCCACGC CTTGCGCGAT
601	TTTATCGACG TAGAAGTCGA CAGGGGACGC GTAACCGGCG ATACGGCGGG
651	TAATTTCCGC TTTTAATTCG TCGTCTTGTT TGTCAAATTC CAACAAGGCT
701	TTGGGGTGGA TACCGATTTG GCGGTTGATG ATAAATTCCA TACGCGCCAA
751	GCCGATGCCT TCGCTGGGCA GGTGGCGGAA GCTGAATGCG AGTTCGGGAT
801	TGCCGACGTT CATCATGACT TTTACAGGTG CTTTAGGCAT GTTGTCCAAA
851	GCAACATCGG TAATTGTAC GTCCAGCAGG CCGGAGTAGA TGAAGCCGGT
901	ATCGCCTTCG GCACAGGATA CGGTAAC TTCGACGTTT TTCAGCAATT
951	CGGTTGCATT GCCGCAGCCG ACAACGGCAG GAATACCCAG TTCGCGCGCG

a501.pcp

1	MVGRALTADA	DIFVLLAAGG	DGKVQHFFDG	RVAFVKRFGY	QAAVAVETEG
51	QLGHVVVRADG	EAVEVLQELF	RQYRVARQLA	HHNQAQAVFA	AFQAVFFQGF
101	DNGFGFAQSA	DERNHDFNVG	QPHFIADAFQ	GFAFQGETVF	EVVGDITRRT
151	TEAQHRVFFM	RFVYVAADQV	GVFVGFEVHG	TDDGFTTRINR	CGQCRHAFGD
201	FIDVEVDVRG	VTGDTAGNER	F*FVVLFEVKF	VQGVGDVTDL	AVDDKFHTRQ
251	ADAFAGQVGE	AECEFGIADV	HHDFYRCFRH	VVQSNIGNLY	VQQAGVDEAG
301	IAFGTGYGNF	LTVFQQFGCI	AAADNGRNTQ	FARDDGGVAG	TSAPVGHGDD
351	SAFHHRFPIW	VGHVGNQYVA	GFDGIHLGSI	FNQAYLALTD	FLTDGAAFAQ
401	DGFFAVDRKA	AQVAAAFFLG	FDGFGTGLQD	VEFAVQAVAS	PFDVHRAAVV
451	FFDGQCVMRQ	LGDDFFVGNGE	AVAVFFGDID	VGYRFAGFCF	VGKNHFDVF*
501	AHGFAQVDGRF	ACFQRGFEHI	EFVGIDCALY	DVFAQTVG*S	DKDDLVTGTG
551	GIEGEHH				

[illegible]

735

	370	380	390	400	410	420
m501.pep	IGHVGN EYVAGFDGIHLGSI FNQAH LALTDFLT DGAAFA XYGFVA VDGEAAQVAVALFLG					
a501	VGHVGNQYVAGFDGIHLGSI FNQAYLALTDFLT DGAAFAQDGF FAVDRKAAQVAAFFLG					
	370	380	390	400	410	420
m501.pep	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGGCVMRQLSNFFVGNGEAVAVFLGDID					
a501	FDGFGTGLQDVEFAVQAVASPFDVHRAAVVFFDGGCVMRQLGDFVGNGEAVAVFFGDID					
	430	440	450	460	470	480
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGLARFERGFEHXXKFVRVDRTLYDVFAQTVRGG					
a501	VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRGFEHIEFVGIDCALYDVFAQTVGXS					
	490	500	510	520	530	540
m501.pep	NKDDLIVXGFGVEGEHHTX					
a501	DKDDLVTGFGIEGEHH					
	550	559				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

```

g502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcccgttt gtcacctgac
51  cgtcgccgtc gcttccgcac aggcgggcgc ggtggacgcg ctcaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca aaccgtccaa
151 agcaaaaaga aaaccctaac cgcgacggc acgttcaaaa tctgcccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 gcgacggtca aaccgtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcgcgggc agccccgcgc ccattcctgc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg cccaaacgca acaacgccgc
451 ctaccaatac atccgcacgc gttcaaagg cggcaacctc gccgccatgc
501 agcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

```

g502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51  SKKKQTQAHG TFKILRPGLF KWEYTLPLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RGNAQTQQR
151 LPIHPHRLQR QPRRHAAX*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

```

m502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcccgttt gtcacctgac
51  cgtcgccgtc gcttccgcac aggcgggcgc ggttagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca amccgtccaa
151 wgcaaaaaga aaaccctaac cgcgacggc acgttcaaaa tctgcccc
201 gggccttttc aaatgggaat acaccaaact t.acaggcaa accatcgctc
251 gcgacggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgcgc ccattcctgc
351 gaacaaarcc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgcccgtc
451 ccaatacatc cgcacgcgct tcaaaggcgc caacctcgcc gccatgcagc
501 tyaa

```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

```

m502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51  XXXKTQAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGX SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQQRRL
151 PIHPHRLQR QPRRHAAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502 . pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 . pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 . pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502 . seq

1	ATGATGAAAC	CGCACAACT	GTTCCAATTC	CTCGCCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTCG
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTTGGC	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCGC	CCATCCTGTC
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502 . pep

1	MMKPHNLFQF	LAVCSLTVSV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKTQTAHG	TFKILRPGLF	KWEYTSPLYK	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQQRRL
151	PIHPHRLQRR	QPRRHAA*			

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502 . pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 . pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSPLYKQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 . pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```

1  ATGatGAAAc  cgcaCaacct  gttccaaTtC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCGGTC  GCTTCCGCAC  AGGCGGGCGC  GGTGGACGCG  CTCAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGCCC
201 GGGCCTCTTC  AAATGGGAAT  ACACTTTGCC  CTACAGACAG  ACTATTGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATTTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATCGGCGGC  AGCCCCGCCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGTTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CGGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GGCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAA
601 GCGGTGGACG  TGTTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```

1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTQVQ
51  SKKKTQTAHG  TFKILRPGLF  KWEYTLPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIGG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  RATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTPQLS  RGAFTFTPPK
201 GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```

1  ATGATGAAAC  CGCACAACTT  GTTCCAATTC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCGGTC  GCTTCCGCAC  AGGCGGGCGC  GGTAGACGCG  CTTAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGACC
201 GGGCCTTTTC  AAATGGGAAT  ACACCAAACC  TTACAGGCAA  ACCATCGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATCTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATAGGCGGC  AGCCCCGCCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGCTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CTGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GGCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAA
601 GCGGTGGACG  TGTTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```

1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTQVQ
51  SKKKTQTAHG  TFKILRPGLF  KWEYTKPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIGG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  LATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTPQLS  RGAFTFTPPK
201 GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG					
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG					
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTLTPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTLTPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF					
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF					
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNGIDYVLRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF					
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF					
	130	140	150	160	170	180


```

                190      200
m502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||
g502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCTG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GGCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51 SKKKTQTAHG TFKILRPLGF KWEYTSPYKQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFFKFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep    MMKPHNLFQFLAVCSLTVSVASAQAGAVDAL KQFNNDADGISGSFTQTQVQSKKKTQTAHG
                |||
m502-1        MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL KQFNNDADGISGSFTQTQVQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep    TFKILRPLGFKWEYTSPYKQTIVGDGQTVWLYD VDLAQVTKSSQDQAIGGSPAAILSNKT
                |||
m502-1        TFKILRPLGFKWEYTKPYRQTIVGDGQTVWLYD VDLAQVTKSSQDQAIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep    ALESSYTLKE DGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                |||
m502-1        ALESSYTLKE DGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                130     140     150     160     170     180

                190     200
a502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||
m502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgtcggcatc ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaaggcggt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaatgcg ttcgttcaga ccgttggtg cgagaaatgc
201 gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSTSNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

```

m503.seq
  1  atgtccgcac cgccggcatc ggcaaccatt ttgttccatg ccgcttcgat
 51  ttccggcatcg agctgttcgg ggaaaggcgt atccaaaatc cattggcgga
101  tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt
151  gccagtgcgg cggaaatgcg ttcgctcaga ccgttggtgtg cgaggaatgc
201  gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

```

m503.pep
  1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
 51  ASAAEMRSLR PLCARNAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

```

m503/g503
      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          ||| ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g503      MSAPSASVILFHAASISASSCSGKGVSKIHWRIPLTRASSETSTSNFARAAEMRSLR
          10      20      30      40      50      60

      69
m503.pep  PLCARNAR
          |||||
g503      PLCARNAR

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

```

a503.seq
  1  ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCATG CCGCTTCGAT
 51  TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA
101  TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT
151  GCCAGTGC GGAAATGCG TTCGCTCAGA CCCTTGTGTG CGAGGAATGC
201  GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

```

a503.pep
  1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
 51  ASAAEMRSLR PLCARNAR*

```

m503/a503 100.0% identity in 68 aa overlap

```

      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a503      MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          10      20      30      40      50      60

      69
m503.pep  PLCARNARX
          |||||
a503      PLCARNARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

```

g503-1.seq
  1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAA ACGTGCGCA TCGCTTTTTT
 51  AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA
101  ATGATGCGTC GGGCAGGTCT TCGGCGGTG CGGAAGAGCG TACGGCAACG
151  GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTTGTTC ATGCCGCTTC
201  GATTTCGGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC
251  GGATTTCTTT GCCGACGCGT GCCAGTTCGG AAACGTCTTC GACATCCAAT
301  TTGCGCAGAG CGGCGGAAAT GCGTTCGTT AGACCGTTGT GTGCGAGAAA
351  TCGCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

g503-1.pep

```

1  MARSLYREAK TWRIAFITLS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51  EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSETSSTSN
101 FARAAMRSL RPLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

m503-1.seq

```

1  ATGGCACGGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
51  AACGTTATCC AAGCCGTTGA TGTTCAGAA GGTTTCCTGT TGTCCAGCGA
101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG
151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTGCGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
251 GGATTCTTTT GCCGACGCGT GCCAGTTCGG CAACGCTTTC GACATCCAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

m503-1.pep

```

1  MARSLYREAN TWCIALTSL KPLMFKKVSC CPANDASGRS SAVAEERTAT
51  EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRIAFITLSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPSASVI					
m503-1	MARSLYREANTWCIALTSLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSETSSTSNFARAAMRSLRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

a503-1.seq

```

1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
51  AACGTTTTC AAGCCGTTGA TATTCAGAA GGTTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTGCGCA TCGAGCTGTT CGGGGAAAGG CGTGTCCAAA ATCCATTGGC
251 GGATTCTTTT GCCGACGCGT GCCAGTTCGG CAACGCTTTC GACATCTAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1.pep

```

1  MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51  EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPPASAT					
m503-1	MARSLYREANTWCIALTSLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

g504.seq

```

1   atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacggt catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgtaa
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgccggaatc cgtactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccacgtgta ccgcacccgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattatTTTT
551 ggctgaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgctgta
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccggtt cgcggggtgc gcttttggtc tatctcggct cggtattgtt
1101 ggttttgggt acagtattta tgttttatgt gcccaaaaaa cgggctgggg
1151 tattgttttc aaacdgc aaa atccgttttg ctatgtcttc ggccgcgagc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

g504.pep

```

1   MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFAWNLR DASREPVVLK ATSIHQFPLE
101 IGKHKYLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQDDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQDQ EARNRFLLS MDAYTGLTEY PAPMLQLLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPKK RAWVLFSNKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

m504.seq..

```

1   atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacggt catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgtaa
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgccgcgcgc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccggtttt gcaggaaacag gattatTTTT
551 ggattaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgctgta
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttctt
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgtc gggtttgag

```

```

1051 atgacccggt ccccggggtgc gcttttgggtc tatctcggtc cgggtgctggt
1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgacgc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
1251 gctcggcaag gacttgaatc atga

```

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

```

m504 . pep . .
  1  ILVQDLPEFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
  51  HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVLK ATSIHQFPLE
 101  IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
 151  IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
 201  IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
 251  TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
 301  RYGLPEWQQD EARNRFLLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
 351  MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWLFS DGK IRFAMSSARS
 401  ERDLQKEFPK HVESLQRLGK DLNHD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

```

m504 / g504

      10      20      30      40      50      60
m504 . pep  ILVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERIRVNHPLTLHGITI
: |||||
g504        MLVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERIRVNHPLTLHGITI
      10      20      30      40      50      60

      70      80      90     100     110     120
m504 . pep  YQASFADGGSDLTFKAWNLDASREPVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
: |||||
g504        YQASFADGGSDLTFKAWNLRDASREPVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
      70      80      90     100     110     120

     130     140     150     160     170     180
m504 . pep  MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKKNYMLPVLQEQ
: |||||
g504        MSEGAREKSLKSTLNDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKKNYMLPILQDK
     130     140     150     160     170     180

     190     200     210     220     230     240
m504 . pep  DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
: |||||
g504        DYFWLTGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKDAPAEI
     190     200     210     220     230     240

     250     260     270     280     290     300
m504 . pep  REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
: |||||
g504        REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKGQQDKMQGYFYEMLYGVMNAALDETIR
     250     260     270     280     290     300

     310     320     330     340     350     360
m504 . pep  RYGLPEWQQDEARNRFLLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV
: |||||
g504        RYGLPEWQQDEARNRFLLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV
     310     320     330     340     350     360

     370     380     390     400     410     420
m504 . pep  YLGSVLLVLGTVLMFYVREKRAWLFS DGK IRFAMSSARSERDLQKEFPKHVESLQRLGK
: |||||

```

743

g504 YLGSVLLVLGTVFMFYVPKKRAWVLSN - KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504 . pep DLNHD
 |||||
 g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504 . seq

1	ATATTGGTTC	AGGACTTGCC	TTTTGAAGTC	AAACTGAAAA	AATTCCATAT
51	CGATTTTTTAC	AATACGGGTA	TGCCGCGCGA	TTTTGCCAGT	GATATTGAAG
101	TAACGGATAA	GGCAACCGGT	GAGAACTCG	AGCGCACCAT	CCGCGTGAAC
151	CATCCTTTGA	CCTTGCACGG	CATCACGATT	TATCAGGCGA	GTTTTGCCGA
201	CGGCGGTTCG	GATTTGACAT	TCAAGGCGTG	GAATTGGGT	GATGCTTCGC
251	GCGAGCCTGT	CGTGTGAAG	GCAACATCCA	TACACCAGTT	TCCGTTGGAA
301	ATTGGCAAAC	ACAAATATCG	TCTTGAGTTC	GATCAGTTTA	CTTCTATGAA
351	TGTGGAGGAC	ATGAGCGAGG	GCGCGGAACG	GGAAAAAGC	CTGAAATCCA
401	CGCTGAACGA	TGTCCGCGCC	GTTACTCAGG	AAGGTAAAAA	ATACACCAAT
451	ATCGGCCCTT	CCATTGTTTA	CCGTATCCGT	GATGCGGCAG	GGCAGGCGGT
501	CGAATATAAA	AACTATATGC	TGCCGGTTTT	GCAGGAACAG	GATTATTTTT
551	GGATTACCGG	CACGCGCAGC	GGCTTGCAGC	AGCAATACCG	CTGGCTGCGT
601	ATCCCTTGG	ACAAGCAGTT	GAAAGCGGAC	ACCTTTATGG	CATTGCGTGA
651	GTTTTTGAAA	GATGGGGAAG	GGCGCAAACG	TCTGGTTGCC	GACGCAACCA
701	AAGGCGCACC	TGCCGAAATC	CGCGAACAAT	TCATGCTGGC	TGCGGAAAAC
751	ACGTGAACA	TCTTTGCACA	AAAAGGCTAT	TTGGGATTGG	ACGAATTTAT
801	TACGTCCAAT	ATCCCGAAAAG	AGCAGCAGGA	TAAGATGCAG	GGCTATTTCT
851	ACGAAATGCT	TTACGGCGTG	ATGAACGCTG	CTTTGGATGA	AACCATACGC
901	CGGTACGGCT	TGCCCGAATG	GCAGCAGGAT	GAAGCGCGGA	ATCGTTTCCT
951	GCTGCACAGT	ATGGATGCGT	ACACGGGTTT	GACCGAATAT	CCCGCGCCTA
1001	TGCTGCTGCA	ACTTGATGGG	TTTTCCGAGG	TGCGTTCGTC	GGGTTTGCAG
1051	ATGACCCGTT	CCCCGGGTGC	GCTTTTGGTC	TATCTCGGCT	CGGTGCTGTT
1101	GGTATTGGGT	ACGTATTGA	TGTTTTATGT	GCGCGAAAAA	CGGGCGTGGG
1151	TATTGTTTTT	AGACGCAAA	ATCCGTTTGT	CCATGTCTTC	GGCCCGCAGC
1201	GAACGGGATT	TGCAGAAGGA	ATTTCCAAAA	CACGTCGAGA	GTCTGCAACG
1251	GCTCGGCAAG	GACTGAATC	ATGACTGA		

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504 . pep

1	ILVQDLPFEV	KLKKFHIDFY	NTGMPRDFAS	DIEVTDKATG	EKLERTIRVN
51	HPLTLHGITI	YQASFADGGS	DLTFKAWNLG	DASREPVVLK	ATSIHQFPLE
101	IGKHKYRLEF	DQFTSMNVED	MSEGAEREKS	LKSTLNDVRA	VTQEGKKYTN
151	IGPSIVYRIR	DAAGQAVEYK	NYMLPVLQEQ	DYFWITGTRS	GLQQQYRWLR
201	IPLDKQLKAD	TFMALREFLK	DGEGRKRLVA	DATKGAPAEI	REQFMLAAEN
251	TLNIFAQKGY	LGLDEFITSN	IPKEQQDKMQ	GYFYEMLYGV	MNAALDETIR
301	RYGLPEWQQD	EARNRFLLS	MDAYTGLTEY	PAPMLLQLDG	FSEVRSSGLQ
351	MTRSPGALLV	YLGSVLLVLG	TVLMFYVREK	RAWVLFSDGK	IRFAMSSARS
401	ERDLQKEFPK	HVESLQRLGK	DLNHD*		

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504 . pep	ILVQDLPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLE	IRVNHP	TLHGITI			
a504	ILVQDLPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLE	IRVNHP	TLHGITI			
	10	20	30	40	50	60
m504 . pep	YQASFADGGS	DLTFKAWN	LG	DASREPVVLK	ATSIHQFPLE	IGKHKYRLEFDQFTSMNVED
a504	YQASFADGGS	DLTFKAWN	LG	DASREPVVLK	ATSIHQFPLE	IGKHKYRLEFDQFTSMNVED
	70	80	90	100	110	120
m504 . pep	YQASFADGGS	DLTFKAWN	LG	DASREPVVLK	ATSIHQFPLE	IGKHKYRLEFDQFTSMNVED
a504	YQASFADGGS	DLTFKAWN	LG	DASREPVVLK	ATSIHQFPLE	IGKHKYRLEFDQFTSMNVED
	70	80	90	100	110	120
m504 . pep	MSEGAEREK	SLKSTL	XDVRA	VTQEGKKYTN	IGPSIVYRIR	DAAGQAVEYK
a504	MSEGAEREK	SLKSTL	XDVRA	VTQEGKKYTN	IGPSIVYRIR	DAAGQAVEYK
	130	140	150	160	170	180
m504 . pep	MSEGAEREK	SLKSTL	XDVRA	VTQEGKKYTN	IGPSIVYRIR	DAAGQAVEYK
a504	MSEGAEREK	SLKSTL	XDVRA	VTQEGKKYTN	IGPSIVYRIR	DAAGQAVEYK

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

1	atgtttcggt	tacaattcag	gctgtttccc	cctttgcgaa	ccgccatgca
51	catcctgttg	accgccctgc	tcaaatacct	ctccctgctg	tcgctttcct
101	gtctgcacac	gctgggaaac	cggctcggac	atctggcggt	ttacctttta
151	aaggaagacc	gcgcgcgcgt	cgtcgccaat	atgcggcagg	cgggtttgaa
201	ccccgacacg	cacagcggtca	aagccgtttt	tgcggaaacg	gcaaaatgcg
251	gtttggaact	tgcccccgcg	tttttcaaaa	aaccggaaga	catcgaaaca
301	atgttcaaag	cgggtacacgg	ctgggaacac	gtgcagcagg	ctttggacaa
351	gggcgaaggg	ctgctgttca	tcacgcgcga	catcggcagc	tacgatttgg
401	gcggacgcta	catcagccag	cagcttcctg	tcaacctgac	cgccatgtac
451	aagccgccga	aaatcaaagc	gatagacaaa	atcatcagg	cgggcagggt
501	gcgcgcgcaa	ggcaaaaacc	cgccccacgg	catacagagg	gtcaaacagg
551	tcatacaagg	cctgcgcgcg	ggcagggcaa	ccatcatcct	gcccgaccac
601	gtccctttct	cgcagggaag	cggcggcggt	tgggcggatt	ttttcggcaa
651	acctgcatac	accatgacac	tggcggcaaa	attggcacac	gtcaaaggcg
701	tgaaaaccct	gtttttctgc	tgcaaacgcc	tgcccgacgg	acaaggcttc
751	gtgttgccca	tccgcccctg	ccaaggggaa	ttgaacggca	acaaaggcca
801	cgatcgccgc	gtgttcaacc	gcaataccga	atattggata	cgccgttttc
851	cgaacgaqta	tctqtttatg	tacaaccgct	ataaaacgcc	gtaa

g505 . pep

1	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	SLSLCLHTLGN	RLGLHAFYLL
51	KEDRARIVAN	MRQAGLNPD	QTVKAVFAET	AKCGLLELAPA	FFKKPEDIET
101	MFKAVHGEH	VQQALDKGEG	LLFITPHIGS	YDLGGYISQ	QLPFLTAMY
151	KPPKIKAIDK	IMQAGRVGRK	GKTAPTGIQG	VKQIIKALRA	GEATIIIPDG
201	VPSPKQEGGV	WADFFGKPAY	TMTLAAKLH	VKGVKTLFFC	CERLPDQGGF
251	VLHIRPQVGE	LNGNKAHDA	VFNRRNTYWI	RRFPTOYLFM	YNRKYTP*

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1369>:

m505.seq (partial)

```

1  GGCATGTTTC GTTTACAATT CAGGCTGTTT CCCCTTTGTC GAACCGCCAT
51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTTGCGGAA ACGGCAAAAG
251 GCGGTTTGGA ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
351 CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTCGCGGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCCACC
601 ACGTCCCCTC CCCTCAAGAA GCGGGGGAAG GCGTATGGGT GGATTCTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAAATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GGCGGACAAG
751 GTTTCGATTT GCACATCCGC CCCGTCCAAG GGGAAATGAA CGGCGACAAA
801 GCCCATGATG CCGCGTGTG CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTTCCGACG CATATC...
```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGHlafYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI DKIMQAGRVRGK GKTAPTS IQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGG EG VVWDFFGKPA YTMTLAAXLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQ G ELNGDKAHDA AVFNRNAEYW IRRFPHTI...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHlafYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLSLSCLHTLGNRLGHlafYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPFAFFRKPEDIETMFKAVHGW EHVQQALDKHEG					
g505	MRQAGLNPDQTVKAVFAETAKGGLLELAPFAFFKKPEDIETMFKAVHGW EHVQQALDKGEG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI DKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFHLTAMYKPPKIKAI DKIMQAGRVRGKGKTAPTGIQG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWDFFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRAGEATIILPDHVPSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKGVKTLFF					
	190	200	210	220	230	
	250	260	270	280	289	
m505.pep	CCERLPGGQGF DLHIRPVQGE LNNGDKAHDA AVFNRNAEYWIRRFPTHI					
g505	CCERLPDGGGFV LHIRPVQGE LNNGKAHDA AVFNNT EYWRFFPTQYLFMYNRYKTP					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

a505.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCCACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAGGCG
251 GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGBAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGCG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATAACAAGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTTC GGCGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGCG ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

a505.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGHLAFYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLELAPA FFRKPEDIET
101 MFKAVHGWHEH VQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGVRGK GKAPTISIQQ VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHD AAVFNRAEYW IRRFPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIMFKAVHGWHEHVQQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIMFKAVHGWHEHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIMFKAVHGWHEHVQQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIMFKAVHGWHEHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGVRGKGKAPTISIQQ					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGVRGKGKAPTISIQQ					
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGVRGKGKAPTISIQQ					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGVRGKGKAPTISIQQ					
	130	140	150	160	170	180
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYMTLAAXLAHVKGVKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYMTLAAXLAHVKGVKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	240
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTHI					
a505	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

m505-1.seq

```

1  ATGTTTCGTT  TACAATTCAG  GCTGTTTCCC  CCTTTGCGAA  CCGCCATGCA
51  CATCCTGTTG  ACCGCCCTGC  TCAAATGCCT  CTCCCTGCTG  CCGCTTTCCT
101 GTCTGCACAC  GCTGGGAAAC  CGGCTCGGAC  ATCTGGCGTT  TTACCTTTTA
151 AAGGAAGACC  GCGCGCGCAT  CGTCGCCAAT  ATGCGGCAGG  CGGGTTTGAA
201 CCGCGACCCC  AAAACGGTCA  AAGCCGTTT  TGCAGAAACG  GCAAAAGGCG
251 GTTTGGAAct  TGCCCCCGCG  TTTTTCAGAA  AACCAGGAAG  CATAGAAACA
301 ATGTTCAAAG  CGGTACACGG  CTGGGAACAT  GTGCAGCAGG  CTTTGACAA
351 ACACGAAGGG  CTGCTATTCA  TCACGCCGCA  CATCGGCAGC  TACGATTGG
401 GCGGACGCTA  CATCAGCCAG  CAGCTTCCGT  TCCCGCTGAC  CGCCATGTAC
451 AAACCGCCGA  AAATCAAAGC  GATAGACAAA  ATCATGCAGG  CGGGCAGGGT
501 TCGCGCAAAA  GGA AAAACCG  CGCTACCAG  CATACAAGGG  GTCAAACAAA
551 TCATCAAAGC  CCTGCGTTCG  GGCGAAGCAA  CCATCGTCCT  GCCCGACCAC
601 GTCCCTCCC  CTCAAGAAAG  CGGGGAAGGC  GTATGGGTGG  ATTTCTTCGG
651 CAAACCTGCC  TATACCATGA  CGCTGGCGGC  AAAATTGGCA  CACGTCAAAG
701 GCGTGA AAAC  CCTGTTTTTC  TGCTGCGAAC  GCCTGCCTGG  CGGACAAGGT
751 TTCGATTGTC  ACATCCGCC  CGTCCAAGGG  GAATTGAACG  GCGACAAAGC
801 CCATGATGCC  GCCGTGTTCA  ACCGCAATGC  CGAATATTGG  ATACGCCGTT
851 TTCCGACGCA  GTATCTGTTT  ATGTACAACC  GCTACAAAAT  GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP  PLRTAMHILL  TALLKCLSL  LPLSCLHTL  GNRLGHLAF  YLLKEDRARI  VAN
51  KEDRARIVAN  MRQAGLNPD  P  KTVKAVFAE  T  AKGGLELAP  A  FFRKPEDIE  T
101 MFKAVHGEH  V  VQALDKHE  G  LLFITPHIG  S  YDLGGYIS  Q  QLPFPLTAM  Y
151 KPPKIKAI  D  IMQAGRV  R  GK  TAPT  SI  Q  VKQIIKAL  R  S  GEATIVLP  D  H
201 VPSPQEG  G  EV  VVDFFG  K  PA  Y  TMTLAA  K  LA  HVKGVK  T  LFF  CCERLPG  G  QG
251 FDLHIRPV  Q  G  ELNGDKA  H  DA  AVFN  RNAE  Y  W  IRRFPT  Q  YL  F  MYNRY  K  MP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLLSLCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKGGLELAPAFFKKPEDIETMFKAVHGEHVQALDKGEG					
	70	80	90	100	110	120
m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKGGLELAPAFFKKPEDIETMFKAVHGEHVQALDKGEG					
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTGIQ					
g505	LLFITPHIGSYDLGGYISQQLPFHLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTGIQ					
	130	140	150	160	170	180
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTGIQ					
g505	LLFITPHIGSYDLGGYISQQLPFHLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTGIQ					
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRSGEATIVLPDHPVSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGKTLFF					
g505	VKQIIKALRAGEATIILPDHPVSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKGKTLFF					
	190	200	210	220	230	
m505-1.pep	VKQIIKALRSGEATIVLPDHPVSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGKTLFF					
g505	VKQIIKALRAGEATIILPDHPVSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKGKTLFF					
	190	200	210	220	230	
m505-1.pep	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX					
g505	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNNTYEWIRRFPTQYLFMYNRYKTPX					
	240	250	260	270	280	290
m505-1.pep	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX					
g505	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNNTYEWIRRFPTQYLFMYNRYKTPX					
	240	250	260	270	280	290

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m50						

m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMPKAVHGWHEHVQQALDKHEG
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMPKAVHGWHEHVQQALDKHEG
	70 80 90 100 110 120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKDQIMQAGRVRGKGTAPTTSIQG
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKDQIMQAGRVRGKGTAPTTSIQG
	130 140 150 160 170 180
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
	190 200 210 220 230 240
m505-1.pep	CCERLPGGQGFDLHIRPVQGEINQDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX
a505	CCERLPGGQGFDLHIRPVQGEINQDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX
	250 260 270 280 290 299

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

g506.seq

```

1  ATGGCGGTAT  TTGATGAAGT  CGGGCGCATC  GCCCATGGCT  GCGGCGGTGT
51  TGTCAAACAA  AGCCTGTTTC  TGC CGTCGT  TCATCAGGTT  GAACAAGGCG
101 CGCGGTGGC  TGAAGTAGTC  GTCATCGTCT  TGGCGGTAGT  CCCAGTGTGC
151 CGCGTCGCCG  TTGATTTTCA  AAGGCGGTTT  GCGAAGTCG  GGTGTTGTGCT
201 GCCATTGGCC  GAAGCTGTTG  GGTTCGTAGT  GCGGCAGGCT  GCCGTAGTTG
251 CCGTCGCGCG  GGCCTTGTC  GTCGCGCTGG  TTGCTGTGAA  CAGGGCAACG
301 CGGACGATTG  ACGGGGATTT  GCGGGAAGTT  CACACCCAAG  CGGTAACGTT
351 GCGCGTCGGC  GTAATTGAAC  AAACGGGCTT  GCAACATTTT  ATCCGGGCTC
401 GCGCCGATAC  CGGGAACGAG  GTTGCTCGGT  GCGAAGGCGG  ATTGTTCCAC
451 ATCGGCGAAG  AAGTTTTTCG  GATTGCGGTT  CAACTCGAAT  TCGCCCACTT
501 CAATCAGCGG  ATAGTCTTTT  TTCGGCCAAA  CTTTGGTCAA  GTCAAACGGA
551 TGATAAGGCA  CTTTTTCGCG  ATCGGCTTCA  GGCATGACTT  GGATGTACAT
601 CGTCCATTTC  GGGAACTCGC  CGCGCTCGAT  GGCTTCGTAC  AGGTGCGGCT
651 GATGGCTTTC  GCGGTCGTCG  GCGATGATTT  TTGCAGCTTC  TTCGTTGGTC
701 AGGTTTTTAA  TCCCTTGCTG  GCTGCGGAAA  TGGAATTTCA  CCCAAAACG
751 TTCGCCCGCT  TCGTTCCAGA  AGCTGTAGGT  ATGCGAACCG  AAGCCGTGCA
801 TATGGCGGTA  GCTGGCGGGA  ATACCGCGGT  CGCTCATCAC  GATGGTAACT
851 TGGTGCAAGG  CTTGCGGCAG  CAGCGTCCAG  AAGTCCAGT  TGTGTTGGC
901 GGAACGCATA  TTGGTGCGCG  GATCGCGTTT  GACGGCTTTG  TTCAGGTCGG
951 GGAATTTGCG  CGGGTCGCGC  AGGAAGAACA  CGGGCGTGTT  GTTGCCGACC
1001 ACATCCCAGT  TGCCTTCTTC  GGTATAGAAT  TTCAACGCAA  AACCGCGGAT
1051 GTCGCGTTCC  GCATCGGCTG  CGCCGCGCTC  GCCTGCCACG  GTGGTGAAAC
1101 GGGCGAACAT  CTCGGTTTTT  TTGCCGACTT  CGCTGAAAAT  TTTGGCGCGG
1151 GTGTATTGCG  TGATGTCGTG  TGTACGGTA  AACGTACCGA  ACGCGCCGA
1201 ACCTTTGGCG  TGCATACGCG  GTTCGGGGAT  GACTTCGCGC  ACGAAGTCGG
1251 CGAGTTTTTC  ATTCAGCCAC  AAATCTTGCG  TCAGCAGGGG  GCCGCGCGG
1301 CCGGCGGTCA  GGCTGTTTTG  ATTGTCGGCA  ACGGGCGCGC  CGTTGTTTCA
1351 GGTCAGATGG  GTTACGGGGC  ATTTGGAGGT  AGTCATCGCT  CTTGTTCTT
1401 TTCTCAGGTT  GGTCAAATGG  GGGGCAAACG  GCTTACAGTA  CGATTTGGCG
1451 GAAAGCGTAT  TCGTAACCGG  TTTCTTGATT  GTAATAAATT  TCTTGAATCG
1501 ACATTTTATT  TTCCTTTTGC  AAAAATATG  GATGCGATTA  TACGCCAAGA
1551 TTTTCGTTAT  TAA

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This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

g506.pep

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1  MAVFDEVGRI  AHGCGGVVKQ  SLFLRVVHGV  EQGARLAEV  VIVLAVVPVC
51  RYAVDFQRRF  GEVGLLLPLA  EAVGFVVRQA  AVVAVGAALS  VALVAVNRAT
101 RTIDGLAEV  HTQAVTLRVG  VIEQTGLQHF  IRARADTGNE  VARCEGGLFH
151 IGEFVGIAV  QLEFAHFNR  IVFFRPNFGQ  VKRMIRHFFG  IGRHDLVDV

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201 RPFRELAALD GFVQVALMAF AVVGDDFCSF FVGQVFNPLL AAEMEFHPKT
 251 FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFQ QRPEVPVVC
 301 GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQKRTAD
 351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGQAVL IVGNGRAVVH
 451 GQMGYGAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFPFAKTM DAIIRQDFRY *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

1 ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
 51 TGCCGAACAA TGCTGTTC TGCGCGTCGT TCATCAGGTT GAACAGGGCG
 101 CGCGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
 151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GCGCAATCG GGTGTGTGCT
 201 GCCATTGGCC GAAGCTGTyG GGTTCGTAGT GCGGCAGGCT GCCGyAGTTG
 251 CCGTCGGCGC GGCCTTGCCC GTyGCGsTgr TTgCTGTgAA CAsGGCAACG
 301 CGGACGATTG ACGGGAATTT GCGGGAAGTT TACGCCCCAA CGGTAGCGTT
 351 GTGCGTCGGC GTAATTGAAC AAACGCGCTT GCAGCATTTT ATCTsGGCTG
 401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
 451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CTCAAACGGA TGATAAGGTA
 501 CTTTTTCGCG GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTT
 551 GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC
 601 GCGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC AGGTTTTTAA
 651 TGCCTTGTTG GGTGCGGAAA TGGAATTCA CCCAAAAACG CTCGCCTGCT
 701 TCGTTCGAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA
 751 GCCGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT TGGTGCAGTG
 801 CTTCCGGCAG CAGCGTCCAG AAGTCCCAGT TGTTTGTGGC AGAGCGCATA
 851 TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG GGAACTTACG
 901 CGGGTCGCGC AGGAAGAACA CGGGCGGTGT GTTGCCGACC ACATCCCAGT
 951 TGCCTTCTTC GGTATAAAAT TTCAAGGCAA AACCCGGAT GTCGCGTTCT
 1001 GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT
 1051 CTCGTTTTTT TTGCCGACTT CGCTGAAGAT TCCTTTGGCG TGCATACGGC
 1101 GTTCGGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTTC AGTCATCGCT
 1151 CTTGTTCTTT TTCTCAGGTT GGTCAAATGG GGGTAAACGG CTTACAGTAC
 1201 GATTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATTT
 1251 CTTGAATCGA CATTTTATTT CCCTTTTGTA AAAACTATGG ATGCGACTAT
 1301 ACGCCAAGAT TTTGCTATT AA

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

1 MAVFDEVGRV AHCGGVVAEQ CLFLRVVHVQ EQGARLAEIV VIVLAVVPVC
 51 RVAVDQRRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT
 101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTNE VARCEGGLFH
 151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRYFFR VCFRHLDDVH
 201 RPFRLAAFD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT
 251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFQ QRPEVPVVC
 301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQKRTAD
 351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVVH
 451 GQMGYRAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFPFVKTM DATIRQDFRY *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGVVAEQCLFLRVVHVQEQGARLAEIVVIVLAVVPVCRAVDQRRF					
	:: ::					
g506	MAVFDEVGRVIAHCGGVVVKQSLFLRVVHVQEQGARLAEVVIVLAVVPVCRAVDQRRF					
	10	20	30	40	50	60

750

	70	80	90	100	110	120
m506 . pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAADVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506 . pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTGLQHFIRARADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506 . pep	VKRMIRYFFRVCFRHDLDVHRPFRKLAAFDGFXXVALMAFAVVGDDFGGFFVGQVFNALL					
g506	VKRMIRHFFGIGFRHDLDVHRPFRCLAALDGFVQVALMAFAVVGDDFCFFVGQVFNPLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506 . pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
g506	AAEMEFHPKTFARFVPEAVGMRTEAVHMAVAGGNTAVAHHDGNLVQCFGQQRPEVPVVCG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m506 . pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIKFQKGTADVAFCIGCAAF					
g506	GTHIGARIAFDGFVQVGEFARVAQEEHGRVVADHIPVAFFGIEFQRKTADVAFRIGCAAL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506 . pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGETGEHLGFFADFAENFGAGVFGDVVCYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506 . pep	IQPQILRQQRARTGGQAVLIVGNRAVVHGMGYRAFGGSHRSCSFSQVGMGGKRLTV					
g506	IQPQILRQQGAARAGGQAVLIVGNRAVVHGMGYGAFGGSHRSCSFSQVGMGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506 . pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRY					
g506	RFGGKRIRNRFLDCNKFLESTFYFPFAKTMDAIIRQDFRY					
	490	500	510	520		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1379>:

a506 . seq

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1   ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATGCG GCGGCGGTGT
51  TGCCGAACAA TGCTGT TTC TGCGCGTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGCGC
151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTT GCGGAAGTCG GGCTGCTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GTCCTGTCC GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGGTTG ACAGGGATTG GCGGAAGTT CACGCCCAAG CGGTAGCGTT
351 GCGCGTCGGC GTAATTGAAC AAACGCGCCT GCAACATTTT ATCTGGGCTG
401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCAAAA CTTTGTGCAA GTCAAACGGA
551 TGATACGGCA CTTTTCCTGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTT GGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT

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651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTTAA TGCCTTGTG GGTGCGGAAA TGGAAATTTCA CCCAAAAACG
751 CTCGCCTGCT TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGTG CTTGCGGCAG CAGCGTCCAG AAGTCCAGT TGTGTTGGC
901 AGAGCGCATA TTGGTGCAGG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTT GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTACGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTTTAT
1351 GGTCAGATGG GTTACAGGGC ATTTGGAGGT ANTATCGCT CTTGTTCTT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAACG GCTTACAGTA CGATTTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTGAATCG
1501 ACATTTTAT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1  MAVFDEVGRV AHCGGGVAEQ CLFLRVVHVQ EQGARLAEIV VIVLAVVPVR
51  RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNR IVFFRPNFGQ VKRMIRHFFR IGFRLDLVDH
201 RPFRLAALD GFVQVALMAF TVVGDDFFGG FVGQVFNALL GAEMEFHFKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRAVVH
451 GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLS
501 TFYFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

```

              10      20      30      40      50      60
m506.pep      MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF
              |||||
a506           MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQVEQGARLAEIVVIVLAVVPVRRVAVDFQRRF
              10      20      30      40      50      60

              70      80      90      100     110     120
m506.pep      GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG
              || |||||
a506           GEVGLLLPLAEAVGFVVRQAQAVVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG
              70      80      90      100     110     120

              130     140     150     160     170     180
m506.pep      VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNRIVFFRPNFGQ
              |||||
a506           VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNRIVFFRPNFGQ
              130     140     150     160     170     180

              190     200     210     220     230     240
m506.pep      VKRMIRYFFRVCFRHDLVDHVPFRKLAALDGFXXVALMAFAVVGDDFFGGFFVGQVFNALL
              |||||
a506           VKRMIRHFFRIGFRHDLVDHVPFRKLAALDGFVQVALMAFTVVGDDFFGGFFVGQVFNALL
              190     200     210     220     230     240

              250     260     270     280     290     300
m506.pep      GAEMEFHFKTLACFVPEAVGMRTAVHMAVAGGDAVAHHHDGNLVQCFGQQRPEVPVVC
              |||||
a506           GAEMEFHFKTLACFVPEAVGMRTAVHMAVAGGDAVAHHHDGNLVQCFGQQRPEVPVVC
              250     260     270     280     290     300

```

752

	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVDHIPVAFFGKIFQGKTADVAFICGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVDHIPVAFFGIELQRKTADVAFICGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQRAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFQVGMGGKRLTV					
a506	IQPQILRQRAARTGGQAVLIVGNRRRAVVHGMGYRAFGGXHRSCSFQVGMGXGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTCCTCTG CTTCAGACGG
101 CCTTTGCGCT CTCGTGCTT GGCAACGTT TGTTCCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGAATTCCTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAATTCGGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTT CTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC CTGCCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGGTTGGTG CAGGTTTTGC CGGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCGT
501 GTACTGCCTG CTGCTGCGAC TGTTCCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNGLFGMGKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLFFDLQLVF LKLHADLLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCTTC GTCGGGCAGG TTTAAGGCTT GGTTCCTCTG TTTCAGACGA
101 CCTTTGCGCT CTCGTGCTT GGCAATCGTT TGTTCCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTCGGGC
251 AGACGCTCCT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAGCTCGGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTT TTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTAAC TCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGGTTGGTG CAGGTTTTGC TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGCTTGTG CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTLOGG CFLRGGGFGF VGQVXGLVFL FQTTFALFVL GNRLFGMGKL

```

51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLVFG NLHRPFRQLG
101 LFFFDLQLVF FKLHADLLLL LMNALXLRLR CLLVAFDALV QVLLMADLFF
151 OTGNLLAOHA ALVAQFMHCL LLRLFGSLOG VYFVV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng)

from *N. gonorrhoeae*:

m507/q507

		10	20	30	40	50	60
m507.pep		MLLLTLQQGGCFLRGGGFVGQVXGLVFLFQTTFALFVLGNRLF	FGMGKLLLLLQRQFAAD				
		:					
g507		MLLPALQQGGGFLSGGGFGLVGVQGLVFLLLQTAFALFVLGNGLF	GMGKLLLLLQRQFAAD				
		10	20	30	40	50	60
		70	80	90	100	110	120
m507.pep		AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQLGLFFFDL	QLVVF	FKLHADLLLL			
		: : :					
g507		AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFDL	QLVFLKLHADLLLL				
		70	80	90	100	110	120
		130	140	150	160	170	180
m507.pep		LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQ	FMHCLLLRLFGSLQG				
		: : :					
g507		LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVY	CLLLRLFGSLQG				
		130	140	150	160	170	180
m507.pep		VYFVV					
		:					
g507		VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

```
a507.seq
1 ATGCTCTTGC TGGCTTTGCA ACAAGCGCGC AGCTTCCTGC GCGGCGGCGG
51 TTTCGGCTGT GTCAGGCAGA TTCAGGGCTT GGTTTTCCTG TTTCAGACGA
101 CCTTTGCGCT CTTCGTGCTT GGCAACGGTT TGTTCCGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTTGCT
201 GGGTTTGGAA GCGCGGCATT AGTGTGGCTT GGGTTTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAATTCCGT
301 TTGCTTTTCT TCCGCTGCA ACTCGTTTTT TTCAAGTCTG ACGCGGATTT
351 GCTGCTGCTC CTGATGGATG CGCTGCATCT CGCGCTGCGC CGCCTGCTTG
401 TCGCGTTCGA TCGGTTGGTG CAGGTTTTGC TGATGGCGGA TTTGTTCTTC
451 CAAACGGCGA ATCTGTTCGC GCAACACGCC GCGTTTGTTC CCCAATTCTG
501 GCACCGGCTG CTGCTGCGAC TGTTCCGGCAG TCTGAAGGC GTGTACTTCG
551 TCGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep

1	MLLLALQQGG	SFLRGGGGFG	VRQIQGLVFL	FQTTFALFVL	GNGLFMGKGL
51	LLLQRQFAAD	AVCLVLLLGLE	GGIECGLGFF	QFGQTALFVG	NLHRPFRQFG
101	LLFFRLQLVF	EKLHADLLLL	LMDALHLRL	RLLVAFDALV	QVLLMADLFF
151	QTGNLFAQHA	AFVAQFVHRL	LLRLFGSLQG	VYFV*	

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLT	LQQGGCFLRGGGF	GFGVQVXGLV	FLFQTTFALFVLGNRLFGMGK	LLLLLQRQFAAD	
a507	:: :	:: :	:: :	:: :	:: :	:: :
	MLLLAL	QQGGSFLRGGGF	GFGVRQIQGLV	FLFQTTFALFVLGNLFGMGK	LLLLLQRQFAAD	
	10	20	30	40	50	60
	70	80	90	100	110	120


```

m507.pep  AVCLVLLGLEGGVERGLGFFQFGQTLFVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL
a507      AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLLFFRLQLVFFKLHADLLLL
           70          80          90          100         110         120

           130         140         150         160         170         180
m507.pep  LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
a507      LMDALHLRLRLLVAFDALVQVLLMADLFFQTGNLFAQHAAFVAQFVHRLLLRLFGSLQG
           130         140         150         160         170         180

m507.pep  VYFVVX
a507      VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGCAG GGTTTGTACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTTTCCTG
151 CACGGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GGCGATTTGC TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLREFFL
51  HGDVFFVQRV YGFGQLVELD VLLVVLELGF IGEGKLLPAF LPVQGLLFEP
101 GDLLPVVFLF RVEFVDGDFG KPVLA VG FQ GKLR L FQTAL LLLAAVRGGL
151 LLVFEFGGGF LQSSDV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAAAGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGCAG GGTTTGCACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTCTCTTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTTGCT GTTCAAGCTG
301 GGCGATTTGC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAGGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLREFLL
51  HNNIFFVQGL YGFAXFFKLD VLLVVLELGF IGEGKLLAF LPVEGLLFLK
101 GDLLPVVFLF LVEFVDGDFG KPVLA VG FQ GKLR L FQTAL LLLAAVRGGL
151 LLVFEFGGGF LQGNV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

755

	10	20	30	40	50	60
m508.pep	MVAFGVDQGF	LLQGGGLGG	LKLRQLGL	QGLHFSVLL	PALFLNLRE	FLHNNIFFVQGL
g508	MVAFGVDQGL	LLQGGGLGG	LKLRQLGL	QGLYAGVLL	PALFLNLRE	FLHGDVFFVQRV
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLD	VLLVLELGF	IGEGKLLA	FLPVEGLLF	FKLGDLLP	VVLFLLVEFVDGDFG
g508	YGFQQLVELD	VLLVLELGF	IGEGKLLA	FLPVEGLLF	FKLGDLLP	VVLFLLVEFVDGDFG
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQ	QKLRRLFQ	TALLLLAA	VRGGLLLV	FEGGGFLQ	GNNDVV
g508	KPVLAVGFQ	QKLRRLFQ	TALLLLAA	VRGGLLLV	FEGGGFLQ	SSDVV
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```

a508.seq
1   ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTGTCAG GGTTTGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTCTCTCTG
151 TACGACAATA TATTCTTCGT CCAAACCTCG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTGTGT GTTCAAGCTG
301 GGCAATTTGC TGTGTTAGT TTTGTTTGTG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAATG GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```

a508.pep
1   MVAFGVDQGF LLLQGGGLGG GLKLRQLGLQ GLYAGVLFPT LLLNLREFLL
51  YDNIFVQTL YGFAQLFELD VLLVLELGF IGEGKLLAF LPIEGLLFKL
101 GNLLLVVFL LVELVDGDFG KPVLAVGFQK GLRRLFQTTL LLLAAVRGGL
151 LLVFEFGGGF LQNGDVV*

```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508.pep	MVAFGVDQGF	LLQGGGLGG	LKLRQLGL	QGLHFSVLL	PALFLNLRE	FLHNNIFFVQGL
a508	MVAFGVDQGF	LLQGGGLGG	LKLRQLGL	QGLYAGVLF	PFTLLNLRE	FLLYDNIFVQTL
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLD	VLLVLELGF	IGEGKLLA	FLPVEGLLF	FKLGDLLP	VVLFLLVEFVDGDFG
a508	YGFAQLFELD	VLLVLELGF	IGEGKLLA	FLPIEGLL	FKLGNLLV	VVLFLLVVELVDGDFG
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQ	QKLRRLFQ	TALLLLAA	VRGGLLLV	FEGGGFLQ	GNNDVVX
a508	KPVLAVGFQ	QKLRRLFQ	TALLLLAA	VRGGLLLV	FEGGGFLQ	NGDVVX
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509.seq

```

1  atgggtcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgttgtag
101 tcttccaagc ctgctgtgtg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgcaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgctga taagggaacg ttgcaatttt ttcaaatcat cgagaaattt
301 ttgggcccga gcataaggct cgagaaagcc gaatttgacg cccatgcccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgcataat gtaggcaatg
401 gcgcggcggt aagggtcttc ggtgcggcg atttcttcgt caggcgagag
451 ggtgcagct gccattacgt cgtcgttgac ttgacgcgg cggtggaaa
501 gcggcagttc gcggtaaaag ttgtcgagtt cgctgcggta aaaacggaac
551 acggcatcgg cgtggcggcg gaaggcaaa cgcagggttt cggcagaaac
601 aaacggattg ccgtcgcggc cgccgcgat ccagccgcg attttaagga
651 tattcggaac gcggacatcg ggataggccg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
751 cagcccggtt tgatttcgt cgttgacgt gagtttgtg cggcgcgttt
801 cgctggtctg ccacaagccc agaagcacgg tgtcgatttc gcggcgagc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttgcg gcagcagcgc
901 gcggatgcgg cggttgaaat tcaaaacggg ttggcgttgc acttcggtcg
951 ggtgcgcggg caaaacggcg gtaacggacg tattgtccaa ctgccgctgc
1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atcttcgtgg atttggcggc
1101 ggcgctcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgtgtcgtgc ggaagtggac aagagtttga
1251 ccgttttcgac aaccaacggc gaggcttctt cgtcaggag gtgaaacagg
1301 gactgtttca aaaattccgc gtccgccgcc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcattgccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcca aaccgttcac actttaacca
1451 ctcatgtccc gaaatgccgt ctgaagtga acgccgccg acggcggcgt
1501 tacaatcgcc cgcaactgtt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctgcggcg gattgggcgc cggcgcacct gcctatctc
1701 gccgcctcgg gggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1  MVAVCDERAV QRTLVAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAFALRQQR
301 ADAAVEIQNG LALHFGRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLR
451 VQDMLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVPKCR LKLNAAARRR
501 YNRPQLFFSE HHHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFFRAY
551 FGRLRRIGR RRPCPISPPR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1  ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTGTCT CTTCTTCAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGCGGTGTTT
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTCGGAAG CAGACGGCTG
251 CCGTTGTGCA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGCGGTT AGGGTTCTTC GCGCGGGCG ATTCTTCGT CGGCGGATTT
451 GTCGGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGTT CGCCGCGATA GAAGCGGAAC

```

```

551  ACGGCATCGG  CGTGGCGGCG  GAAGGCAAAG  CGCAGGGTTT  CGGCAGAAAC
601  AAACGGATTG  CCGTCGCGGT  CGCCGCCGAT  CCAGCCGCCG  ATTTTGAGGA
651  TGTCCGAAC  GCGGACGCCG  GGATAGGCCG  TCTGAAAGTC  GTGTTCCATC
701  TTGCGGTAGA  GCTTGGGCAG  GGCTTCGAAA  AAGCTCATCG  GGAAGATGGA
751  CACGCCGTTG  TTGATTTCTG  CGTTGACGCT  GAGTTTGTGG  CGGCGCGTTT
801  CGCTGGTCTG  CCACAAGCCC  AGCAGGATAG  TGTCTGATTc  GCgGCGCAGC
851  CGTGCCAGCG  CGTCGGCATT  GGTGCAGCGT  TCgCGTTGCG  GCAACAGTGC
901  GCGGATGCGG  CGGTTGAAGC  TTAAGACGCT  TTGGCGTTGC  ACTTCGGTCG
951  GGTGCGCGGT  CAAAACGGCG  GTAACGGACG  TATTGTCCAA  CTGCCGCTGC
1001  ACCGATTTGC  CGTCGGCTTT  CCCCCTTTG  AGCCTGCGGA  CGGTTTCCGT
1051  CAGGTGCGCT  TCCGCGCCGC  CGCGTCCGCG  TTCTTCGTGG  ATTTGGCGGC
1101  GCGTTCGTG  GTGCACGTCT  TCGGCGATGT  TCAAAATCTG  GGCGAACAGG
1151  CCGCAGGCCA  AGGTTAAATC  GTGGGTTTGT  TGTTCTGCCA  ATTGCGGCAA
1201  TACTTTTCA  ATCAATGCCG  CGCTGTCTGC  GGAAGTGGAC  AAGAGTTTGA
1251  CTGTTTCGAC  AACCAACGGC  GAGGCTTCTT  CGTGCAGGAG  GTTGAACAGG
1301  GATTGTTTCA  GAAATTCCGC  GTCCGCCGCC  AAAGCCGCGT  CCTTTGGATT
1351  GTTCAGAATA  TGCAGTTGCA  TGATTTTCT  CTCTCGTCTG  CCGTAAATAT
1401  TGTAAATGTA  CCCCAAATGC  CGCATCCGTG  CCAAACCGTT  CACACTTTAA
1451  CCGCCCGTGT  CCCGAAATGC  CGTCTGAAGT  TGAACGCCGC  CCGACGGCAG
1501  CGTTACAATC  GCCCGCAACT  GTTTTtTTCC  GAACATCATC  ATGACCACGA
1551  CCGAACACGA  CAACGACGAT  GCATTCTCTG  TCGGTTACAG  CCGCCACATC
1601  CTCTTGACG  AAATCGGCAT  CGAAGGGCAG  CAGAACTTT  CCGCCGCGCA
1651  TATTTTGGTC  GTCGGCTGCG  GCGGTTTGGG  TGCCGCCGCA  CT.GCCCTAC
1701  CTTGCCGCTT  CGGGTGTCGG  CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

```

m509.pep
1  MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVKAEHGYGT DEVCQTAFGK QTAAVVDKGT LQFFQIIQKL
101  LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
151  VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201  KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFKAHREDG
251  HAVVDFVVD AEFVAARFAGL PQAQQDSVDF AAQPCQRVGI GAAAFALRQQC
301  ADAAVEAXDG LALHFGRVVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351  QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401  YFFNQCRADV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451  VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNAARRQ
501  RYNRPQLFFS EHHHDHDRTR QRRCI PAAVQ PPHPLGRNRH RRAAETFRRA
551  YFGRRLRRFG CRRTXPTLPL RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

```

m509/g509
      10      20      30      40      50      60
m509.pep  MVAVCDKRAVQRTLMAQFAQGGGLFLLFVQAVVVVFQACVLEKLGHNHIGVFACVLAQVERH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509      MVAVCDERAVQRTLVAQFAQGGGLFLLFVQAVVVVFQACVLEKLGHNHIGVFACVLAQVERH
          10      20      30      40      50      60

      70      80      90      100     110     120
m509.pep  HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAFAAHTQTER
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509      HVEAEHGHGTDEVCQTAFGKQAAAVVDKGTLQFFQII EKFLGRSIRLEKAFAAHAQTER
          70      80      90      100     110     120

      130     140     150     160     170     180
m509.pep  ARFAHSARHNVDGAAGVFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g509      ARFAHSARHNVDGAAGVFFGAGDFFVREGCQCHYVVVDFDAADGKRQFAVKFVEFAAV
          130     140     150     160     170     180

```

	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFGRNKR	IAVAVAADPAADFEDVRNADAG	IGRLKVVFHLAVELGQ			
g509	KTEHGIGVAAEGKAQGFARNKR	IAVAVAADPAADFKDIRNADIG	IGRLKVVFHLAVEFGQ			
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFKAHREDGHAVVDFVDAEFVA	ARFAGLPQAQQDSVDFAAQPC	QRVGIGAAAFALRQQC			
g509	GFKAHREDGHAVVDFVDAEFVA	ARFAGLPQAQKHGVDFAAQPC	QRVGIGAAAFALRQQR			
	250	260	270	280	290	300
	310	320	330	340	350	360
m509.pep	ADAAVEAXDGLALHFGRVRGQ	NGNGRIVQLPLHRFAVGFP	RFEPADGFRQAAFRAAASG			
g509	ADAAVEIQNGLALHFGRVRGQ	NGNGRIVQLPLHRFAVGFP	RFEPADGFRQAAFCVVAG			
	310	320	330	340	350	360
	370	380	390	400	410	420
m509.pep	FFVDLAAAFVVHVFGDVQNLGE	QAAGQXIVGLLFVQLRQYFF	NQCRAVVGSGQEFDCFD			
g509	IFVDLAAAFVVHVFGDIQNLGE	QAPGRQIVGLPFVQLRQYFF	NQCRAVVGSGQEFDRFD			
	370	380	390	400	410	420
	430	440	450	460	470	480
m509.pep	NQRRGFFVQVEQGLFQKFRVR	RQSRVLWIVQNMQLHDFSLSS	AVNIVNVPQMPHPCQTV			
g509	NQRRGFFVQVEQGLFQKFRVR	RQSRVLWIVQNMQLHDFPLI	-AVNTVNVNVPQMPHPCQTV			
	430	440	450	460	470	
	490	500	510	520	530	540
m509.pep	HTLTARVPKCRCLKLNAARRQ	RYNRPLFFSEHHHDRTTRQ	RRCI PAAVQPPHPLGRNRH			
g509	HTLTTHVPKCRCLKLNAARRR	RYNRPLFFSEHHHDRTTRQ	RRRT PAAVQPPHPLGRNRH			
	480	490	500	510	520	530
	550	560	570			
m509.pep	RRAAETFRRAYFGRRLRRFG	CRRTCPTLPLRV SAR				
g509	RRAAEAFRRAYFGRRLRRIG	RRRPCISP PRGSAR				
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

```

a509.seq
1  ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGCT TGTTTTTGCT CTTCGTTGAG GCTGTTGTAG
101 TCTTCCAAGC CTGCGTGT TGAAAAGCTCG GCAACCACAT CGGCGTGT TT
151 GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201 ATACGGAACG GATGAGTCT GCCAAACGGC CTTCGGCAAG CAGGCGGCTG
251 CCGTTGTCTG TAAGGGAATG TTGCAATTTT TTCAAATCAT CGAGAAATTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCAATG
401 GCGCGACGGT AGGGTTCTTC GGCGCGGGCG GTTCTTCTCGT CGGGCGATTT
451 GTCGGACAAC GCCATCACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCTGAGT CGCCACGGTA AAAACGGAAC
551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601 GAACGGATTG CCGTCGCGGT CGCCGCGGAT CCAGCCGCGG ATTTTGAGGA
651 TGTCCGGAAC GCGGACATCG GGATAGGCCG TCTGAAAGTC GTGTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751 CACGCCGTTG TTGATTTCTG CTGTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTTC GCGGCGCAGC
851 CGTGCCAGCG CGTCGGCATT GGTACAGCGT TCGCGTTGCG GCAGCAGCGC

```

```

901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTGC
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTCGGCTTT CCCCCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTTCGTG GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCA ATTGCGGCAA
1201 TACTTTTTC AATCAATGCCG CGCTGTCTGC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCGC GTCCGCCGCC AAAGCCCGCT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCCG ACGGCAGCGT
1501 TACAATCGCC CACAACGTG TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGGCAGCAG AAACCTTCCG CCGCGCATAT
1651 TTTGGTCGTC GGCTGCGGCG GTTTGGGTGC CGCCG.CCCT GCCCTATCTC
1701 CCCGTTCCG GCATCGGCAC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

```

a509.pep
1  MVAVCDERTV QWTLMAQFAQ QGGLFLLFVE AVVVFOACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGNGATVGFF GAGGFFVGRF
151 VGQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIAVAVAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKAHRKDG
251 HAVVDFVVD AEFVAARFAGL PQAQQDSVDF AAQPCQRVGI GTAFALRQQR
301 ADAAVEIQDG LALHFGRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRADV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNV PMPHPCQTVH TLTARVPKCR LKLNAARRQR
501 YNRPQLFXSE HHHDHDRTRQ RRCIPAAVQP PHPLGRNWHR RAAETFERRAY
551 FGRRLRRFGC RXPCPISPLP ASAR*

```

m509/a509 93.0% identity in 575 aa overlap

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFOACVLEKLGNHIGVFACVLAQVERH					
	: :	: :	: :	: :	: :	: :
a509	MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVFOACVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509.pep	HVKAEGHYGTDEVCQTAFGKQTAAVVDKGT LQFFQIIQKLLCRSIRLEKA EFAAHTQTER					
	: : :	: :	: :	: :	: :	: :
a509	HVEAEHGYGTDEVCQTAFGKQAAAVVDKGM LQFFQIIEKFLCRSIRLEKA EFAAHTQTER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVDGAAVGFAGDFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
	: :	: :	: :	: :	: :	: :
a509	ARFAHSARHNVGNGATVGFFGAGGFFVGRFVGQRHHIAVDFDAADGERQFAVEFVEFATV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFGGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
	: : : :	: :	: :	: :	: :	: :
a509	KTEHGIGVAAEGKTQGFGRNERIAVAVAADPAADFEDVRNADIGIGRLKVVFHLAVELGQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFKAHREDGHAVVDFVVD AEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAAAFALRQQC					
	: : :	: :	: :	: :	: :	: :
a509	GFKAHREDGHAVVDFVVD AEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGTAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360

760

```

m509.pep  ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPRFEPADGFRQAAFRAAASG
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      ADAAVEIQDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPRFEPADGFRQAAFRAAASG
          310      320      330      340      350      360

          370      380      390      400      410      420
m509.pep  FFVDLAAAFVHVFGDVQNLGEQAAGQGXI VGLLFVQLRQYFFNQCRAVVGSQGEFDCFD
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      FFVDLAAAFVHVFGDVQNLGEQAAGQGXI VGLLFVQLRQYFFNQCRAVVGSQGEFDRFD
          370      380      390      400      410      420

          430      440      450      460      470      480
m509.pep  NQRRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMPHPCQTV
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      NQRRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLI-AVNTVNVVPQMPHPCQTV
          430      440      450      460      470

          490      500      510      520      530      540
m509.pep  HTLTARVPKCRLKLNAARRQRYNRPQLFFSEHHHDH DTRQRRCIPA AVQPPHPLGRNRH
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      HTLTARVPKCRLKLNAARRQRYNRPQLFXSEHHHDH DTRQRRCIPA AVQPPHPLGRNWH
          480      490      500      510      520      530

          550      560      570
m509.pep  RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRVSARX
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509      RRAAETFRRAYFGRRLRRFGCRXPCPISPLPASARX
          540      550      560      570

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1  atgccttcgc ggacaccgca gggaaaaagg ggttattcct gccccaaagcg
51 ggatagtgcc ttttggcagg cgttggtccat atcgggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgcccgttca gggagggttt caataggctcg
151 tggacgacgt tgagcgcggc cataatgacg attttttcgc tgtccgcgac
201 gcgccgcct tcgcgcatgg ctccggcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcggtgatg acttcgatgt agacttggtc gatgttcac ctttaaatcct
351 tattgctgcg tttcctgccg ttgggggagg cgcgctgcc gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1  MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51 WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTTCCT GCGCCAAGCG
51 GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGC TGTCGCGGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAG GGTGAGCCGG
301 GGCGTGCAWG ACTTCsAtGT GGACTTGTTG GATGTTTCAT CTTTAATCCT
351 TATTGCTGCG TTTCTGCGCA TTGGGGGAGG CCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51 WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FQWALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
g510	MPSRTPQGKRGYSCPKRDSA FQWALSISVILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPV RX					
	:					
g510	FPAVGGGALPV RX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

1	ATGCCTTCGC	GGACACCGCA	GGGAAAAGG	GGTTATTCCT	GCGCCAAGCG
51	GGATAGTGCT	TTTTGGCAGG	CGTTGTCCAT	ATCGGCTATT	TTACGCGCAA
101	AATCGCCGAT	TGCCAAATCG	CCGCCGTTCA	GGGAGGTTTT	CAACAGGTCG
151	TGGACGACGT	TGAGCGCGGC	CATAATGACG	ATTTTTTCGC	TGTCCGCGAC
201	GCGTCCGCCT	TCGCGGATGG	CTTCGGCTTT	GCCGTTGAGC	ATTCCGACTG
251	CCTGCAACAG	TGTGTCTTTT	TCTTCTGCCG	GCGTGTGAC	GGTCAGCCGG
301	G.CGTGCATG	ACTTCGATGT	GGACTTGTTT	GATGTTTCATC	CTTTAATCCT
351	TATTGCTGCG	TTTCTGCCG	TTGGGGGAGG	CGCGCTGCCA	GTGCGCTGA

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

1	MPSRTPQGKR	GYSCAKRDSA	FWQALSISAI	LRAKSPIAKS	PPFREVFNRS
51	WTTLSAAIMT	IFSLSATRPP	SRMASALPLS	IPACNSVSF	SSAGVLTVSR
101	XVHDFDVL	FDVHPLILIAA	FPAVGGGALP	VR*	

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FQWALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
a510	MPSRTPQGKRGYSCAKRDSA FQWALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPV RX					
	:					
a510	FPAVGGGALPV RX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

1	atgaaagtgc	ttgttttagg	tgcgggtgtt	gccggcgat	cctccgtgtg
---	------------	------------	------------	-----------	------------

g512.pcp

m512.seq (partial)

m512.pep (partial)

m512/g512

```

                                10      20      30
m512.pep                      VLERYGVPYRRLKPEECAEFEPALARVTAK
                                |||||
g512      TDMNFEGRRKKGTLQIFRQTEEVEAAKQDIAVLERYGVPPYRRLKPEECAEFEPALARVTAK
              130      140      150      160      170      180

                                40      50      60      70      80      90
m512.pep      IAGGLHLPPADATGDWRLF TENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGG LK
              |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g512      IVGGLHLPPADATGDCRLFTENLYKLCQEKGVRFYFNQTISRIDHNGLRIKAVETKQGG LK
              190      200      210      220      230      240

                                100      110      120
m512.pep      QMPLSARSVASAGRFWRSWISICPFIPSKAIP
              |||||:|||||
g512      QMPLSARSAASAGLCWRSWISICPFIPSKAIP

```

763

250 260 270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
1  ATGAAAGTGC TTGTTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCGCGTGC
51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAAACCACT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCGAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GCGGTGCCGT ACCGCCGTCT
501 GAAGCCCGAA GAATGCGCAG AATTGAGGCC TCGCTGGCA CGCGTTACCG
551 CCAAATTGCG CGGCGGCCTG CACCTGCCCC CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAGGAAA AGGGCGTACG
651 GTTTCATTTC AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAAACCGT TGAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
1  MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
51  YTPWAAAPGI PTKALKWLFK SHPLLFRPD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMFR RFEAQTMNMF EGRKKGTLQI FRQTKVEEAA
151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVEVK QGGLKQMPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVPYRRLKPEECAEFEPALARVTAK
a512                                |||||
TGMNFEGRKKGTLQIFRQTKVEEAAKQDIAVLERYGVPYRRLKPEECAEFEPALARVTAK
130      140      150      160      170      180

m512.pep                                40      50      60      70      80      90
                                IAGGLHLPADATGDWRFLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVEVKQGGLK
a512                                |||||
IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVEVKQGGLK
190      200      210      220      230      240

m512.pep                                100      110      120
                                QMPLSARSVASAGRFWRKWSISICPFIPSKAIPX
a512                                |||||
QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
250      260      270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
1  ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
51  TTCGCAAGGT ATGATTCAA TGCTGGGCGT GTTTGTGCGT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGCG CGGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
351 GGTCTATTTC GGCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

764

501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep
 1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKGK DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq
 1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATTCAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTC GCGCGGTTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep
 1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKGK DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m513.pep	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMXLRDYTAKLKMKGKDPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHP					
	130	140	150	160	170	180
	190					
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

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```

1  ATGAACGAGA  ACTTTACCGA  ATGGCTGCAC  GGCTGGGTCG  GCGCCATCAA
51  CGATCCGATG  TGGTCATACT  TGGTTTATNT  GCTTTTGGGT  ACGGGGCTTT
101 TCTTCACCGT  AACCACGGGC  TTTGTCCAAT  TCCGCCTGTT  CGGGCGCAGC
151 ATCAAAGAAA  TGCTCGGCGG  CCGCAAACAG  GGGGACGACC  CTCACGGCAT
201 CACGCCGTTT  CAGGCATTTG  TAACCGGCCT  TGCCAGCCGC  GTGGGCGTGG
251 GCAATATCGC  GGGCGTGGCC  ATCGCCATCA  AAGTCGGCGG  ACCGGGCGCG
301 GTGTTTTTGA  TGTGGGTAAC  CGCCTTAATC  GGTATGAGTT  CGGCGTTTGT
351 CGAATCTTCG  CTGGCGCAGC  TCTTTAAAGT  CCGCGACTAC  GACAACCACC
401 ATTTCCGGGG  CGGCCCTGCC  TACTACATCA  CTCAAGGGCT  GGGGCAGAAA
451 TGGCTGGGCG  TGTTGTTTCG  CCTGAGCCTG  ATTTTCTGTT  TCGGCTTTGT
501 GTTTGAAGCG  GTTCAGACCA  ATACCATTGC  CGATACCGTC  AAAGCGGCGT
551 GGGGTTGGGA  GCCTCATTAT  GTCGGCGTCG  CCCTGGTGAT  TTTAACCGCG
601 CCGATTATCT  TCGGCGGCAT  CAGGCGCATA  TCTAAAGCGG  CGGAAATCGT
651 CGTCCCCCTG  ATGGCGGTTT  TGTACCTCTT  TATCGCGCTT  TTCATCATTT
701 TGACCAATAT  TCCGATGATT  CCGGACGTGT  TCGGTCAGAT  TTTTTCGGGC
751 CGGTTCAAAT  TCGACGCGGC  AGCAGGCGGC  TTAAGCGGCG  GTCTGATTTC
801 GCAAACGATG  ATGATGGGCA  TCAAACGCGG  CCTGTATTCC  AACGAGGCGG
851 GTATGGGTTC  CGCGCCGAAC  GCCGCCGCCG  CCGCCGAAGT  GAAACACCCT
901 GTTTCGCAAG  GTATGATTCA  AATGCTGGGC  GTGTTTGTGC  ATACCATCAT
951 CGTTTGTCT  TGCACCGCCT  TCATCATCTT  GATTTACCAA  CAGCCTTACG
1001 GCGATTTGAG  CGGTGCGGCG  CTGACGCAGG  CGGCGATTGT  CAGCCAAGTG
1051 GGGCAATGGG  GCGCGGGCTT  CCTCGCCGTC  ATCCTGTTTA  TGTTTGCCTT
1101 TTCCACCGTT  ATCGGCAACT  ATGCCTATGC  CGAGTCCAAC  GTCCAATTCA
1151 TCAAAGCCA  TTGGCTGATT  ACCGCCGTTT  TCCGTATGCT  GGTTTTGGCG
1201 TGGGTCTATT  TCGGCGCGGT  TGCCAATGTG  CCTTTGGTCT  GGGATATGGC
1251 GGATATGGCG  ATGGGCATTA  TGGCGTGGAT  CAACCTTGTC  GCCATCCTGC
1301 TGCTCTCGCC  CTTGGCGTTT  ATGCTGCTGC  GCGATTACAC  CGCCAAGCTG
1351 AAAATGGGCA  AAGACCCCGA  GTTCAAACCT  TCCGAACATC  CGGGCCTGAA
1401 ACGCCGTATC  AAATCCGACG  TTTGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```

a513.pep
1  MNENFTEWLH  GWVGAINDPM  WSYLVYXLLG  TGLFFTVTTG  FVQFRLFGRS
51  IKEMLGGRKQ  GDDPHGITPF  QAFVTGLASR  VGVGNIAGVA  IAIKVGPGPA
101 VFWMWVTALI  GMSSAFVESS  LAQLFKVRDY  DNHHFRGGPA  YYITQGLGQK
151 WLGVLFALSL  IFCFGVFEEA  VQNTNIADTV  KAAWGWEPHY  VGVALVILTA
201 PIIFGGIRRI  SKAAEIVVPL  MAVLYLFIAL  FIILTNIPMI  PDVFGQIFSG
251 AFKFDAAAGG  LLGGLISQTM  MMGIKRGlys  NEAGMGSAPN  AAAAAEVKHP
301 VSQGMQMLG  VFVDTIIVCS  CTAFIILYQ  QPYGDLGSA  LTQAAIVSQV
351 GQWGAGFLAV  ILFMFAFSTV  IGNYAYAESN  VQFIKSHWLI  TAVFRMLVLA
401 WVYFGAVANV  PLVWDMADMA  MGIMAWINLV  AILLLSPLAF  MLLRDYTAKL
451 KMGKDPEFKL  SEHPGLKRRR  KSDVW*

```

m513/a513 100.0% identity in 191 aa overlap

```

m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||
a513 260 270 280 290 300 310
DAAAGLLGLISQTM MMGIKRGlys NEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
m513.pep TIIVCSCTAFIILYQ QPYGDLGSAAL TQAAIVSQV GQWGAGFLAV ILFMFAFSTVIGNY
|||||
a513 320 330 340 350 360 370
TIIVCSCTAFIILYQ QPYGDLGSAAL TQAAIVSQV GQWGAGFLAV ILFMFAFSTVIGNY

100 110 120 130 140 150
m513.pep AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMMGIMAWINLVAILL
|||||
a513 380 390 400 410 420 430
AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMMGIMAWINLVAILL

160 170 180 190
m513.pep LSPLAFMLLRDYTAKL KMGKDPEFKL SEHPGLKRRR KSDVW
|||||

```

a513 LSPLAFMLLRDYTAKLKMKGKDEPKLSEHPGLKRRRIKSDVWX
440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq
1 atggttcaaa tacaggttgt gcgcgcgcgc ggcgttgccc gtggtctgca
51 ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg
101 ccgtttttgaa tcacgaagcg cgcgcgcggtg gcaacacctt ccgcatacaa
151 atagctgctg cggaaagagc gggggatgtg cggttcttcg cgcaggttga
201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt
251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag
301 cccgcccga acggtggtat cgaagaggac ggggttagctg cctgtcggga
351 tgctgcggct gccgagtcgg cgcgaagtgc ggccggcggc ggtttgaccg
401 atggtttcgg ggctgtccat atccggatgg cggcaggcgg aatcgtacca
451 gtagtcgcgc tgcattccgt tttcgtcggc ggccagcagc ctgcaggaaa
501 tgctgtggtg cgtgctttgc cgtgtgcgg caaaaccgtg ggtgttgccg
551 taaacgtatt ggtactgtcc ggtttgcacc gccgcgcctt cggagttttc
601 gatgcggctg tccgtgtcca acgctgcctg ttcgcatgtt tttgccaaagc
651 cgacggcggc ttccgtatcc aaatcccatt cgtggtaaag gtcggggctg
701 ccgatgtgtt gcgccatcaa ctccgggtcg gcaagtccgg cgcaaccgtc
751 ttcggcgggtg tggcgggcga tgcggcggc ggccgagacg gtgtcgcga
801 gggcttggtt ggagaagtcg gcggtgcgg ccgcgcctt gcgtttgccg
851 acgtaaacgg taatgtccag cgatttgtcc tgctggaact cgatttgttc
901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tcgctgaagt
951 cggttcggc ggccggtcgg cccgctgctt ttgccaagtc gaggctgcgg
1001 cggcagaggt cgaggagttc ggaagcgggt tggttgaaca gcataacaat
1051 ctttcttggg ggagcgttgt ggcattttta

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep
1 MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGNTFRK
51 IAAAERAGDV RFFAQVEEIG QDFADAVDQ ETALAVERRA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GDDAAGNAVV RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLEDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVAFA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)
1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
101 GCGCCGCCCG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCGAAAC
151 GGTGGTATCG AAGAGGACCG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC
201 CGAGTCGGCG CAAAGTGCAG CGGGCGGCGG TTTGACCGAT GGTTCGGGG
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCACT AGTCGCGCTG
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCGGTA AACGTATTGG
401 TAATGGCCCG TTGCAACGCG CGCGCCTTCG GAGTTTTCGA TCGCTCATC
451 CTCGTTACAG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGGCGGCTk
501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CGGGGTGCGC GATGTGTTTT
551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CGGCGGTGTG
601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGCAAG GCTTTTTCGG
651 AGAAGTCGGC AGTACTGGCG CGGCCTTTCG GTTTGCGGAC GTAAACGGTA
701 ATGTCCAGCG ACTGTCTCTG CTGGAACCTG ATTTGTTsGA TTTsGCCCAG
751 CCGCACGCTG ACGCTTTGTC CCAATGATTG GCTGAAATCG GCTTCGGCGG
801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGGCGCG GCAGAGGTGCG
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
901 TGCTTTGCGG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

Homology with a predicted ORF from *N. gonorrhoeae*

m515/q515

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m515.pep                                     10      20      30
                                         GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                           ::| | | | | | | | | | | | | | | | | |
g515    AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
           30          40          50          60          70          80

           40          50          60          70          80          90
m515.pep    VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
           ||||| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g515    VERAAGECADEVSDQPARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
           90         100        110        120        130        140

           100        110        120        130        140        150
m515.pep    GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
           ||||| | | | : | | | : | | | | | | | | | | | | | | | | : | | | | | | :
g515    GGIVPVVALHSVFVGDDAAGNAVVRALPVCCKTVGVAVNVLVLSGLHRRAFGVFDAAVR
           150        160        170        180        190        200

           160        170        180        190        200        210
m515.pep    VQGGLFALFCQADGGXRIQIPFVKVGVADVFCCHQTGIGKSGATVFGGVAGVDVGGFDGV
           || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g515    VQRCLFALFCQADGGFRIQIPFVKVGVADVLRHQLGVGKSGATVFGGVAGDVGGGADGV
           210        220        230        240        250        260

           220        230        240        250        260        270
m515.pep    LQFFFEVGGSTGAFAFADVNGNVQRLVLELDLXDQAQPHADALSQXFAEIGFGGGRCAR
           || : | | | | : : | | | | | | | | | | | | | | | | | | | | | | | | | |
g515    AQGLFGEVGGAGAFAFADVNGNVQRFVLELDLFDFAQAHADALSERFAEVGFGGGRAR
           270        280        290        300        310        320

           280        290        300
m515.pep    RFCQVERAAAAEVEEFGSGVVEQHNNLSXXCFAAF
           ||||| | | | | | | | | | | | | | | | | : ||
g515    CFCQVERAAAAEVEEFGSGVVEQHNNLSWWSVVAF
           330        340        350

```

a515.seq

1	ATGTTTCAAA	TAAAGTTGT	GCGCGCCGCC	GGCGTTGCCC	GTGGTCTGCA
51	TTCCGAGTTT	GCGCGCGCTG	TAAGTCTGA	GGAAATAGCC	TTCGACAATG
101	CCGTTTGTAA	TCACGAAGCG	CGGTGCGGTG	GCAACGCCTT	CCGATCAAAA
151	ATAGCTGCTG	CGGAAAGAGC	GGGGATGTG	CGGTTCTTCG	CGCAGGTTGA
201	GGAAATCGGG	CAGGACTTTT	TTGCCGATGC	TGTCGATCAG	GAAACTGCTT
251	TGGCGGTAGA	GCGCTCCGCC	GGAGAGTGCG	CCGACGAGGT	GTCCGATAAG
301	ACCGCCCGAA	ACGGTGGTAT	CGAAGAGGAC	GGGGTAGTTG	CCTGTCGGGA
351	TGCTGCGGCT	GCCGAGTCGG	CGCAAAGTGC	GGCGGGCGGC	GGTTTGACCG
401	ATGGTTTCGC	GGCTGTCCAT	ATCCGGATGC	CGGCAGGCGC	AATCGTAGCA
451	GTAGTCGCGC	TGCATGCCGT	TTTCGTCGGC	GGCAACGACG	CTGCAGGAAA
501	TGCTGTGGTG	CGTGCTTTGC	CGGTTGCGGC	CAAAACCGTA	GGTGTTGCCG

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551 TAAACGTATT GGTAATGGCC GGTTCGACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCNNNGC GGC GCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGCTGAAACT CGATTTGTTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGAT TCGCTGAAAT
951 CGGCTTCGGC GGC GGTGCG CCCGTCGCTT TTGCCAAGTC GAGCGTGGC
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGTTGAACA GCATAGAAAT
1051 CTTTCTTGAT GATGCTTTGC GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1422; ORF 515.a>:

```

a515.pep
1  MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNVLNHEA RCGGNAFRK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADSVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGL FALFCQADGG FRIQIPFVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVXX GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*FAEIGFG GGCARRFCQV ERAAAEVEEF GSGVVEQHRN
351 LS**CFAAF*

```

m515/a515 92.1% identity in 304 aa overlap

```

m515.pep                                     10      20      30
                                         GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                         ::| | | | | | | | | | | | | | | | | |
a515      AEEIAFDNVLNHEARCGGNAFRKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
           30      40      50      60      70      80

           40      50      60      70      80      90
m515.pep  VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGLTDGFGAVHIRMAA
           | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VERSAGECADEVSDKTARNGGIEEDGVVACRDAAAESAQSAAGGLTDGFGAVHIRMAA
           90      100     110     120     130     140

           100     110     120     130     140     150
m515.pep  GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLVMAGLHRRAFGVFDALIL
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLVMAGLHRRAFGVFDALIL
           150     160     170     180     190     200

           160     170     180     190     200     210
m515.pep  VQGGFLFALFCQADGGXRIQIPFVKVGVADV FCHQTGIGKSGATVFGGVAGDV DGGFDGV
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VQGGFLFALFCQADGGFRIQIPFVKVGVADVLRHQLGVGKSGATVFGGVAGDVXXGADGV
           210     220     230     240     250     260

           220     230     240     250     260     270
m515.pep  LQGFGEVVGSTGAFAFADVNGNVQRLVLLLELDLXDAQPHADALSQXFAEIGFGGGCAR
           | | : | | : | | | | | | | | | | | | | | | | | | | | | | | |
a515      AQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLFDFAQPHADALSQXFAEIGFGGGCAR
           270     280     290     300     310     320

           280     290     300
m515.pep  RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
           | | | | | | | | | | | | | | | | | | | | | | | |
a515      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
           330     340     350     360

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1423>:

```

g515-1.seq
1  ATGGTTCAAA TACAGTTGT GCGCGCCGCC GGCCTTGCCC GTGGTCTGCA

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```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTTGA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CCGTCTCTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCTGCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CCGTGTGCGG CAAAACCGTG GGTGTGCGG
551 TAAACGTATT GGTAGTGTC GGTTCGACC GCCGCGCCTT CGGAGTTTTT
601 GATGCGGCTG TCCGTGTCCA ACGCTGCTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCGTATCC AAATCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GGCGGCGACG GTGTCGCGCA
801 GCGCTTGTTC GGAGAAGTCG CGGTGCGCG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGATTTGTCC TGCTGGAAC CGATTTGTTC
901 GATTTTCGCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCCTGAAGT
951 CCGCTTCGCG GCGGTCGCG CCCGCTGCTT TTGCCAAGTC GAGCGTGGCG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAA
1051 CTTTCTTGGT GGAGCGTTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGNTFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFQCV ERAAAEEVEF GSGVVEQHNN
351 LSWWSVVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGTTTGT GCGCGCCGCC GCGGTGCGCC GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTTGA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CCGTCTCTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCTGCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CCGTGTGCGG CAAAACCGTG GGTGTGCGG
551 TAAACGTATT GGTAAATGGC GGTTCGACC GCCGCGCCTT CGGAGTTTTT
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCGTATCC AAATCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGATGGC GGCTTTGACG GTGCTTGTGA
801 GCGCTTTTTT GGAGAAGTCG GCAGTACTGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCC TGCTGGAAC CGATTTGTTC
901 GATTTTCGCC AGCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEIEA FDNAVLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVK VGVADVLFHQ TGIGKSGATV
251 FGGVAGDVGG GFDGVLQGGF GEVGSTGAFF AFADVNGNVQ RLVLELDLF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

	10	20	30	40	50	60
g515-1.pep	MVQIQVVRAAGVARGLHSEF	ARAVTAEIEAFDNAVLNHEARR	GGNTFRIKIAAAERAGDV			
m515-1	MVQIQVVRAAGVARGLHTEF	ARAVTAEIEAFDNAVLNHEAR	CGGNAFRIKIAAAERAGDV			
	10	20	30	40	50	60

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	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGVADVLRHQ					
m515-1	GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVFCCHQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLLLELDLF					
m515-1	TGIGKSGATVFGGVAGDVGGFDGVLQGGFGEVGGSTGAFAFADVNGNVQRLVLELDLF					
	250	260	270	280	290	300
	310	320	330	340	350	360
g515-1.pep	DFAQAHADALSERFAEVGFGGGRARCFQVERAAAEVEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GCGGTTGCCG GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACGTCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTGTAA TCACGAAGCG CCGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CCGTCTCTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTGATCAG GAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGGC CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGGCG GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTGCGG
551 TAAACGTATT GGTAAATGGC GGTTCGACC GCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGCGGGCGGA TGTGCGCGGC GCGCGGACG GTGTGCGCGA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CCGGCCTTTT GCGTTGCGG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGCTGAAACT CGATTTGTTC
901 GATTTCGCC AGCCGCACGC TGACGCTTTG TCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEIEA FDNVLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAGNAVVR RALPVCCKTV GVAVNVLMVA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEIEAFDNVLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEIEAFDNVLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNGGIEEDGVVACRDAAA					

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m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
	70 80 90 100 110 120
a515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
	130 140 150 160 170 180
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
	130 140 150 160 170 180
a515-1.pep	GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGADVLRHQ
	190 200 210 220 230 240
m515-1	GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGADVLFCHQ
	190 200 210 220 230 240
a515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
	250 260 270 280 290 300
m515-1	TGIGKSGATVFGGVAGDVGGGDFGVLQGFGEVGGSTGAFAFADVNGNVQRLVLELDF
	250 260 270 280 290 300
a515-1.pep	DFAQPHADALSQX
	310
m515-1	DFAQPHADALSQX
	310

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

g516.seq

```

1  atgtttgtcc gtaaaacgac cgccgccgtt ttggcggcaa ccttgatact
51  gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacgtt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatcccga agattcggcg aagctgacgg
251 gccttttgaa ggccgggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccg gtcaaattcg aagcgcccgg
351 cagccagaat ttcagtaccg gaggtccttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcgggtcaa
451 ctcgacaatc ggaccattta cagcgctgc gtatccgcca aaggcaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaatg
551 tgcccgccga tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttgttga tattggatgc
651 ggcggccgcg gtgctggctt tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

g516.pep

```

1  MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSVLMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNILEYTP PLLILDAAAA VLVLPMALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

m516.seq

```

1  ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGCGC CTTCCGGTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCGGCG AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```

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```

501 CTACGCCACA CCGCAAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG
551 TGCCTGCCGA TATTTATTAC ACGGTACTG AAGAACATAC CGACAAATCC
601 AAGCTGTTTG CAAATATCTT ATATACGCCC CCCTTTTGA TACTGGATGC
651 GCGGGGCGCG GTACTGGCCT TGCCTGCGGC GGCTCTGGGT GCGGTCGTGG
701 ATGCCGCCCG CAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

```

m516.pep
  1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV
  51 VAEDNAQLEK GSLVMMGGKY WFVVPEDSA KLTGILKAGL DKPFQIVEDT
 101 PSYARHQALP VKLESPGSQN FSTEGLCRLY DTDKPADIAK LKQLGFEAVK
 151 LDNRTIYTRC VSAKGYYAT PQKLNADYHF EQSVPADIYY TVTEEHTDKS
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

```

m516/g516
      10      20      30      40      50      60
m516.pep MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKQIRAFGVVAEDNAQLEK
          |||||:|||||:| |||||:|||||:|||||:|||||:|||||:|||||
g516      MLFRKTTAAVLAATLILNGCTMLRGMNPNVSQTITRKHVDKQIRAFGVVAEDNAQLEK
          10      20      30      40      50      60

      70      80      90      100     110     120
m516.pep GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g516      GSLVMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSQN
          70      80      90      100     110     120

      130     140     150     160     170     180
m516.pep FSTEGLCRLYDTDKPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGYYATPQKLNADYHF
          ||| |||||:| |||||:|||||:|||||:|||||:|||||:|||||
g516      FSTGGLCLRYDTGRPDDIAKLKQLEFKAVKLDNRTIYTRCVSAKGYYATPQKLNADYHF
          130     140     150     160     170     180

      190     200     210     220     230     239
m516.pep EQSVPADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|:|:|
g516      EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLLILDAAAAVLVLPMALIAAANSSDK
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

```

a516.seq
  1 ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT
  51 GAACGGCTGT ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTCGGTGTG
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
 201 CGGGAAATAC TGGTTCGTCT TCAATCCTGA AGATTCGGCG AAGCTGACGG
 251 GCATTTTGAA GGCCGGGTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC
 301 CCGCGCTTTG CCTACCAAGC CTGCGCGGTC AAATCGAAT CGCCCGCCAG
 351 CCAGAATTTT AGTACCGAAG GCCTTTGCCT GCGCTACGAT ACCGACAGAC
 401 CTGCCGACAT CGCCAAGCTG AAACAGCTTG AGTTTGAAGC GGTGCAACTC
 451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCCGCCAAG GCAAATACTA
 501 CGCCACACCG CAAAACTGA ACGCCGATTA TCATTTTGAG CAAAGTGTGC
 551 CTGCCGATAT TTATTACACG GTTACGAAAA AACATACCGA CAAATCCAAG
 601 TTGTTTGAAG ATATTGCATA TACGCCACC ACGTTGATAC TGGATGCGGT
 651 GGGCGCGGTG CTGGCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT
 701 CCTCAGACAA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

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```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51 VAEDNAQLEK GSLVMMGGKY WFVVPEDSA KLTGILKAGL DKQFQMVPEPN
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIAKL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDVAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

              10      20      30      40      50      60
m516.pep      MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDDKDQIRAFGVVAEDNAQLEK
              |||||:||||:| ||| :|||||
a516           MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVDDKDQIRAFGVVAEDNAQLEK
              10      20      30      40      50      60

              70      80      90      100     110     120
m516.pep      GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
              |||||:|||||:|||||:|||||:|||||:|||||
a516           GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKQFQMVPEPNRFA-YQALPVKLESPASQN
              70      80      90      100     110

              130     140     150     160     170     180
m516.pep      FSTEGLCLRYDTPDKPADIACLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
              |||||:|||||:|||||:|||||:|||||:|||||
a516           FSTEGLCLRYDTPDRPADIACLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
120           130     140     150     160     170

              190     200     210     220     230     239
m516.pep      EQSVADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX
              |||||:|||||:|||||:|||||:|||||:|||||
a516           EQSVADIYYTVTKKHTDKSKLFENIAYTPTTLILDVAVGAVLALPVAALIAATNSSDKX
180           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1  atgcatcggg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
51 cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 cccgtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacg
151 tgcgtctttc aatcccgatt tgatgttttt gggcaggctg atttggtctg
201 tgcgcgggt aatgacggct ttcgcgccga agccgatgag ggtcaggaac
251 attttcattt gttcgggcgt ggtgttttgc gcttcgtcga ggatgatgta
301 tgcgcggttg agcgtcctgc cgcgcataata ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagaggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1  MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSCHAVQFLT
51 CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDPLGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1  ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTTT TGACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACGTTGTGCA GTTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCGATTTCOA
351 TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

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451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT
51 RIFXSRFDVF GOVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGQEAQFLA GFDGWAH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

m517.pep	10	20	30	40	50	60
	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
g517	10	20	30	40	50	60
	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGGMEIQSCHAVQFLTCVFQSRFDVF					
m517.pep	70	80	90	100	110	120
	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
g517	70	80	90	100	110	120
	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
m517.pep	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKR TKVGIDFLGQVSGQEAQFLAGFDGWAH					
	: : : :					
g517	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKRTEVGVDFLGQVSGQEAQFLTGFDGRPN					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGACCAAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGCCGTGCA GTTCTCAGC
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTCATT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCCGTG AGCGTCTGCG CGCGCATATA GGCGAGCGGG GCAATCTCAA
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTCGAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT
51 RIF*SRFDVF GOVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGNLQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
151 VTGQKTQFLA GFDGRPH*

m517/a517 93.4% identity in 167 aa overlap

m517.pep	10	20	30	40	50	60
	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
a517	10	20	30	40	50	60
	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
m517.pep	70	80	90	100	110	120
	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
a517	70	80	90	100	110	120
	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLQTF					

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```

          70          80          90          100          110          120
          130          140          150          160
m517.pep  FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX
          ||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||
a517      FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKTQFLAGFDGRPHX
          130          140          150          160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1   atgacgtttt cggcggcaaa gctcaacatt tcggcactga tgttggtgtct
51  ttcggcagga atgaccgttt tactttccgc ttttttactg ctccgaccgg
101 aaggcagcat cttattcaac cattttttca gcataaatat tctgaccgga
151 agagcggcat ctccacgggc aaccgtgttc agactgcata aggcggtacg
201 attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
251 tccgaatcac gccgcctcct cggcgggcaa cgcttcatta taacagattg
301 ccccttaaaa aatcagaccc tgcttttgtg gcggagtctg aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1   MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RLHQAVRFHK MPKTISKMRN NYAVRITPPP RAATLHYNRL
101 PLKSDPAFV AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1   ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTGCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCAT GCATAAATAT TCTGACCCGA
151 AGAGCGGCAT CTCCACAGGC AACCGTGTTT AGACGGCATC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCG TAGAACTAC GCCGTCCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATTT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1   MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPOATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
101 AAGLVRERRR RCAVILSNR KKSDPAFVAE SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPOATVF
          ||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||
g518      MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPRATVF
          10          20          30          40          50          60

          70          80          90          100          110
m518.pep  RRHQA-RFARC-RTINKRRRNYAVRITPPSXA ATRHYNRLPSAAGLVRERRR RCAVILSN
          | ||| || : ||: || ||||| || |||||
g518      RLHQAVRFHK MPKTISKMRN NYAVRITPPRAATLHYNRLPL-----
          70          80          90          100

          120          130
m518.pep  GRKKSDPAFVAE SEI
          ||||| |||||
g518      --KKSDPAFVAE SEI
          110

```

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTITACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTTCa GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCACGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 .....AAAAAAT CAGACCCTGC TTTGTGGCA GAGTCTGAAA
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*
```

m518/a518 79.9% identity in 134 aa overlap

	10	20	30	40	50	60
m518.pep	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF					
a518	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF					
	10	20	30	40	50	60
	70	80	90	100	110	119
m518.pep	RRHQA-RFARCRITINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSNG					
a518	RRHQAVRFRKMPTINKRRRNYAVRITPPSXAATRHYNRLPS-----					
	70	80	90	100		
	120	130				
m518.pep	RKKSDPAFVAESEIX					
a518	-KKSDPAFVAESEIX					
		110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatcct gttggcagcc gtcgccgttt tcggcttcaa
51  atcctttgtc gtcaccccc agcaggaagt ccacgttgct gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatatt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actggtgacg
251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgatatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgctgctctc gccctcgatg aagccgccgg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctacggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccgcct tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaaag ttgccgaaat cgggaaacct
901 aattttcggc ggcataaaaa attttcgcca gaagcaaaaa cggccaaata
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPOQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```

777

```

101 SNYIMAITQL AQTTLSRVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANAEAN
251 RQIAAALQTQ SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
301 NFRRHEKFSP EAKTAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

```

m519.seq (partial)
1   ..TCCGTTATCG GCGGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51  AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGTTTCC GCCGCAAGAA
151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA
251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTGCGGAC ATCGGCAGCC
551 TGATTTCTGC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

```

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

```

m519.pep (partial)
1   ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51  ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGSQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLLISAGMK IIDSSKTAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

```

m519/g519

m519.pep                               10      20      30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||
g519      YFQVTDPKLASYGSSNYIMAITQLAQTTLSRVIGRMELDKTFEERDEINSTVVSALDEAA
          90      100     110     120     130     140

m519.pep          40      50      60      70      80      90
GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGSQREAE
|||||
g519      GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLAGSQREAE
          150     160     170     180     190     200

m519.pep          100     110     120     130     140     150
IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAEAIRQIAAALQTQGGADAV
|||||
g519      IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAEANRQIAAALQTQSGADAV
          210     220     230     240     250     260

m519.pep          160     170     180     190     200
NLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK
|||||
g519      NLKIAEQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRHEKFSP EAKTAK
          270     280     290     300     310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

```

a519.seq
1   ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT

```



```

201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCGG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

a519.pep

```

1  MEFFIILLAA VVVFGEKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLSRVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519/a519 99.5% identity in 199 aa overlap

```

m519.pep                               10      20      30
SVIGRMELDKTFEERDEINSTVVAALDEAA
a519      YFQVTDPKLASYGSSNYIMAITQLAQTTLSRVIGRMELDKTFEERDEINSTVVSALDEAA
           90      100     110     120     130     140

m519.pep           40      50      60      70      80      90
GAWGVKVLRYEIKDLVPPQEILRSMQAITAEREKRARIAESEGRKIEQINLASGQREAE
a519      GAWGVKVLRYEIKDLVPPQEILRSMQAITAEREKRARIAESEGRKIEQINLASGQREAE
           150     160     170     180     190     200

m519.pep           100     110     120     130     140     150
IQQSEGEAQAANASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTGGADAV
a519      IQQSEGEAQAANASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTGGADAV
           210     220     230     240     250     260

m519.pep           160     170     180     190     200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
a519      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
           270     280     290     300     310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

g519-1.seq

```

1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAGGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CTTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCGG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA

```

801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVA AFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
 101 GGC GTTCCA TCGCGCCCTG ACGGCGCGTT TGAATATTTT GATTCCCTTT
 151 ATCGACGCGG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTTGTTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
 451 GTGAAGGTTT TGC GTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
 551 GTATCGCCG ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAATGCGG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
 751 CGTCAAATTG CCGCGGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVA AFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEG RKIEQINLASGQREAEIQSEGEAQA AVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEG RKIEQINLASGQREAEIQSEGEAQA AVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	KRARIAESEG RKIEQINLASGQREAEIQSEGEAQA AVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEG RKIEQINLASGQREAEIQSEGEAQA AVNASNAEKIARINRAKGEAESLR					

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATG CCGCCGCCCT TCAAACCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFQKSFV VIPOQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 QREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFQKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              |||||
m519-1      MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAQITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAQITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

```

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```

m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in *E. coli* as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in *E. coli*. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttccttg
301 gcaatgcccg tgccgccgaa caattcgacc aagacatcga cgtctttacg
351 cgcgaaacagt tcgaacggat cttttgacaa gggcgggcga cgggcccatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgccccaa gcggcgggaa atttcctctg cgttgtcccg caacacggga
501 gccgcaccgc cgccgaccgt acctaacgct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDLILFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCCTGCGC TTCTTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCC CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

```

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```

301  GCAATGCCGG  TACCGCCGaa CAATTCGACG  ACGACATCGA  CGTCTTCACG
351  TGCGACCACT  TCGAACGGAT  CTTTGACAAA  GGCTGc .CGG  ACGGGCAGGT
401  TTGTCGGGCT  TTTTCTTCAC  TCAAATCGCA  CACGGCAGAA  ATACGGATTT
451  CGCGCCCCAA  GCGACGGGAA  ATTTCTCCG  CGTTGTCCG  CAACACGGCA
501  GCCGTACCGC  CGCCGACCGT  ACCCAAACCT  AAAAGACCGA  TGTTTACTGG
551  CTTCATTGTG  TCTCCTTGTA  AGCCGACTGA  AATGTAAATA  TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
  1  MPALLSVHXA  NALPFSRISX  RMKLLVPLIM  PAMDILILFAA  KPSRRALMIG
 51  IPPATAASNW  TMTFCFSASG  KISLPYSASS  FLLAVTMCLP  FSMAFNTASL
101  AMPVPPNNST  TTSTSSRATS  SNGSLTKAXR  TGRFVGLFLH  SNRTRQKYGF
151  RAPSDGKFPF  RCXATRQPYR  RRPYPNLKDR  CLLASLCLLV  SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

```

m520/g520

      10      20      30      40      50      60
m520.pep  MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW
          |||||:::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
g520       MPALLSIRANALPFSRISERMKLLVPLIMPAMDILILFAAKPSRTALMIGIPPATAASNW
          10      20      30      40      50      60

      70      80      90     100     110     120
m520.pep  TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS
          |||||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
g520       TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS
          70      80      90     100     110     120

      130     140     150     160     170     180
m520.pep  SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPFRCXATRQPYRRRPYNLKDR
          ||||:|::|:|:||||:|:|||||:|||||:|||||:||||:|:||||:|
g520       SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATRQPHRRRPYLSLKDR
          130     140     150     160     170     180

      190
m520.pep  CLLASLCLLVSRKCKY
          |||||:|||||:|||||
g520       CLLASLCLLVSRKCKY
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
  1  ATGCTGCGC  TTCTTTCAGT  ACATCGG .CA  AACGCGCTGC  CTTTTTCGCG
 51  CATTTCGGAG  AGGATGAAGT  TGCTGGTGCC  GTTAATAATG  CCGGCGATGG
101  ATTTAATCCT  GTTTGCCGCC  AAACCTTCGC  GCAGGGCTTT  GATGATTGGG
151  ATACCGCCCG  CTACTGCCGC  TTCAAATTGG  ACGATGACGT  TTTGTTTTTC
201  CGCCAGCGGG  AAGATTTCTG  TGCCGTATTC  GGCGAGCAGT  TTTTGTGTTG
251  CGGTAACGAT  GTGTTTGCCG  TTTTCAATGG  CTTTCAACAC  CGCATCTTTG
301  GCAATGCCGG  TACCGCCGAA  CAATTCGACG  ACGACATCGA  CGTCTTCACG
351  TGCGACCACT  TCGAACGGAT  CTTTGACAAA  GGCTG .CGG  ACGGGCAGGT
401  TTGTCGGGCT  TTTTCTTCAC  TCAAATCGCA  CACGGCAGAA  ATACGGATTT
451  CGCGCCCCAA  GCGACGGGAA  ATTTCTCCG  CGTTGTCCCG  CAACACGGCA
501  GCCGTACCGC  CGCCGACCGT  ACCCAAACCT  AAAAGACCGA  TGTTTACTGG
551  CTTCATTGTG  TCTCCTTGTA  AGCCGACTGA  AATGTAAATA  TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
  1  MPALLSVHRX  NALPFSRISE  RMKLLVPLIM  PAMDILILFAA  KPSRRALMIG
 51  IPPATAASNW  TMTFCFSASG  KISLPYSASS  FLLAVTMCLP  FSMAFNTASL
101  AMPVPPNNST  TTSTSSRATS  SNGSLTKAXR  TGRFVGLFLH  SNRTRQKYGF

```

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151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCPATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTTGGC GGGCTTTTTT
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSILTAAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTGTC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTC GGGCTTTTTT
351 TTCGCTTAAG TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```

101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
m520-1	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSLRATSSNGSLTKAADGQIWRAFSSLK					
m520-1	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKRREISSALSRTAAAPPPTVPKPKRPMFTGFIVSPCKPTEMX					
m520-1	SHTAEIRISRPKRREISSALSRTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCGTTGC CGTATTCGCG GAGCAGTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTGC GACCAAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTG GGGCTTTTTC
351 TTTCACTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCAAGCGCAC
401 GGGAAATTTT CTCCGCGTTG TCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSF LLAVTMCLPF SMAENTASLA MPVPPNNSTT TSTSSRATSS
101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
m520-1	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
m520-1	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKRREISSALSRTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX					
m520-1	SHTAEIRISRPKRREISSALSRTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

```

1  ATGAAATCAA AACTCCCTT AATCCTAATC AACCTTTCCC TGATTTCAGG
51  CCCATTGGGT GCGAATGCGG CCAAATCTA TACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG

```

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```

151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCTGC CCCAAACTCC
201 CGAACCGGCA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCAGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301 CAAGCACCTG TAAATAACAG CAGACGCTCC ATTCTcgaag caGaattaag
351 cAatgaacgc aaagccctGa ctGaAGCCCA AAAAATGTTA TCACAagcac
401 gtCtGGCAAA AGGCGgcaAC AtcaaCCatc aaaAaatcaa cgcattgtaa
451 AGCAATGTTt tggacAGACA GCAAAATaTC Caagcactgc aaaGAgAATt
501 GGGACGTATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

```

g521n.pep
  1 MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCHSTD
 51 LPIGNYSSER YILPQTPEPA PPSNNGQAV KYKAPVKTVS KPAKSNTPPQ
101 QAPVNSRRS ILEAELSNER KALTEAQKML SQARLAKGGN INHQKINAL*
151 SNVLDROQNI QALQRELGRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1473>:

```

m521.seq
  1 ATGAAATCAA AACTCCTCTT AATCCTAATC AACTTTTCCC TGATTTCAG
 51 CCCATTGGGT GCGAATGCGG CCAAATCTA sACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCAsCAAG CCGTCCAAA GCTGCCACTC AACCGATTTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACGCC
201 CGAACCGGTA TCATCACCGT CAAACGGCGG ACwGGTTGTC AAATATAAAG
251 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCArTAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGCTGGC AAAGGGCGGC AACATCAACC ATCAAGAAAT AAATGCATTA
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATTCAAGCCC TGCAAAGGGA
501 ACTGGGGCGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

```

m521.pep
  1 MKSKLLLLILI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTD
 51 LPIGNYSSER YIPQTPEPV SSPSNNGXVV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNSRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDROQN IQALQRELGR M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

```

m521/g521

      10      20      30      40      50      60
m521.pep  MKSKLLILINFLSLISSPLGANAAXIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g521      MKSKLPLILINLSLISSPLGANAAXIYTCTINGETVYTTKPSKSCHSTDLPPIGNYSSER
          10      20      30      40      50      60

      70      80      90      100     110     120
m521.pep  YIPQTPEPVSSPSNNGGXVVVKYKAPVKTVSKPAKSXTPPPQQAPSNNSRRSILETELSNE
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g521      YILPQTPEPAPSPSNNGGQAVKYKAPVKTVSKPAKSNTPP-QQAPVNSRRSILEAELSNE
          70      80      90      100     110

      130     140     150     160     170
m521.pep  RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX
          ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g521      RKALTEAQKMLSQARLAKGGNINHQKINALXSNVLDROQNIQALQRELGRMX
      120     130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

```

a521.seq
  1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAG

```


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```

51 CCCATTGGGT GCGAATGCGG CCAAAATCTA CACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCCAAA GCTGCCTCTC AACCGATTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACATC
201 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAAG
401 CACGTCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATCCAAGCAC TGCAAAGAGA
501 ATGGGACGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI NFSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCLSTDL
51  PPIGNYSSER YIPPQTSEPT PSPSNGGQAV KYKAPVKTVS KPAKSNTPPP
101 QQAPSNNSRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSVLDRQQN IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

```

              10      20      30      40      50      60
m521.pep      MKSKLLLLILINFSLISSPLGANAAXIXTCTINGETVYTXKPSKSCSTDLPPIGNYSSER
              |||||  |||||  |||||  |||||  |||||  |||||
a521           MKSKLPLILINFSLISSPLGANAAXIYTCTINGETVYTTKPSKSCSTDLPPIGNYSSER
              10      20      30      40      50      60

              70      80      90      100     110     120
m521.pep      YIPPQTPEPVSSPSNGGXVVVKYKAPVKTVSKPAKSXTPPPQQAPSNNNSRRSILETELSNE
              |||||  |||  |||||  :|||  |||||  |||||  |||||  |||||  |||||  |||||
a521           YIPPQTSEPTPSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNNSRRSILETELSNE
              70      80      90      100     110     120

              130     140     150     160     170
m521.pep      RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a521           RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX
              130     140     150     160     170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
51  caaaaaagca aaagccaaaa tccgcacccat ccgcatttgg gcgtgggtca
101 ttttgcggtt gctcgcttca accgccctgc tctcccaatg cgcgatgtcc
151 aaaccgcagg caaaacagaa aattgtcgag tcttgcataa aaaatattcc
201 gtttgctgaa aaatggcaga acgatttgaa agcgcgcggc ttggatgagg
251 acaatacccg tctcgccgtc gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcgggtc
351 acaagaacag cttgacctgc tcggcggcgc aaacgcgttt gaaactcgag
401 acaacaatg tgtcgcggat ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMs
51  KPQAKQKIVE SCMKNIPFAE KWQNDLKARG LDADNTRLAV DYCKMWEQP
101 LDGLSEKQIS SFGKLGAEQ LDLLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51  CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGATTGCGT GCGTGGGTCA
101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAA ACGATTGCGG GGCCCGCGGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

```

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301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWWILALLAL TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEQP
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGKLGAQEQ					
	: :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKCMWEQPLDGLSEKQISSFGKLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	: :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG
 51 CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTTGG GCATGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
 201 GTTTGCCGAA AAATGGCAAA ACGATTGCG GGCCCGCGGT TTAGATTCAA
 251 ACAATACCCG CCTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWWILALLAS TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKCMWEQP
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGKLGAQEQ					
	: :					
a522	SCVKNIPFAEKWQNDLRARGLDSDNNTRLTVDYCKCMWEQPLDRLSEKQISSFGKLGAQEQ					
	70	80	90	100	110	120

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```

                130      140
m522.pep      LDLLGGANAFEARDKQCVADLKSEX
                |||||:|||||
a522          LDLLGGANAFETRDKQCVADLKSEX
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

```

g523.seq
1  atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
51 gacgggaacg gtttatcttt tggttgtagc cgcggctttg gcgggttcgg
101 gacttgcccta cgggctgact ggcagcacgc ctgccgccgt cttgaccgcc
151 gactgctttt ccgcgctggg catttggttc gtacatgcca aaaccgccgt
201 gggaaaagtt gaaacggatt catatcagga tttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt ttttatcgc
301 ggtacgcact ggcaggcgca aaatacgggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcacgtgcc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

```

g523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKYAEILRYT GGNRYEVFVR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

```

m523.seq (partial)
1  ..GCCGTCTTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGTT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GncGCTCTGC TTTCCGCGCT GGGTATTnG
151 TTCGTACACG CCAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTGGAT GCCGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251 ACCGTACGA AGTTTtTAT CGCGTACGc ACTGGCAGGC TCAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACTCGC GCCCTCATTG TCCGAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

```

m523.pep (partial)
1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLG AGQYVEILRH TGGNRYEVFY RGTHWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng) from *N. gonorrhoeae*:

m523/g523

```

                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTXALLSALGIXF
                |||||:|||||
g523          MTVWFVAAVAVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTAALLSALGIWF
                10      20      30      40      50      60

                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLGAGQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
                |||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA
                70      80      90      100     110     120

                120
m523.pep      LIVRKEGNLLIITHP
                |||||:|

```

g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

```
a523.seq
  1 ATGACTGTAT GGTGTGTTGC CGCTGTGTCG GTCTTAATCA TCGAATTATT
 51 GACGGGAACG GTTTATCTTT TGGTGTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

```
a523.pep
  1 MTVWFVAAVA VLIIELLTGT VYLLVVSAAAL AGSGIAYGLT GSTPAAVLTA
 51 ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*
```

m523/a523 94.4% identity in 126 aa overlap

```

              10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF
              |||||
a523           MTVWFVAAVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF
              10      20      30      40      50      60

              60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
              |||||
a523           VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
              70      80      90      100     110     120

              120
m523.pep      LIVRKEGNLLIITHPX
              |||||
a523           LIVRKEGNLLIIAKPX
              130
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

```
g525.seq
  1 atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
 51 agcggcggct gccgaaatgg ttcaaatacga aggcggcagc taccgcccgc
101 tttatctgaa aaaagatacc ggcttgatta aagtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 ccccaaatgg caaaaaggca ggatcggttc caaacaggca gaaccgcgtt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcgaattga aacagccggt taccaatatt tcctggtttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttcgcc acgcagaaaa aacggctcaa acgaaccgcg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaaagca ccgccgaac tactggggtg tttatgatat
551 gcacgggctg a
```

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

```
g525.pep
  1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKKRLKRTT
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

790

```

m525.seq
1  ATGAAGTATG TCCGGTTATT TTWCCTCGGC GCGGCACTCG cCrrCACTCA
51  ArCGGCGGCT GcCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCrC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGc GCCGAAGgCG
301 GgCGAATTAA AACAAACCGGT AACCAATGTT TCCTGGwTTG CCGCCAACgC
351 CTAtTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA A.CGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC
501 TGCACGATGT CGGCA.AAGG CCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

```

m525.pep
1  MKYVRLFXLG AALAXTQXAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNV SWXAANAYCA AQGKRLPTID EWEFAGLASA TQKXRLKTR
151 LQPHYSRLVC RRRTERPARC RXKAARTGA FMICTG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

```

m525/g525

          10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
          |||||  |||||  |||||  |||||  |||||  |||||
g525      MKYVRLFFLTALAGTQAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
          10      20      30      40      50      60

          70      80      90      100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
          |||||  |||||  |||||  |||||  |||||  |||||
g525      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNIWFAANAYCA
          70      80      90      100     110     120

          130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQKXRLKTRRLQPHYSRLVCRRTTERPARCRXKAARTTGA
          |||||  |||||  |||||  |||||  |||||  |||||
g525      AQGKRLPTIDWEFAGLASATQKXRLKTRRLQPHYSRLVCRRTTERPARCQSTARTTGV
          130     140     150     160     170     180

m525.pep  FMICTGX
          |||||
g525      FMICTGX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

```

a525.seq
1  ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51  AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGATTAA AACAAACCGGT AACCAATGTT TCCTGGTTTC CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCCCTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
501 TGCACGATGT CGGCAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGTCTG A

```

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This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
  1 MKFTRLLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
          ||::||: | |||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      MKFTRLLFLCAALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
          10      20      30      40      50      60

      70      80      90     100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVNTVSWXAANAYCA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGDLKQPVNTVSWFAANAYCA
          70      80      90     100     110     120

      130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCQXVARTTGA
          130     140     150     160     170     180

m525.pep  FMICTGX
          |||||
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
  1 ATGAAGTACG TCCGGTTATT TTTCCTCGGC ACGGCACTCG CCGGCACTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGCGCAGC TACCGCCCCG
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGACC GCCGAACTA CTGGGGTGT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAAC TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
  1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKDRPNYGV YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNLFGRFAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
  1 ATGAAGTATG TCCGGTTATT TTTCCTCGGC GCGGCACTCG CCGGCACTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGCGCAGC TACCGCCCCG
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

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```

151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAGGCCCT
501 GCACGATGTC GGCAGAGGCC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```

1  MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHWK NGSRSYAPKA
101 GELKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKGLHDV GKGRPNYWGV YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/g525-1 97.6% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLGAALAGTQAAA	AEMVQIEGGSYRPLYLKKDT	GLIKVKPFKLDKYPVTNAEF			
g525-1	MKYVRLFFLGTALAGTQAAA	AEMVQIEGGSYRPLYLKKDT	GLIKVKPFKLDKYPVTNAEF			
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQWQKGRIGSKQA	EPAYLKHHWMKNGSRSYAPK	AGELKQPVNTVSWFAANAYCA			
g525-1	AEFVNSHPQWQKGRIGSKQA	EPAYLKHHWMKNGSRSYAPK	AGELKQPVNTISWFAANAYCA			
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTIDWEFAGLASAT	QKNGSNEPGYNRTILDWYAD	GGRKGLHDVGKGRPNYWGV			
g525-1	AQGKRLPTIDWEFAGLASAT	QKNGSNEPGYNRTILDWYAD	GGRKGLHDVGKDRPNYWGV			
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWETEDFNSSLLS	SGNANAQMFCSGASIGSSDS	SNYAAFLRYGIRTSLQSKYV			
g525-1	YDMHGLIEWETEDFNSSLLS	SGNANAQMFCSGASVGS	SDSNYAAFLRYGIRTSLQSKYV			
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLGFRCTSRX					
g525-1	LHNLGFRCSRX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```

1  ATGAAGTTTA CCCGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51  AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAAC TG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA CTGGTATGCG GATGGCGACC GGAAGACCT
501 GCACGATGTC GGCAGAGGTC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

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This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLFLFC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGDRKDLHDV GKGRPNYWGV YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

```

              10      20      30      40      50      60
m525-1.pep  MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
a525-1       MKFTRLFLFLCAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              10      20      30      40      50      60

              70      80      90     100     110     120
m525-1.pep  AEFVNSHPQWQKGRIGSKQAEPAAYLKHWMKNGSRSYAPKAGELKQPVTNVSWFAANAYCA
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
a525-1       AEFVNSHPQWQKGRIGSKQAEPAAYLKHWMKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
              70      80      90     100     110     120

              130     140     150     160     170     180
m525-1.pep  AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVVGKGRPNYWGV
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
a525-1       AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVVGKGRPNYWGV
              130     140     150     160     170     180

              190     200     210     220     230     240
m525-1.pep  YDMHGLIEWETEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
a525-1       YDMHGLIEWETEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV
              190     200     210     220     230     240

              250
m525-1.pep  LHNLGFRCTSRX
              |||::|||::|||
a525-1       LHNLGFRCTSRX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atggtttttac cagtctcctt ttttcagcct gtccagttgg cggcgggtcgc
51  gcttgggtcgg tctgccgtcg ggatgggagg aagtgatgag gctgaattgg
101 tcgagctggtt tgcactcttc cctcaatgct gccgttttcg cgtcttcttc
151 atacagaagc cgcgcctcgg gtgccgggag gcgttggtgg ttcaaacttc
201 taaccttgat tttatgggga aggggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tggttttact gtttttgact ttcgagccgt ttacttgaac
301 cctacccagt tcgatatgct tttgcgcaag ggaacgggtc ttgaaaaaac
351 gtgccgcgcc aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatac gattttggtt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLPSVFFQP VOLAAVALGR SAVGMGGSDA AELVELFALF PQCCFRFRVFF
51  IQKPRLGCRALVVQTFNLD FMKGIERQV DNIADVGFV VDFDRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
51  GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTWTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT

```


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201 TAACCKTGAT TTTATAGGGA AGGG.AATTk AgCkTCaGty GrTwATaTCG
 251 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA CTTGAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGTTC GAAATAATTG AATTGTGTTT GAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

m527.pep
 1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLV
 51 IQKPRXGCRA ALVVQTFNND FIGKXNXASV XXIADVYGFT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRXRVLV	FIQKPRXGCRA
g527	MVLPSVFFQP	VQLAAVALGR	SAVGMGGSDA	AELVELFALF	PQCCRFRVFF	FIQKPRLGCR
	10	20	30	40	50	60
	70	80	90	100	110	120
m527.pep	ALVVQTFNND	FIGKXNXASV	XXIADVYGFT	VFDLRAVYLN	PTQFDVLLRK	GTGLEKTCRP
g527	ALVVQTFNLD	FMGKGIERQV	NDIADVYGFT	VFDLRAVYLN	PTQFDMLLRK	GTGLEKTCRP
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGR	IVLVFHTILF	EIIEFVSSLA			
g527	KPFVQPHGGR	IVLVFHTILF	EIIEFVSSLA			
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

a527.seq
 1 ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
 51 GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
 101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC
 151 ATACAGAAGC CGCGCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
 201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
 251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA CTTGAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGTTC GAAATAATTG AATTGTGTTT GAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

a527.pep
 1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLV
 51 IQKPRLGCR ALVVQTFNLD FIGKGIERQV DNIADVYGFT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRXRVLV	FIQKPRXGCRA
a527	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRFRVLV	FIQKPRLGCR
	10	20	30	40	50	60

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	70	80	90	100	110	120
m527.pep	ALVVQTFNXXDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
a527	ALVVQTFNLDFIGKGIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaaattc gggtaataaa atatacggca acggctgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggtg gtatgagtgt ttgtccttgt
101 ccggctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggccgagaga gtccgctgtc tttagaggac tacgagatac cgctttcaga
201 cgcaaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatcct
251 acttttatag gaaaataggg aagtttgaag cctgcgggtt ggattggcgt
301 acgctgacg gcaaaccttt ggttgagagg ttcaaacagg aaggtttcga
351 ctgtttgtaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGTA
351 CTGCTTGGAA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
g528	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPLSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
g528	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE					
	70	80	90	100	110	120

796

```

m528.pep      K
               |
g528           KQGLRRNGLSERVRW

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

```

a528.seq
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGCAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

```

a528.pep
1   MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW*

```

m528/a528 95.0% identity in 121 aa overlap

```

               10      20      30      40      50      60
m528.pep      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
               |||||
a528           MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLED
               10      20      30      40      50      60

               70      80      90      100     110     120
m528.pep      YEIPLSDGNSSVRANEYESAQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE
               |||||
a528           YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLK
               70      80      90      100     110     120

m528.pep      K
               |
a528           KQGLRRNGLSERVRWX
               130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

```

g528-1.seq
1   ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGCAGA GTCCTCGTGC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAAATCTT
251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GGTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGGA AAGCAGGGGT TCGCGCGCAA CGGCCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

```

g528-1.pep
1   MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

```

m528-1.seq
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

```

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```

51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GGCGGCCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTACAGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGAA AAGCAGGGGT TCGGCGCAA CCGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51 GGESPPSLGD YEIPLSDGNNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

              10      20      30      40      50      60
g528-1.pep  MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
              ||||:||||| |||:||||| |||||:||||| |||||:||||| |||||:||||| |||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
              10      20      30      40      50      60

              70      80      90      100     110     120
g528-1.pep  YEIPLSDGNNRSVRANEYESAQKSIFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
              |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
m528-1      YEIPLSDGNNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
              70      80      90      100     110     120

              130
g528-1.pep  KQGLRRNGLSERVRWX
              |||||:|||||
m528-1      KQGLRRNGLSERVRWX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1 ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GGCGGCCGAGA GTCCGCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTACAGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTAAA AAGCAGGGGT TCGGCGCAA CCGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

              10      20      30      40      50      60
a528-1.pep  MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
              |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
              10      20      30      40      50      60

              70      80      90      100     110     120
a528-1.pep  YEIPLSDGNNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
              |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
m528-1      YEIPLSDGNNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
              70      80      90      100     110     120

              130
a528-1.pep  KQGLRRNGLSERVRWX
              |||||:|||||
m528-1      KQGLRRNGLSERVRWX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

```
g529.seq (partial)
  1 atgacccata tcaaacccgt cattgccgcg ctgcactca tgggcttgc
 51 cgcctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggtcgcaccg cctgatcaaa ctggaagtcc cgcctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc gggtcgggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccagcggatg
251 ccggaagtat tgaaaagcgt caaaggcgct cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgctgt tgacggcaaa tcccccgccg aaatctccgc
351 cgctttctg.
```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

```
g529.pep (partial)
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
 51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAF..
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

```
m529.seq
  1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
 51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTTCGACCG CCTGATCAAA CTTGAAGTCC CACCTGATTG GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCCGGCG CCGTCCGCGC
201 CAGCGATTTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCTGA CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451 CCCCAGACA GCTTGCCTCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GGCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGCGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAAGC AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGT GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTGCGCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGCG AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TCGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

```
m529.pep
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
 51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAELVLSV KGVRLERDGS
101 QRWLVDGKS PAEIWPLLKA FWQENGFDIK SEEPALIGME TEWAENRAKI
151 PQDSLRLRLFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDQTV WQSPSPDPNL EAAFLTRFMQ YLGVDGQQA NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFVQ
301 KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELRL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

          10          20          30          40          50          60
g529.pep  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA
```

```
a529.seq
1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAGGCC
101 GGTGCAACCG CCGTATCAAA CTCGAAGTCC CACCTGATTT GAACAAACCC
151 GACCAAGGCA ACCTGTACCG CCTGCCTGCC GGTTCGGGCG CGCTCCGCGC
201 CAGCGATTTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAGGCGTC AAAGGTGTCT GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTGCA CGGCAAGTCT CATGCGCGAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCGGAAGAAC
401 CCGGCATCGG ACAAAATGGAA ACCGAGTGGG CGGAAAACCG TGCCAAAATC
451 CCCCAAGACA GCTTGCGCCG CCTATTCGAC ACAGTCGGTT TGGGCGGCAT
501 CTACTCCACC GGCAGCGCGC ACAAAATCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAAGCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTTGGGCG
701 TTGACGACA GCAGGCGGAA AACGCATCGG CAAAAAAACC TACCCTTCCC
751 GCCGCCAAGC AAATGGCGCG TATCGAAGCG AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAATGGC GGCACACCGC GACTCGCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCTTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAC CCGGCCTGTT
951 CAAACGCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCCGAG CATGTGCCCA ACGGCTCGCG CATCGTCTTG
1051 CTCACAAAGC ACGGCAGCGC AATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TGCGTTAA
```

a529.pep

1	<u>MTHIKPVIAA</u>	<u>LALIGLAACS</u>	GSKTEQPKLD	YQSRSHRLIK	LEVPPDLNNP
51	DQGNLYRLPA	GSQAVRASDL	EKRRTPAVQQ	PADAEVLKSV	KGVRLEDRGS
101	QRWLVDGKS	HAEIWPLLKA	FWQENGFDIK	SEEPAIQMSV	TWAEARNRAKI
151	PQDSLRLRFD	TVGLGGIYST	GERDKFIVRI	EQGKNGVSDI	FFAHKAMKEV
201	YGGKDKDTTV	WQPSPSDPNL	EAAFLTRFMQ	YLGVDGQQAE	NASAKKPTLP
251	AANEMARIEG	KSLIVFGDYG	RNWRRTALAL	DRIGLTVVGQ	NTERHAFLVQ
301	KAPNESNAVY	EQKPGLFKRL	LGKGKAKEPA	EQFELIVYAE	PVANGSRIVL
351	LNKDGSAAYG	KDASALLGKL	HSEL*		

	10	20	30	40	50	60
m529.pep	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA					
a529	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m529.pep	GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDGKSPAEIWPLLKA					
a529	GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDGKSHAEIWPLLKA					
	70	80	90	100	110	120
	130	140	150	160	170	180

800

```

m529.pep  FWQENGFDIKSEEP AIGQMETEWAENRAKIPQDSLRLRLFDKVGLGGIYSTGERDKFIVRI
a529      FWQENGFDIKSEEP AIGQMETEWAENRAKIPQDSLRLRLFDTVGLGGIYSTGERDKFIVRI
          130      140      150      160      170      180

          190      200      210      220      230      240
m529.pep  EQGKNGVSDIFFAHKAMKEVYGGKDKD TTVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
a529      EQGKNGVSDIFFAHKAMKEVYGGKDKD TTVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
          190      200      210      220      230      240

          250      260      270      280      290      300
m529.pep  NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTVLALDRIGLTVVGQNTERHAFLVQ
a529      NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTALALDRIGLTVVGQNTERHAFLVQ
          250      260      270      280      290      300

          310      320      330      340      350      360
m529.pep  KAPNESNAVTEQKPGLFKRLLGKGAEKPAEQPELIVYAE PVANGSRIVLLNKDGSAYAG
a529      KAPNESNAVTEQKPGLFKRLLGKGAEKPAEQPELIVYAE PVANGSRIVLLNKDGSAYAG
          310      320      330      340      350      360

          370
m529.pep  KDASALLGKLHSELRX
a529      KDASALLGKLHSELRX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga ggcgcgcaat gacgggtttg atatgggtca tcgtgtcatc
51 ctgtgtgatg gatattaaag tgtttgcgat gttatgccgt ccgaacgggt
101 cagacggcat ggctatat taaagttgtcc tgaggctttc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgcacg
201 tgcggtccgc atccgccaa ggcggatacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgcgtaaat cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCVM DIKVFVMLCR PNGSDGMAIF KVVLR LSGRR
51  GLLPVRLPSA ERAAGARAVR IRPRRIPPIS VRRDWVRRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  wTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGT CATC
51  sTGtGTGATG GATATTAAAG TGtYtGTTGC GwTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGAckTTTGC wTGtCCGTTT yCCGTcAGCG GAACGAGCGG CAGGCGGACG
201 TGCGGTTCGC ATCTGCCCAg GCGGATACC GCCATTTCG GTGCGGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CCGTcGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCVM DIKVXVAXCR PNGSDGMXIF KVVLR LSGRR
51  GLLXVRFPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

```

m530/g530

m530.pep  XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPNGSDGMXIFKVVLR LSGRRGLLXVRFPSA 60
          |||

```

```
a530.seq
1  ATGAGTGC GA GCGCGCAAT GACGGGTTTG ATATGGGTCA TCGTGTCATC
51  CTGTGTGATG GATATTAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTTTTGC CTGTCCGCC TCCGTACAGC GAACGAGACCG CAGGCGGACG
201 TGCGGTTCGC ATCTGCCACC GCGCGATACC GCCCATTCGG GTGCGGCGGG
251 GCTGGGTTGC CAGAACAATG TGTCGTAAAT CGGAATCAGC GGTGCGTTGA
```

a530.pep

1	MSASAAMTGL	IWVIVSSCVM	DIKFVVALCR	PNGSDGMAIF	KVVLRLSGRR
51	GLLPVRLPSA	ERAAGGRAVR	ICPGRIIPIS	VRRGVVRRTW	CRKSESAGR*

	10	20	30	40	50	60
m530.pep	XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA					
a530	MSASAAMTGLIWVIVSSCVMDIKVFVALCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA					
	10	20	30	40	50	60
	70	80	90	100		
m530.pep	ERAAGGRAVRICPGRIPPISVRRGWVRTWCRKSESVGRX					
a530	ERAAGGRAVRICPGRIPPISVRRGWVRTWCRKSESAGR					
	70	80	90	100		

g531.seq

```
1  ATGACCGCCC TACTCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
51  GGCAGGCATC GTCTATCCCG CCCTGCCCGG CTTGGCATTG ATGTTTGCCG
101 GAACATGGCT GCTTGCCCTAT GCCGGCGGCT ATCAAATCTA CGGCGCAGGC
151 ATCTTGTTGA CGGTTCGGACT CATCAGCCTT GGCGGCATAC TGGCGGACTA
201 TATGGCAGGC ATGTTGGGGG TAAAATACAC TGGGGCAGGC AAACCTGCCG
251 TCCGAGGTGC ATTGGCCGGC AGCATCATCG GCATATTTTT CTCCCTTCCC
301 GGAATAATC TCGGCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
351 TCGGGCGCAAT ATGCTTCAGG CAGGTAAGC GGCGCTGGGT ACGCTGTTGG
401 GGCTTGTCGT CGGCACGGCG TTCAAAATCG GCTGCGCCGT ATCCATCTTG
451 TTTATCCTGT TGGTGAAATA CATCGCATAC CTGTTTTTAA
```

g531.pep

1	<u>MTALLVILAL</u>	<u>ALIAVGTAGI</u>	<u>VYPALPGLAL</u>	<u>MFAGTWLLAY</u>	AGGYQIYGAG
51	<u>ILWTVGLISL</u>	<u>GGILADYMag</u>	<u>MLGVKYTgAG</u>	<u>KLAVRGALAG</u>	<u>SIIGIFFSLP</u>
101	<u>GLILGPFIGA</u>	<u>AAGELIDRRN</u>	<u>MLQAGKAGLG</u>	<u>TLLGLVVGTa</u>	<u>FKIGCAVSIL</u>
151	<u>FILLVKYIAY</u>	LF			

```
m531.seq
  1  ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
 51  GGCGGGCATC GTTTaCCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
101  GAACATGGCT GCTTGCCTAT GCCGGCGGCT ACCAAATCTA CGGCGCGGGC
151  GTTTTGTGGA CGGTCGGACT CATCAGCCTT GCCGGCATACT TGGCGGACTA
201  TGTGGCAGCG ATATGGGGGA CAAAATATAC CGGAGCGGGC AAGCTCGCCG
251  TTCGCGGCGC ATTGGCCGGC AGCATCATCG GCATATTTTT TCTCCCTCCC
301  GGAATAATAC TCGGTCCCTT TATCGGCGCG GCGGCAGGCG CACTGATCGA
```


m531.pep

1 MTVLTVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGTYKTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

Homology with a predicted ORF from *N. gonorrhoeae*

m531/g531

		10	20	30	40	50	60							
m531.pep		MTVLT	VILAL	ALIAV	GTAGI	VYPAL	PGLAL	MFAGT	WLLAY	AGGYQ	IYGAG	VLWTV	GLISL	
		:										:		
g531		MTALL	VILAL	ALIAV	GTAGI	VYPAL	PGLAL	MFAGT	WLLAY	AGGYQ	IYGAG	ILWTV	GLISL	
			10	20	30	40	50	60						
		70	80	90	100	110	120							
m531.pep		AGILAD	YVAGI	WGTYT	GAGKL	AVRGAL	AGSI	IIGIFF	SLPGL	ILGPF	IGAA	AGELI	ERRN	
		:		:	:	:							:	
g531		GGILAD	YMGML	GVKYT	GAGKL	AVRGAL	AGSI	IIGIFF	SLPGL	ILGPF	IGAA	AGELI	DRRN	
			70	80	90	100	110	120						
		130	140	150	160									
m531.pep		MLQAG	KAGLG	TLLGL	VVGTA	FKIGCA	VSILF	ILLVK	YIAYL	F				
g531		MLQAG	KAGLG	TLLGL	VVGTA	FKIGCA	VSILF	ILLVK	YIAYL	F				
			130	140	150	160								

a531.seq

1	ATGACCGCCT	TGCTCGTCAT	CCTCGCCCTC	GCCCTGATAG	CCGCCGGTAC
51	GGCGGGCATC	GTTTACCCCG	CCCTGCCCGG	ATTGGCATTG	ATGTTTGCCG
101	GAACCTGGCT	GCTCGCCTAC	TCCGGCGGGT	ACCAATCTA	CGGCCGGGGC
151	GTTTTGTGGA	CGGTCCGACT	CATCAGCCTT	CGCCGCATAC	TGGCGGACTA
201	TGTGGCAGGC	ATATGGGGGA	CAAAATATAC	CGGAGCGGGC	AAGTCGCCG
251	TTCGCGGCGC	ATTGGCCGGC	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGACTAATAC	TCGGTCCCTT	TATCGGCGCG	GCGGAGGCG	AACTGATCGA
351	ACGGCGCAAT	ATGCTTCAGG	CAGGTAAAGC	GGGCTGGGT	ACGCTGTTGG
401	GGCTTATCGT	CGGTACGGCG	TTCAAAATCG	GCTGCGCCGT	ATCCATCTTG
451	TTTATCTGTT	TGGTGAATA	CATCGCCTAC	CTGTTTTTAA	

a531.pep

1 MTALLVILAL ALIAAGTAGI VYPALPGLAL MFAGTWLLAY SGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGTTYGTAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGELIERRN MLQAGKAGLG TLLGLIVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

	10	20	30	40	50	60
m531.pep	MTVLT	VILALALIA	VG	TAGIVYPAL	PGLALMFAG	TWLLAYAGGYQIYGAGVLWTVGLISL
	:	:	:	:	:	:
a531	MTALL	VILALALIA	AG	TAGIVYPAL	PGLALMFAG	TWLLAYSGGYQIYGAGVLWTVGLISL
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADY	VAGIWG	TKYTGAGK	LAVRGALAGS	IIGIFFSLPGLIL	GPFIGAAAGELIERRN

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```

a531      |||||
          AGILADYVAGIWGTYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERRN
          70      80      90      100      110      120

          130      140      150      160
m531.pep  MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          |||||
a531      MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acaggcggat tcgectgatt tgggtgtacgg
51  ttggaagac aggccgccgt tcggaatgc gctcttgagc gcggttacc
101 atcttttggc gattttcgtg ccgatgatta cgcgcgcgct gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgctgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggccaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTCG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CCGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTTCGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGCTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGCGATT ACCGATTTCG GCGGCGGGCT CGGCGCGAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAAGAA TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCGG CTGTTGCGCA TGAGCGGCAT
651 TGCGGTGCGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCGCGTACCG
751 TTTAAATACG GTTTTGCTTT CGACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCTTG
901 CGCGGCGGCG TGTGCTGCTG CCGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTCAGA
1001 TGACCGCGCT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCCGTG TTGGGCGGCG CGATGGTTT GATGTTTCGGC TTAATTGCGA
1151 TTGCGGCGCT GCGGATTTTG GTCAGTCACG GCATCCGCAG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CCGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACTGCT CCGTCTTGTT CCAAACTCT ATTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVF GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```

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201 VLVFNCKMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLPPV
 251 FKYGFAPDWH AFIVAGAIPL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
 301 RGGLADGLV SVIATLGLS PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
 451 EAAVKFDTDH LEH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

g532/m532

	10	20	30	40	50	60
g532.pep	MAETMKKQADSPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVGGALELPVEMT					
	:	:				
m532	MSGQLGKGADAPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVGGALELPVEMT					
	10	20	30	40	50	60

	70	80	90	100	110
g532.pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLS IQRYRHDCARRGDERGRFEX				
m532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLS IQSVNFSFVTVMIALGAGMKEGGLTKDAM				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

a532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAGGAT AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTCG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CGGTGAATTT CTCGTTTCGT
301 ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT TTCGGCGTGG CTCTGCGCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATCGGCTTGA GTTTGGTACA
501 CGTCGGTATT ACCGATTTCG GCGGCGGCTT CGGCGCAAAG GCGGACGGCA
551 CGTTCGGCTC GATGAAAAAC TTGGGGCTGG CATCGCTGGT GCTGCTGATT
601 GTGCTGGTGT TCAATTGCAT GAAAAACCG CTGCTGCGGA TGAGCGGCAT
651 TGCGGTCGGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC GGCACTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTTAAATATG GTTTTGCTTT TGACTGGCAC GCATTTATTG TGGCGGGTGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTG ACGGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCTTG
901 CGCGGCGGCG TGTTGGCGGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGACA AAACAACGGC GTGATTACAG
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGA CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCCGC TTGATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
1201 GTAATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTGCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACCTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSMAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV

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805

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
251 FKYGFAFDWH AFIVAGAI FL LSVFEAVGDL TATAMVSDQP IEGEETYKRL
301 RGGVLADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

m532.pep	MSGQLGKGADAPDLVYGLED	RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
a532	MSGQLGKGADAPDLVYGLED	RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
m532.pep	AYLVSMAMVASGVGYTLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM	
a532	AYLVSMAMVASGVGYTLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM	
m532.pep	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK	
a532	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK	
m532.pep	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLMSGIAVGLIAGYIVALFLGKVDFSALQ	
a532	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLMSGIAVGLIAGYIVALFLGKVDFSALQ	
m532.pep	NLPLVTLVPVFFKYGFAFDWHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEETYKRL	
a532	NLPLVTLVPVFFKYGFAFDWHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEETYKRL	
m532.pep	RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASRHVGKYIAVILVLLGLFPVVG	
a532	RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASRHVGKYIAVILVLLGLFPVVG	
m532.pep	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF	
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF	
m532.pep	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX	
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

```

g535.seq
1  atgccctttc ccgttttcag acaantattt gcttngtcct tgctacggtt
51  ttttgccgta ggteggatc tcgaatccga catttccaac agcgggtttt
101 cggaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatttaca tcgcttccaa ttctcgaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagtga tggtcagtcg ggcggattcg
251 ctttgtctg cggcacgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttcgggc tgtttgaagt

```

806

```

351 catcgatgat tttgtcccgt tgtacggtgg tttggcgcgt gttgccgtag
401 ctgtcgaagg cgggtttttt gacggacagg tagtgcaata cttctggcgg
451 gatttcttcg acgaagcggg atgcatgcc gaattgggtt tgtccgtgca
501 gcatgcgttg ctgtgccatg gtgatgtaga ggcgtttgcg ggcgcgggtg
551 atggcgacgt acatgaggcg gcgtttcttct tcgaggccgc cgcgctcggc
601 aaggctcatt tcgctgggga aacgcccctc ttccataccg gtgaggaaga
651 cggcggttga ttccaagcct ttggcggcgt ggacggtcat cagttggacg
701 gcttttttcg ctgcccctgc ttggttttcg ccggattcga gggcggcgtt
751 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

```

g535.pep
  1 MPFPVFRQXF AXSLLRFFAV GRILESDISN SGFSETINAS NVFFVGYEYP
 51 ACISNLHRFQ FRKLGIOFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
101 DVLSDAEACV GLRLFEVIDD FVPLYGGLAR VAVAVEGGFF DGQVVQYFWR
151 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
201 KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
251 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

```

m535.seq
  1 atGCCCTTtC CCGTTTTcAG ACGGCCTTTT GCTTTGTCCT TACTtACGTT
 51 TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTTCCAAC AGCGGTGTTT
101 CGGAAACAAT AGACGCGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
151 TACATTTCAA ATTTACATCT CTCCAATTT CGCAAACCTG GTGTCCAAC
201 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTCCGCT
251 TTATCTGCGG CATCGATAAT CACGCCGGTG CCGAATTTGG CGTGCCGGAC
301 GTTTTGTCG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GGCGCGTGTT GCCGTAAC
401 TCGTAGGCAG GCTTTTGGAC GGACAGGTAG TGCAATACTT CCGGTGGGAT
451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
501 TGCGTTGTTG CGCCATGGTG ATGTAGAGGC GTTTGCGGGC GCGGGTGATG
551 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
601 GCTCATTTTC CTGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
701 TTTTCGCCTG CGCCTGCCTG GTTTTCACCG GATTCGAGGG CGGCATTGCT
751 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

```

m535.pep
  1 MPFPVFRFPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
 51 YISNLHLFPQ RKLGVQLFHA LFAEIDGQSG GFAFICGIDN HAGAEFGVAD
101 VLSDTETCVG LGLFVVDDF IFGCGGLARV AVTVVGRFLD GQVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEENGEGGV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

```

m535/g535
      10      20      30      40      50      59
m535.pep MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ
|||||: || ||| ||||: || ||||| ||||: ||||| ||||| ||||| ||
g535      MPFPVFRQXFAXSLLRFFAVGRILESDISNSGFSETINASNVFFVGYEYPACISNLHRFQ
      10      20      30      40      50      60

      60      70      80      90     100     110     119
m535.pep FRKLGVLQFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVDD
|||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
g535      FRKLGIOFFHALFAEVDGQSGGFAFVCGIDNHAGAEFGVTDVLSDAEACVGLRLFEVIDD
      70      80      90     100     110     120

```



	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	: : : :						
g535	FVPLYGGLARVAVAVEGGFFDQGVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACAC						
	: : : : : :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVEFQAFGGVDGHELDGFFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIAXEGENGE			GGGVV			
	: :			: :			
g535	LVFAGFEGGVAQEGEDG			EGGIV			
	250	260					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

a535.seq	(partial)					
1	TTCAGACGGC	CTTTTGCCTT	GTCCTTGCTA	CAGTTTTTTG	CCATAGGTCG	
51	GATTCTCGAA	TCCGACATT	CCAACAGCGG	TTTTTCGGAA	ACGATAGACG	
101	CGTCAAATAT	TTTTGTCCGA	TACGAGTATC	CAGCCTGCAT	TTCAAATTTA	
151	CATCGCTTCC	AATTTTCGCA	ACTTGGTGTC	CAACTCTTTC	ACGCCCTGTT	
201	TGCCGAAATT	GATGGTCAGT	CGGGCGGATT	CGCCTTTATC	TGCGGCATCG	
251	ATAATCAACG	CGGTGCCGAA	TTTGGCGTGG	CGGACGTTTT	GTCCGATACG	
301	GAACCTCGC	TAGGTTTTGG	GCTGTTTGTA	GTGTCGATG	ATTTGTCTTT	
351	TGGGCGCGGC	GGTTTGCGCG	GTGTTGCCAT	AGCGGTCGTA	GGCGGGTTTT	
401	TTGACGGACA	GGTAGTGCAA	TACTTCGGGG	GGGATTTCTT	CGACGAAGCG	
451	GGAGACGATG	CCGAATTGGG	TTTGTCCGTG	CAGCATTCGT	TGTTTGCGCC	
501	TGGTGATGTA	GAGGCGTTTT	CGGGCGCGGG	TGATGGCGAC	GTACATCAGG	
551	CGGCGTTCTT	CTTCGAGGCC	GCCGCGTTCG	GCAAGGCTCA	TTTCGCTGGG	
601	GAAGCGGCCT	TCTTCCATGC	CGGTGAGGAA	TACGGCGTTA	AATTCCAAGC	
651	CTTTGGCGGG	GTGCGACGGT	ATGAGTTGTA	CGGCTTTTTT	GCCCCGCGCT	
701	GCTTTGGTTTT	CGCCGAGATC	GAGAGCAGCA	TTGCTTAGGA	AAGCGAGGAT	
751	GGGGAAGGCG	GGGTCGTCTG	A			

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

a535.pep (partial)

1	FRRPFALSL	QFFAIGRILE	SDISNSGFSE	TIDASNIFVG	YEYPACISNL
51	HRFPQFRKLGV	QLFHALFAEI	DGQSGGFAFI	CGIDNHAGAE	FGVADVLSDT
101	ETCVGLGLFV	VDDFVFGRG	GLARVAIAV	GGFFDGQVVQ	YFGRDFFDEA
151	GDDAELGLSV	QHALLRHGDV	EAFAGAGDGD	VHQAATFFEA	AAFGKAHFAG
201	EAAFFHAGEE	YGVKFQAFGG	VHGHELYGFF	ARALVFVAGF	ESSIA*ESED
251	GEGGVV*				

m535/a535 88.7% identity in 256 aa overlap

```

      10      20      30      40      50      60
m535.pep  MPFPVFRPPFALSLLTFFAVSQILVSDISNSGVSETIDASNVEFVGYEYPTYISNLHLFQF
          |||||::||| |||||:|||||:|||||:|||||
a535      FRPPFALSLLQFFAIGRILESDISNSGFSETIDASNIFVGYEYPACISNLHRFQF
          10      20      30      40      50

      70      80      90      100     110     120
m535.pep  RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF
          |||||:|||||:|||||:|||||:|||||:|||||
a535      RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF
          60      70      80      90      100     110

      130     140     150     160     170     180
m535.pep  IFGCGGLARVAVTVVGRLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG
          :|||:|||||:|||||:|||||:|||||:|||||
a535      VFGRGGLARVAIAVVGGFDFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG
          120     130     140     150     160     170

```

808

	190	200	210	220	230	240
m535.pep	AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACACL					
a535	AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL					
	180	190	200	210	220	230
	250	260				
m535.pep	VFTGFEGGIXEGENEGGVVX					
a535	VFAGFESSIAXESEDGEGGVVX					
	240	250				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

g537.seq

```

1  atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51  tttctaccat acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
101 cgtccgcacc gcaaatcagg gacggcggcg atgcgctgca ctacctcaac
151 cgcatccgca cacaaatcgg tttgcacgcg ctggcacacg cgccggtttt
201 ggaaaattcc gcccgcaggc acgcacgcta tctcacgctc aatcccgaag
251 acggacacgg cgaacaccat cccgacaatc cgcactacac cgcacaaaag
301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgccga atcgtccgac agcgacatcc
401 gcacgcagca acgccaagtg gacgctttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca taccgacgaa gcaggtgcgg catttggtgcg
501 cgaaaacggc aaaaccgtcc tcgtattcaa tcagggcaac ggcagcttcg
551 agcgcgcctg tgcaaaagga aggcggcagc cggaagcagg acggaaatat
601 taccgcaacg cttgccacaa cggcgcgcc gtttatgctg acgaagccat
651 gcccgtaacg gaattgcttt ataccgccta tccggttggc ggcggcgcg
701 tgctttattt ttacggggaa cgtcccgaac ccgtgccgga atatgaaatc
751 acaggaatc ctgccagcat tgatttttcc gaggcggcag gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgccccgtca
851 gggttttaac cgccggcaac gaccctaacg gcaggtgac cgcgcaccaa
901 ttgcgccttt tcccgctcaa acccttgga taccggcacg tttatacggc
951 ggtattcgac tatgtccgca acggacggca cgcgaggcgg aaatggcagt
1001 ttagaaccgg aaaaccgat tacccttatt ttgaggtaaa cggcggcgag
1051 acacttgctg ttagaaaagg cgaaaaatat ttcattccact ggcgcggacg
1101 ctggtgtctg gaagcgtgta cccgttatcc ctaccggcgg cagttcggga
1151 acagcctgtc catactccgg cacgaagcgg gcggcattgt cttcagcgtc
1201 agcggaatgg cgggaagcgg catcaggctt actccggaag acagcccgga
1251 acgcggtgta accctttatt tgcaggattg a

```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

```

1  MKSLFIWLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
51  RIRTQIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DALMSAIYHR
151 LSLDRHTDE AGAAFVRENG KTVLVFNQGN GSFERACAKG RRQPEAGRKY
201 YRNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDVPPEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPVRVLTAGN DPNGRLLTAHQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERGV TLYLQD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

m537.seq (partial)

```

1  ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCAGGCGT
51  TTTCTACCAT ACCCAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGTTTTT
201 GGAAACTCC GCCCGCAGC ACGCAAGCTA CCTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG

```

```

301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
451 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

```

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

```

m537.pep (partial)
  1 MKSLFIRLLLL LGSAAGVFIYH TXQXSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
151 LSLDRHTDE SGAA...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

```

m537/g537

          10      20      30      40      50      60
m537.pep  MKSLFIRLLLLGSAAGVFIYHTQXQSLPAGELVYPSAPQIRDGGDALHYLNRIIRAQIGLHK
          |||||  |||||  |||||  |||||  |||||  |||||
g537       MKSLFIWLLLLGSAAGVFIYHTQNQSLPAGELVYPSAPQIRDGGDALHYLNRIQTIGLHA
          10      20      30      40      50      60

          70      80      90     100     110     120
m537.pep  LAHAPVLENSARRHASYLTLNPEDGHGEHHDPNPHYTAQKLTERTRLAGYLYNGVHENIS
          |||||  |||||  |||||  |||||  |||||  |||||
g537       LAHAPVLENSARRHARYLTLNPEDGHGEHHDPNPHYTAQKLTERTRLAGYLYNGVHENIS
          70      80      90     100     110     120

          130     140     150     160
m537.pep  TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA
          |||||  |||||  |||||  |||||
g537       TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN
          130     140     150     160     170     180

g537       GSFERACAKGRRQPEAGRKYRNNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE
          190     200     210     220     230     240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

```

a537.seq
  1 ATGAAATCCC TTTTATTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
 51 TTTCTATCAT ACCCAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGCG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT
201 GGAAATTCG GCGCCGAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGTCG
501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG
551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT
651 GCGCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
751 ACGGGCAATC CTGCCAGCAT TGATTTTTTC GAGGCGGCAG GCAAAATTAC
801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCCGTCA
851 GGGTTTAAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
951 GGTATTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
1001 TTAGAACCCG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG
1051 AACTTGCAGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GGCGCGGACG
1101 CTGGTGTGTT GAAGCGTGTG CCCGTTATAC CTACCGGCAG CGACCCGGCA

```


810

```

1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTACAGCGTT
1201 GACGGAATGG CGGGCAGCCG CATCACGCTT GCACCGGAAG GAGAAACGGA
1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

```

a537.pep
1  MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
51  RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
151 LSLDRHTDE AGAAVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPEYEI
251 TGNPASIDFS EAAGKITMKS FKLYQKNEI RPVRVLTAGN DPNGLRTAYQ
301 FALFPLKPLE YGTYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPSRLSIGR HKAGGIVFSV
401 DGMAGSRITL APEGETERGV TLYLQD*

```

m537/a537 98.2% identity in 164 aa overlap

```

              10      20      30      40      50      60
m537.pep      MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLNLRIRAQIGLHK
              |||||
a537           MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLNLRIRAQIGLHK
              10      20      30      40      50      60

              70      80      90      100     110     120
m537.pep      LAHAPVLENSARRHASLYLTNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
              |||||
a537           LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
              70      80      90      100     110     120

              130     140     150     160
m537.pep      TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA
              |||||
a537           TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN
              130     140     150     160     170     180

a537           GRFERHCAQGRNQPEAGRKYRACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE
              190     200     210     220     230     240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

```

g538.seq
1  atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg
51  cgtcatgctg gtgggcgtaa tgttgataa agatgatacg ggcagcaatg
101 ccgcccgtct gaacgggttt cagacggcat tggcggaaag cgtcagagctg
151 gtcaaaagcg cgggcggcga ttccgtacgc gtggagactg ccaaacgcga
201 ccgcccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt
251 cggaagcagt tgccgcagac ggcattgatt tggtcgtatt caaccacgaa
301 cttactccca cgcaggaacg caatttgaa aaaatcctcc aatgccgcgt
351 attggacaga gtggggctga ttctggcgat ttctgcccgc cgcgcccgca
401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttggcg
451 ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat
501 cggcatgaaa gggccgggcg aaaccaaact ggaaaccgac cgccgattaa
551 ccgcccacat gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
601 cagcgcgccc tgcgcgcgaa gtcccgcgag tcgggcagaa tcaaacggtt
651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc
701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
751 acgacggcgc ggcggctgta catcagtcgc gcatgcagca ttatcctgac
801 cgataccgtc ggattcgtca gcgatctgcc gcacaaactg atttccgcct
851 tttccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcacgtc
901 gtcgatgctg ccgcccggaa cagcgggcag cagattgaag acgtggaaaa
951 cgtactgcaa gaaatccatg cccacgatat tccgtgcatc aaggtgtaca
1001 acaaaaccga cctgctgccc tctgaagaac aaaacacggg catatggcgc
1051 gacgctgccc gaaaaattgc cgccgtccgc atttccgttg ctgaaaatac

```

This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:

g538.pep

```

1  MSGRTGRNSA TQAQPERVML VGVMLDKDDT GSNAARLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHE
101 LTPTQERNLE KILQCRVLDR VGLILAI FAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLTAHRINA LKKQLANLKK
201 QRALRRKSRE SGRIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
251 TTARRLYISP ACSIIILDTV GFVSDLPKHL ISAFSATLEE TVQADVLLHV
301 VDAAARNSEQ QIEDVENVLQ EIHADIPCI KVYNKTDLLP SEEQNTGIWR
351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

m538.seq

```

1  ATGACAGGCA GAACAGGCGG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GGCAGTAGTG
101 CCGCCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CAGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTCACGCCCA CGCAGGAACG CAACCTTGAA AAAGAACTsa AATGCCGCGT
351 ATTGGACAGG GTAGGGCTGA TTCTGGCGAT TTTCGCTCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CGCAATTGAG CCATTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGCGGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAAC TGGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGATAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TGCGCCGCAA GTCnCGCGAA TCGGGCACAA TCAAAACGTT
651 TGCGCTGGTC GGCTATACAA ATGTCGAAA ATCCAGCCTG TTCAACCGGC
701 TGACAAAGTC GGGCATATAT GCAAAGGACA AGCTTAGTCC CGAATGCAGC
751 ATTATCCTGA CCGATACCGT CGGATTCGTn AGCGATCTGC CGCacAAACT
801 GATTTCCGCC TTTTCgCC.A CGCTGGAAGA AACCGCGCAA GCCGATGTGC
851 TGCTGCACGT CGTCGATGCC GCCGCTCCGA ACAGCGGACA GCAGATTGAA
901 GACGTGGAAG ACGTACTGCA AGAAATCCAT GCCGGCGATA TTCCGTGCAT
951 cAAGGTGTAC AACAAAACCG ACCTGCTGCC GTCTGAAGAA CAAAACACGG
1001 GCATATGGCG CGACGCTGCG GGAAAAATTG CCGCCGTCCG CATTTCGTT
1051 GCTGAAAATA CCGGTATAGA CGCACTGCGC GAAGCcATTG CCGAGTCTTG
1101 TGCCGCCGCA CCAAACACAG ACGAAACCGA AATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

m538.pep

```

1  MTGRTGGNGS TQAQPERVML VGVMLDKDGT GSSAARLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHE
101 LTPTQERNLE KELKCRVLDR VGLILAI FAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LIKQLANLKK
201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDKLSPECS
251 IILTDTVGFV SDLPKHLISA FSXTLEETAQ ADVLLHV VDA AAPNSQQQIE
301 DVENVLQEIH AGDIPCIKVY NKTDLLPSEE QNTGIWRDAA GKIAAVRISV
351 AENTGIDALR EAIAESCAAA PNTDETEMP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/g538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
	: : : :					
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHEL TPTQERNLE KELKCRVLDR					
	: :					
g538	VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHEL TPTQERNLE KILQCRVLDR					

812

	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQ EGR LQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
g538	VGLILAI FARRARTQ EGR LQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQ RALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
g538	RRLTAHRINALKKQLANLKKQ RALRRKSRESGRIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGFVSDLP HKLISAFSXTLEETAQADVLLHV					
g538	AKDQLFATLDTTARRLYISPACSIILTDTVGFVSDLP HKLISAFSATLEETVQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEI HAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
g538	VDAAARNSGQQIEDVENVLQEI HAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
g538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1   ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCCA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCCGCAC GGGCAAGCGC GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTTGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCGCCCCG CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGGCGC
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAACT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TGCGCCGCAA GTCCCGCGAA TCGGGCACAA TCAAAACGTT
651 TGCGCTGGTC GGCTATACCA ATGTCCGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCTGCA GCGATCTGCC GCACAACTG ATTTCCGCCT
851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAAAA
951 CGTACTGCAA GAAATCCATG CCGGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGA CCTGCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTTG CTGAAAATAC
1101 CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1   MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLVVFNHE
101 LTPTQERNLE KILQCRVLDR VGLILAI FAR RTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

```

813

201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILTDTV GFVSDLPKLI SAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERV	MLGVMLDKDGTGSSAAR	LNGFQTALAEAVELVKA	AGGDSVR		
a538	MTGRTGRNGSTQAQPERV	MLGVMLDKDGTGSSATRL	NNGFQTALAEAVELVKA	AGGDSVR		
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTG	KAAELSEAVAADGIDL	VFNHELTPTQERNLEKEL	KCRVLD		
a538	VETAKRDRPHTALFVGTG	KAAELSEAVAADGIDL	VFNHELTPTQERNLEKIL	QCRVLD		
	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRL	QVELAQLSHLAGRLIRGY	HLQSQRGGIGMKGPGETK	LETD		
a538	VGLILAI FARRARTQEGRL	QVELAQLSHLAGRLIRGY	HLQSQRGGIGMKGPGETK	LETD		
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANL	KKQALRRKSRESGTIKTF	ALVGYTNVGKSSLFNRLT	KS		
a538	RRLIAHRINALIKQLANL	KKQALRRKSRESGTIKTF	ALVGYTNVGKSSLFNRLT	KS		
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSI	IILTDTVGFVSDLPKLI	SAFSXTLEETAQADVLLH	V		
a538	AKDQLFATLDTTARRLYI	SPECSI IILTDTVGFVSD	LPHKLISAFSATLEETAQ	ADVLLHV		
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQ QIEDVEN	VLQEIHAGDIPCIKVYN	KTDLLPSEEQNTGIWRD	AAGKIAAVR		
a538	VDAAAPNSGQ QIEDVEN	VLQEIHAGDIPCIKVYN	KTDLLPSEEQNTGIWRD	AAGKIAAVR		
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAE	SCAAAPNTDETEMPX				
a538	ISVAENTGIDALREAIAE	YCAAAPNTDETEMPX				
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

```

1  atggaggatc tgcaggaaat cgggttcgat gtcgccgccg taaaggtagg
51  tcggcagcgc gaacatcatc gtctgcatca taccagtcgc ggcaacggca
101 aggcggacga tgtattgttt gcgttccttt tggttggcgg cttcgatttt
151 ttgcgcgtca taggggtgcgg cgggtgtacc tgtctgccgg attttcaaca
201 gaatgtcggg gaggcggatt ttgccgtcgt cccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaaag
301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgctgagca
351 tcagcactgc ttcgtgcgtg ccattatggg ttccacaaa gtcggatttg
401 acttcgggca ggtcgtagag gcggatttgg tcgaggattt cttggggcgg
451 cagttcgggt ttttcgcgt cggcgggtgc tcgtttgtaa taactgccca
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcgcggg cttcgccttc gtagcggacg gtcagatgca ggttttcggg
601 aacgtccagc ccgcagtgga aacaggtttt tttcatggca tttcgggttc

```

814

```

651 gtctgtgttt ggtgcggcgg cacaatactc ggcaatggct tcgcgagctg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccggtgtt tgttcttcag acggcagcag
801 gtcggttttg ttgtacacct tgatgcacgg aatatcgtgg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgct gttccgggcg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgcacgg tttcttccaa
951 ggtggcggaa aaggcggaaa tcagtttggt cggcagatcg ctgacgaatc
1001 cgacggtatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgcgctcg tgtcgagagt ggcgaaaagc tggctcttcg catatatgcc
1101 cgacttggtc agccggttga acaggctgga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

```

g539.pep
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVVQ ADLVEDFLGR
151 QFGFLRVGGA SFVITAQAGI DDALCDCLTA DAAGFAVFAF VADGQMVFV
201 NVQPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPFLRA
301 AASTCSSTS ACTVSSKVAE KAEISLCGRS LTNPTVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

```

m539.seq (partial)
1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGC GG GTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAc GCGGCaGcGg
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAACACCGC CTCGCGCGTG CCGCGTGGG TTTCCACAAA GTCGGATGG
401 ACTTCGGGCA GGTCTGACAG GCGGATTGG TCGAGGATT CTGCGGCGG
451 CAgCTCGGTT TTTTGCGCGT CGGCGGTGCG TTGTTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaAgG
551 GTTCGCGGTT CTTCGTTTTT GTAACGGACA GTCAGGTGGA GGTGTTCCGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTTT
751 CCCGCGACGT CGCGCCATAT GCGCGTGTTC TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATTT
851 CTTCGAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGgcG.AA AAGGCGGAAA TCAGTTTgTG CCGCAGATCG CTnACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

```

m539.pep (partial)
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVGFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGLFLRVGGA LFVITAQARV NNALCDRLTA GAQGFVAVFV VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTCSSTS ACAVSSSVAX KAEISLCGRS LTNPTVSVRI MLHSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

```

m539/g539
10 20 30 40 50 60
m539.pep MEDLQEIGFDVAAVKVGRQREHHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
|||||
g539 MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```

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	10	20	30	40	50	60
m539 . pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	70	80	90	100	110	120
	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
m539 . pep	130	140	150	160	170	180
	LARAAGVGHKVGGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	130	140	150	160	170	180
	FVRAIMGFHKVGGLDFGQVVQADLVEDFLGRQFGFRVGGASFVITAQAGIDDALCDCLTA					
m539 . pep	190	200	210	220	230	240
	GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS					
g539	190	200	210	220	230	240
	DAAGFAVFAFVADGQMVFVGNVQPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS					
m539 . pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHMVFVFCSSDGRSVLLYTLMHGISPAWISCSFTSTSSICCPFLGA					
g539	250	260	270	280	290	300
	ATEMRTAAIFPAASRHMVFVFCSSDGRSVLLYTLMHGISWAWISCSFTSTSSICCPFLFRA					
m539 . pep	310	320	330	340		
	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	310	320	330	340	350	360
	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRAVVSRVAKS					
g539	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539 . seq
1   ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGCGCGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTG TACGCAAAAG
301 CTGCTGTTCG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCGC CTGCGCGGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTTCGTACG GCGGATTTGG TCGAGGATT CTTGGGGCGG
451 CAGCTCGGTT TTTTGCGCGT CGGCGGTGCG TTGTTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
551 GTTTCGCGGT CTTCGTTTTC GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGCG GGCAATTTT
751 CCCGCAGCGT CGCGCCATAT GCCCGTGTTT TGTTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGCGGAA AAGGCGGAAA TCAGTTTGTG CGGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CGCGCGTCTG TGTCGAGTGT GGCGAAAAGC TGGTCTTTCG CATATATGCC
1101 CGACTTGGTC AGCCGGTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539 . pep
1   MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF

```

816

```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVGHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFLRVGGA LFVITAQARV NNALCDCLTT GAAGFAVFEV VTDGOMQVFG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTTCSSTS AAVSSSSVAE KAEISLCGRS LTNPTVSVRI MLHSGMLYSR
351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

```

              10      20      30      40      50      60
m539.pep     MEDLQEIGFDVAAVKVGRQREHRLHHPQPGNGEADDVLFAFFLVGGFDLRLVIGCGGVA
              |||
a539          MEDLQEIGFDVAAVKVGRQREHRLHHPQPGNGEADDVLFAFFLVGGFDLRLVIGCGGVA
              10      20      30      40      50      60

              70      80      90     100     110     120
m539.pep     YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
              |||
a539          YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
              70      80      90     100     110     120

              130     140     150     160     170     180
m539.pep     LARAAGVGHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA
              |||
a539          LARAAGVGHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDCLTT
              130     140     150     160     170     180

              190     200     210     220     230     240
m539.pep     GAQGFAVFEVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS
              || |||
a539          GAAGFAVFEVFTDGMQVFGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS
              190     200     210     220     230     240

              250     260     270     280     290     300
m539.pep     ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA
              |||
a539          ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA
              250     260     270     280     290     300

              310     320     330     340
m539.pep     AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG
              |||
a539          AASTTCSSTSACAVSSSVAEKAEISLCGRSLTNPTVSVRIMLHSGMLYSRRRAVVSSVAKS
              310     320     330     340     350     360

a539          WSFAYMPDLVSRLNRLDLPTLVX
              370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

g540.seq

```

1  atgccgcct cccgacgcg caacgggggtg tttatcaaa acggcaaaact
51 tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
101 tgccggtgac gaaccgatg ccgtctgaac cttcagacgg catcggtgtg
151 ttattgttcc actcggacgg gtgcagggtc gtattgtgtc gattcgtcgc
201 cgtaatacag cacgccgagt ttgacgggga tgcgtccctg cgatttgagg
251 tgggcgttgg aatcgcgcaa ggaatacgcg cagccgcagt attcctgctg
301 gtagaagttt tcgcggttgc tgatttcaat catacgcgcg ccgccgcgcg
351 ctttgcgcca gttgaagtcc caataggcca catcatcgta aggcgcggcg
401 gcacggtgtc cgcagtcgtt gatttgcgcc atatttttcc agcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

g540.pep

```

1  MPPSRGNGV FYQNGKLANA VSACRLPNRQ TFPVPVNPMP PSEPSDGIGC

```

```
m540.seq (partial)
1 ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTTGT
51 CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCGTC GCCGTAATAC
101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTGC GGTGGGCATT
151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCTCTG TGGTAGAAGT
201 TTTACGCTTT GCTGATTTC ATCATGCGCG CGCTGCCGCC GCCTTTGCGC
251 CAGTTGAAAT CCCAATACAC CACATCATCG TAAGGCGCGG CGGCGCGGTG
301 TCCGCAGTCG TTGATTTGCG CCATATTTT CCAGCGTGA
```

```
m540.pep      (partial)
      1      ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
     51      GIPQGIGTTA IFLLEVETFT ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
    101      SAVVDLRHIF PA*
```

[illegible]

a540.seq	1	51	101	151	201	251	301	351	401
	ATGCCGTCCT	TGCCAATGCG	TGCCGATGCC	TTATTGTGCC	CGTAATACAG	TGGGCGTTGG	GTAGAAGTTT	CTTTGCGCCA	GCGCGGCGGC
	CCCGACGCGG	GTTTCGCGATT	GAACCCGATG	ACCCGGATGG	CACGCCGAGT	AATCCCTCAG	TCACGTTTGC	CTTGAAATCC	CGTCAGTCGTT
	CAACGGGGTG	GCAGATTGCC	CCGTCTGAAC	GTCCAGGTTT	TTGATGGGGA	GGAATAGGCA	TGATTTCAAT	CAATACACCA	AATCTGGTTC
	TTTTATCAAA	AAACCGGCAA	CTTCAGACGG	GTATTGTGTC	TTCTGCCCTG	CAACCGCAAT	CATACGCGCG	CATCATCGTA	ATGTTTTTCC
	ACGGCAAAC	ACCTTTCCCG	CATCGGGTGT	GATTCGTCGC	TGATTTGCGG	ATTCTGCTG	CTGCCGCCGC	AGGCGGGCG	A

a540.pep (partial)

1	MPSSRRGNGV	FYQNGKLANA	VSDCRLPNRQ	TFVPMPNPM	PSEPSDGIGC
51	LFVHPDGCRF	VLCRFVAVIQ	HAEFDGDSAL	*FAVGVGIPQ	GIGTTAIFLL
101	VEFTFADFN	HTRAAAFAP	VEIPIHHIIV	RRGGAAAADV	NLVHVFP

818

m540/a540 92.8% identity in 111 aa overlap

```

                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                |||||
a540      GNGVIFYQNGKLANAVSDCRLPNRQTFVPMPNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
              10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHARAAAFAFVEIPIH
              |||||
a540      AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHTRAAAFAFVEIPIH
              70      80      90      100     110     120

                                100     110
m540.pep      HIIVRGGAVSAVVDLRHIFPAX
              |||||
a540      HIIVRGGAAAANLVHVF
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

```

g542.seq
1  atgccgaaat ggtcgcgcat acggcggttc agcgtccttt cgctgatgtt
51 cagcgcggct gtcagccggt tgacttggtg tgcgccgccg tcgaacgcgg
101 cattcagggt gcggtgaag tcttcagacg gcatagcgtc tgcttcgcc
151 gtttgccccg ccgccggtc gatgccgtct gaaaccgtgt cccacaaatc
201 cgacagcagc cgcaacacgt ccgcctcgcg gcgcaatgtt tcgccccaaat
251 gcccctttgg gacggtttgc aggcaggatg ccgccaagcc gcgcaggttt
301 gggggcaaat cccatatacct gaccggttcg cggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

```

g542.pep
1  MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFRVLK SSDGIASASA
51  VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF
101 GKGSHILTGS R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

```

m542.seq
1  ATGCCGAAAT GGTGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT
51  CAGCGCGTCT GTCAGCCGGT TGACTTGGTG TGCGCCGTCG GCAAACGCGG
101 CATTTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCGG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
301 GGGGGCAAAT CCCATATCCT GACCGGTTTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

```

m542.pep
1  MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVLK SSDGIASASA
51  VCPAAGSMPS ETVSHKSDSS RNTSASRAMF RPNAPLGRNV SPKCPFGTAF
101 RQDAAKPRRF GKGSHILTGS R*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

```

m542/g542

                                10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSASVSRLTWCAPSANAAFRVLKSSDGIASASAVCPAAGPMPS
              |||||
g542      MPKWSRIRRC SVLSLMFSAVVSRLTWCAPP SNAAFRVLKSSDGIASASAVCPAAGSMPS
              10      20      30      40      50      60

                                70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASXRNVS PKCPFGTA FRQDAAKPRRF GKGSHILTGSRX

```

```
a542.seq
1  ATGCCGAAAT  GGTGCGGCAT  ACGGCGTTGC  AGCGTCCTTT  CGCTGATGTT
51  CAGCGTGCTC  GCCAGCCGGT  TGACTTGATG  TGCGCGCCCG  GCAAACGCGT
101 CATTCAGGAT  CGGGCTGAAG  TCTTCAGACG  GCATAGCGTC  TCGTTCGCGC
151 GTTGTCCCGG  CCGCCGCCCC  GATGCCGTCT  GAAACCGTGT  CCCACAAGTC
201 CGACAGCAGC  CGCAACACGT  CCGCCTCGCG  GCGCAATGTT  TCGCCCCAAT
251 GCCCCTTTGG  GACGCTTTC  AGGCAGGATG  CGGCCAAGCC  GCGCAGGTTT
301 GGGGCGAAAT  CCCATATCCT  GACCGGTTGC  CGGTAA
```

a542.pep

1	MPKWSRIRRC	SVLSLMFSVS	ASRLT*CAPP	ANAAFRMLRK	SSDGIASASA
51	VCPAAGPMPS	ETVSHKSDSS	RNTSASRRNV	SPKCPFGTAF	RQDAAKPRRF
101	GGKSHILTGS	R*			

	10	20	30	40	50	60
m542.pep	MPKWSRIRRCVLSL	MFSASVSRLTWC	APSANAAFRVRLK	SSDGIASASAVCP	AAGPMPS	
a542	MPKWSRIRRCVLSL	MFSVSASRLTXC	APPANAAFRMRLK	SSDGIASASAVCP	AAGPMPS	
	10	20	30	40	50	60
	70	80	90	100	110	
m542.pep	ETVSHKSDSSRN	TASAXRNVSPKC	PFGTAFRQDAAK	PRRFGGKSHILT	GSRX	
a542	ETVSHKSDSSRN	TASARRNVSPKC	PFGTAFRQDAAK	PRRFGGKSHILT	GSRX	
	70	80	90	100	110	

```
g543.seq
1 atggtttgtc ggttatttgc cgcggttttt ggctttcaac tcggcaatca
51 gcccgctgat gccttttggt ttgatgattt cgccgaattg gttgcggtac
101 acggtaacca ggctcgtgcc ttcgatggcg acgttgtaggt tacgggtattt
151 gccgcgcgtt tggtaggtgg taaagttccat attgacgggc ttctgacggc
201 ggatgccgac ttcggcagcg acgacgattt ccttgccgcc tttattgacg
251 atgggattgt ctttgacgtt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgcggatca gcagggtttg aaattctttg gccaacgcgtt
351 gtttttgcg gtccggacgc gtacgccaa ggttgccgac cgccaatgcg
401 gtcatacgtt ggaaatcgaa atagggaacc gcataggctt cggcttttgg
451 gcgtgcagaa gccgcgtcgc cgcttttttag catgggtcaaa acctgtgtgg
501 cgttttggcg gattttgtcc atctgcgtcg ccggggaggc aactgccatg
551 ccgatgtcga aaataccgat gcccaatgcg ctgatgaagg aggatttttt
601 cacgatgtct ttcttgaaaa tggatgtgta tgtttattct gcggcttttt
651 ccgcattgcc gccctcagcg tttttctcgg cgaagctggg catgaattta
701 ccgatcaggt tttccagaac cattgcagaa ctggttacgg agatgggtgc
751 gccggcagca aggtttttccg tatcgccgcc ctgctgcage ccgatgtact
801 gttcgcccaa aagtcgccga gtcaggattt gcgcggaaac gtactgtctg
851 aactgatact tgccgtccaa atcaaggcgc accctgcctt gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgccc gaccaatacg cctgcggatt
951 tgacgggggc attgacctt aaaccgccga tgtcgccgaa atcggcataa
1001 accgcgtaag tttgtccga ccgcgcgaac gccgcgcgc ccgccacgcg
1051 gaaagcgaga aaggcaaccg ccgcccgcgc gatcaagacg aacagtcgga
1101 cccaaaattc caatatgttc tttttcatta a
```

g543.pep
1 MVCRLFAAVF GFQLGNQPVDF AFGFDDFAEL VAVHGNQARA EDGDVVGTVF

m543.seq

m543 . pep

m543/q543

	10	20	30	40	50	60
m543 .pep	MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDGVVGTFTAAALVGGEVH					
g543	MVCRLFAAVFGFQLGNQPVDAFGFDFAELVAVHGNQARAFDGDGVVGTFTAAALVGKGKH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543 .pep	VDGFLPGYADFGADDDFFAAFIDDGIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR					
	:	:	:	:	:	:
g543	IDGLLTGDADFGTDDDFLAALIDDGIVFDVDGRVFEFQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180

821

```

m543.pep  VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
g543       VGRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLCGVLADLSHCVGRGG
           130      140      150      160      170      180

           190      200      210      220      230      239
m543.pep  KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIAAGVIFLGKTRHEFADKV
g543       KCHADAQNTDAQCADEGGFFHDXV--FPENGCVCLFCGFFRIAALSFLGEAGHEFTDQV
           190      200      210      220      230

           240      250      260      270      280      290      299
m543.pep  FQNHCRGTGYGDGVAGSKVFRVAALLQPDVLLAQKSRSQDLRGNVAAELILAVQIEAHPRL
g543       FQNHCRGTGYGDGVAGSKVFRVAALLQPDVLLAQKSRSQDLRGNVTAELILAVQIKAHPR
           240      250      260      270      280      290

           300      310      320      330      340      350      359
m543.pep  IGFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNR
g543       IGFRVKPDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRAARHAESEKGNR
           300      310      320      330      340      350

           360      370      379
m543.pep  RRANQDEQSDPKFQYVLLHX
g543       RRADQDEQSDPKFQYVLFHX
           360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1  ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTTTAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATCTTTTG GCCAACGCTT
351 GTTTTTGCGC GTCGGACGCG GTGCGCCAAG GGTTGCCGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGGGCGGTG TTGGCATCAC CGCTTTTTTA GATGCTCAAT ACTTGAGTGG
501 CGTTTTGACG GATTTGGTTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCCTAGTT TGAATATGAT GGCATACGTT TATTGCGCGG
651 CTTTTTCCGC ATTGCCGCCG TCGGCATTTT TCTCGGCAAA ACTCGTCATG
701 AATTTGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTGCGC GGAAACGTCG
851 CTGCTGAAC TACTTTGCC GTCCAAATCG AGGCGCACC TCGCCTGATA
901 GGATTTCCGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCGT
951 CGGATTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1  MAYGLLAHVX SLQLXNQSVH AFREDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQQL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRGTGYGD
251 GVAGSKVFRV AALLQPDVLL AQKSRSQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQTADV AEIGINGVSF VRTAERRTAG

```

822

351 HAESEKGNRR RANQDEQSDP KFQYVLFH*

m543/a543 96.0% identity in 378 aa overlap

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGGEVH					
a543	MAYGLLAAXSLQLXNQSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGGEVH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAAFIIDGIVFDVDVGVFQHRAGIGADQQGLKFFGQRLFLR					
a543	VDGFLPGXADFGADDDFFAAFIIDGIVFDVDVGVFQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m543.pep	VGRGAPRVADRQCCHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG					
a543	VGRGAPRVADRQCCHTLEIEIGNRIGFGFLAGGVGITAFXDAQYLSGVLTDLVYRVGRGG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m543.pep	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFQGGFFRIAAVGI FLGKTRHEFADKVF					
a543	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFQGGFFRIAAVGI FLGKTRHEFADKVF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m543.pep	QNHCRGTGYGDGVAGSKVFRVAALLQPDVLLAQKSRSQDLRGNVAAELILAVQIEAHPRLI					
a543	QNHCRGTGYGDGVAGSKVFRVAALLQPDVLLAQKSRSQDLRGNVAAELILAVQIEAHPRLI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m543.pep	GFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
a543	GFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
	310	320	330	340	350	360
	370	379				
m543.pep	RANQDEQSDPKFQYVLLHX					
a543	RANQDEQSDPKFQYVLFHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

```

1  atgaaaaaaa tactcaccgc cgccgcgcgc gactgatcg gcatcctcct
51  cgccaccgct ctcacccccg acagtaaaac cgcccccgc ttctccctgc
101 cgcacctgca cggaaaaacc gttccaacg ccgacctgca aggcaaagtc
151 accctgatta atttttgggt tcctcctgt ccgggttggt tgagcgaaat
201 gccccaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
251 tcctcgccgt tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301 gtcaaagact acggactgcc gttaccgct atttatgatg cggacaaagc
351 cgtcggacag gcattcggca cacagggtta tccgacttcc gtccttatcg
401 gcaaaaaagg cgaaatcctc aaaacttatg tcggcgaacc cgatttcggc
451 aaactctacc aagaaatcga taccgcgctg gcgcaatag

```

This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>:

g544.pep

```

1  MKKILTAAAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGV
51  TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIKKEIL KTYVGEPDFG

```

151 KLYQEIDTAL AQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1587>:

```
m544.seq
1  ATGAAwAAAAA TACTCACCGC CGCCGTCGTC GCACTGATCG GCATCCTCCT
51  TGCCATCGTC CTCmTCCCCG ACAGCAAAAC CGCGCCCGCC TTCTCCmTGC
101 CCGACCTGCA CGGAAAAACC GTTTCCAACG CCGACCTGCA AGGCAAAGTA
151 ACCCTGATTA ATTTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGAwAT
201 GCCCAAAATC ATTAACACGG CAAATGACTA TAAAwCAAA AACTTCCAAG
251 TACTTGCCGT CGCCAGCCC ATCGATCCGA TAGAAAGCGT CCGCCAATAT
301 GTCAAAGACT ACGGTTTGCC GTTTACCGTC ATGTATGATG CGGACAAAGC
351 TGTCGGACAG GCGTTCGCA CACAGGTTTA TCCGACTTCC GTCCTTATCG
401 GCAAATAAGG CGAAATCTC AAAACCTACG TCGGCGAACC CGATTTCGGC
451 AACTCTACC AAGAAATCGA TACGCGCGTG GCGCAATAG
```

This corresponds to the amino acid sequence <SEQ ID 1588; ORF 544>:

```
m544.pep
1  MXKILTAADV ALIGILLAIV LXPDSKTAPA FSXPDLHGKT VSNADLQGV
51  TLINFWFPSC PGCVSXMPKI IKTANDYKXK NFOVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGK*GEIF KTYVGEPDFG
151 KLYQEIDTRV AQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

```
m544/g544

          10      20      30      40      50      60
m544.pep  MXKILTAADVVALIGILLAIVLXPDSKTAPAFSXPDLHGKT VSNADLQGVTLINFWFPSC
          | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g544       MKKILTAADVVALIGILLATVLPDSKTAPAFSLPDLHGKT VSNADLQGVTLINFWFPSC
          10      20      30      40      50      60

          70      80      90     100     110     120
m544.pep  PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTV MYDADKAVGQ
          | | | | | : | | | | | : | | | | | | | | | | | | | | | | | | | | | |
g544       PGCVSEMPKVTKTANDYKXKDFQVLAVAQPIDPIESVRQYVKDYGLPFTVIYDADKAVGQ
          70      80      90     100     110     120

          130     140     150     160
m544.pep  AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX
          | | | | | | | | | | | | | | | | | | | | : | | |
g544       AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX
          130     140     150     160
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1589>:

```
a544.seq
1  ATGAAAAAAA TACTCACCGC CGCCGTCGTC GCACTGATCG GCATCCTCCT
51  TGCCATCGTC CTCATCCCCG ACAGCAAAAC CGCGCCCGCT TTCTCCCTGT
101 CCGANCTGCA CGGAAAAANC GTTTNCAACG CCGACCTGCA AGGCNAAGTT
151 ANCCTGATTA ANTTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGAAAT
201 GNCCANAATC ATTAACACGG CAAATGACTA TAAAAACAAA AACTTCCAAG
251 TCCTTGCCGT CGCCAGCCC ATCGATCCGA TAGAAAGCGT CCGCCAATAT
301 GTCAAAGACT ACGGTTTGCC GTTTACCGTC ATGTATGATG CGGACAAAGC
351 TGTCGGACAG GCGTTCGCA CACAGGTTTA TCCGACTTCC GTCCTTATCG
401 GCAAAAAAGG CGAAATCTC AAAACTTATG TCGGCGAACC CGATTTCGGC
451 AACTCTACC AAGAAATCGA TACCGCGCTG GCACAATAG
```

This corresponds to the amino acid sequence <SEQ ID 1590; ORF 544.a>:

```
a544.pep
1  MKKILTAADV ALIGILLAIV LIPDSKTAPA FLSXLHGKX VSNADLQGV
51  XLIXFWFPSC PGCVSEMXXI IKTANDYKNK NFOVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG
```

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151 KLYQEIDTAL AQ*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544.pep	MXKILTA	AVVALIG	ILLAIVL	XPDSKT	APAFSX	PDHLGK
a544	MKKILTA	AVVALIG	ILLAIVL	IPDSKT	APAFSL	SXLHGK
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVS	XMFKI	IKTAND	YKXKN	FQVLAV	AQPIDP
a544	PGCVS	EMXXI	IKTAND	YKXKN	FQVLAV	AQPIDP
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQ	VYPTSV	LIGKXG	EIFKTY	VGEPDF	GKLYQE
a544	AFGTQ	VYPTSV	LIGKXG	EILKTY	VGEPDF	GKLYQE
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547.seq

```

1  atgttcgtag ataacggatt taataaaacg gtagcgagtt ttgccccaaat
51  cgtcgaaact ttcgacgtat tcttcttttag gaacgattgc gcctttttta
101 cgcagatgaa acagcgggtgc ggttgggtct gctcgttggg atatctcggt
151 gatataattta caagatgcgg cttcgagatt ccgaaccgct ccttttaaaga
201 gcttggggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg
251 ccgaagtcga gatggatgcc cattacttcc cttactcag aaaatattta
301 aaatttataa tgttacatat agttacaaat attagagttt tttgtgtgtg
351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaaccgaa
401 aaaagcgggt tgttttttgt tgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547.pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEDMA HYFPLLRKYL
101 KFIMLHIVTN IRVFCVCVKE LLTILVKNLN PNGKKRFVFC C*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547.seq

```

1  ATGTTTCGTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTSTA
101 CGCAGATGAA ACAGCGGTGC GGTTGGGTCT GCTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCTC CTTTAAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTTT AGGACTAATG
251 CCGAAGTCGA GATGGATGCT CATTACTTCC CTTACTCAG AAAATATTTA
301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTTGTGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTG TCTCCAAACG
401 GAAAAAAGCG GTTGTGTTTT TGTGTGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547.pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEDMA HYFPLLRKYL
101 KFIMLHIFTN IKVFXVCVKE ELLTILVKNL SPNGKKRFVF CC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

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	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRRKYLKFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRRKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
g547	ELLTILVKNLSPNGKKRFVFCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547.seq
1  ATGTTCGTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACAATTGC ACCTTTTTTA
101 CGCAGATGAA ACAGCGGTGC GGTGGGTCT GCTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG CTTGAGATT CCGAACCGCT CCTTTAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
251 CCGAAGTCGA GATAGATGCT CATTACTTCC CCTTACTCAG AAAATATTTA
301 AAATTATATA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTT.TGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTAGT T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547.pep
1  MFVDNGFNKT VASFAQIVET FDVFFFRNNC TFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEIDA HYFPLLRRKYL
101 KFIMLHIFTN IKVFXCVCVK ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRRKYLKFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRRKYLKFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548.seq
1  atgttttccg taccgcgttc ctttttgccg ggcgttttcg tacttgccgc
51  gcttgccgcc tgcaaacctc aagacaacag tgcggcgcaa gccgcttctt
101 caagtgcata cgcgcgggct gcggaaaatg cggcaaagcc gcaaacgcgc
151 ggtacggata tgcgtaagga agacatcggc ggcgatttca cactgaccga
201 cggcgaaggc aagcctttca gcctgagcga ttgaaaggc aaggtcgtga
251 ttctgtcttt cggcttttac cactgtcccg atgtctgccc gacagggtt
```


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```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggtg ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acgggcgggcc aaaacctgcc ggatcatcaag cagcaatacc gcgtggtttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccgggtgc gtatcttatc gataaaaacg gtgagggtgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ AASSSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFTLTDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAQ FNPDFIGLTA
151 TGGQNLPIVK QQYRVVSAKI NQKDDSENIL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTTCGG TACCGCGTTC CTTTTTGCCG GCGTTCCTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAATG CGGCAAAGCA AnACACGCGC
151 GGTACGATA TGCGTAAGGA AGACATCGGC GCGGATTTCa CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTCATCAAG CAGCAATACc GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCGGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTTCTCG
601 CTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKQXTR
51 GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAQ FNPDFIXLTA
151 TGGQNLPIVK QQYRVVSAKV NQXDDSENIL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG					
	:					
g548	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQAASSSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTLTYSDTLKQLGGQAKDVKV					
	:					
g548	GDFTLTDGEGKPFSLSDLKGKVVILSFGFTHCPDVCPTGLTYSDTLKQLGGQAKDVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTP EIIGKYAQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENIL					
	:					
g548	FVSIDPERDTP EIIGKYAQFNPDFIGLTATGGQNLPIVKQQYRVVSAKINQKDDSENIL					
	130	140	150	160	170	180

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```

                190      200      210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                |||||
g548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTC CG TACCGCGTTC CTTTTTGCCG GCGTTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TGCGTAAGGA AGACATCGGC GCGGATTTCA CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCG GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTCTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR
51 GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTTEL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

```

                10      20      30      40      50      60
m548.pep      MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAENAAXQXTRGTDMRKEDIG
                |||||
a548          MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAENAAXQXTRGTDMRKEDIG
                10      20      30      40      50      60

                70      80      90      100     110     120
m548.pep      GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV
                |||||
a548          GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV
                70      80      90      100     110     120

                130     140     150     160     170     180
m548.pep      FVSIDPERDTP EIIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKV NQXDDSENYL
                |||||
a548          FVSIDPERDTP EIIIGKYAKQFNPDFIGLTATGDQNLPIVKQQYRVVSAKV NQKDDSENYL
                130     140     150     160     170     180

                190     200     210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                |||||
a548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51 tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```

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```

151 caaatctgca atcggacggg ttgccacgcc gctttccatc gctgctttgg
201 cggcagccgt agcgacgcga ggcagcaggc ggaatcgaa cggagtagga
251 atcaggtatt ccgcgccgaa ttcgaatttc ttaccgtaag cggcaaccac
301 ttcttcgggt acttcttcca tcgccaaatc tgccaaagca tacacgcagg
351 cgcgtttcat ttcttcgttg atggtggttg cgcgcacatc caacgcgccc
401 cggaagatga acgggaagca caatacgttg ttcacttggt tcgggaagtc
451 ggagcggccg gtaccgataa ccacgtccgg acgggtttct ttcgccagcg
501 gcggcaggat ttccggattc gggttggcca tggcgaacac gatgggtttt
551 tcgttcacatc tgttcaacat ttcaggcgtc agcaggtttg cgcggagag
601 gcccaagaag atgtctttgc ctttaaccgc atcggaagt acgcgcggc
651 cgttgctctt aacggcgtag aatttttttg attcgtccat gcggtctttg
701 tcttcgcggg tttggtaaat cacgcctttg gagttgcaaa cggttacgtt
751 ttcacgtttc aagcccaaat ccagcagttg gttcaggcag gcaatcgcg
801 cggcacctgc gccggagcac accaaagtcg cttcttcgat tttacggccg
851 gtataacgca gggcgttcaa tacggcggcg gcggtaatga tggccgtgcc
901 gtgctggcca tcatgaaata cggggatttt gcagcgtttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

```

g550.pep
  1 MITDRFHLFH FPVSFIYQSD NKMPPESSD GILTTNGLQL PFAQLGSVSF
 51 QICNRTGCHA AFHRCFGGSR SDARQQAGIE RSRNQVFRAE FEFLTIVSGNH
101 FFGYFFHRQI CQSIHAGAFH FFVDGGCADI QRAPEDEREA QYVVHLVREV
151 GAAGTDNHVR TGFFRQRQD FRIRVGHGEH DGFFVHRVQH FRRQQVCAGE
201 AQEDVFAPNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251 FTFQAQIQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301 VLVIMKYGDF AAFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

```

m550.seq (partial)
  1 ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
 51 GTTTGGACTC GTCCATACGG TCTTTGTCTT CGCGGGTTTG GTAAATCAGC
101 CCTTTGGAGT CGCAAACGGT CACGTTTTCG CGTTTCAAGC CCAAATCCAG
151 CAATTGGWTC AAGCAGGCAA TCGCGGCCGC ACCTGCGCCG GAACACACCA
201 AAGTCGCTTC TTCGATTTTA CGGCCGGTAA AACGCAKGGC GTTCAATACG
251 GCGGCGGCGG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
301 GATTTTGCAG CGTTTGCATA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

```

m550.pep (partial)
  1 ..DGIGKHALAV VFNGVELFGL VHTVFVFAGL VNHAFGVANG HVFAFQAQIQ
 51 QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101 DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

```

m550/g550
                                     10      20      30
m550.pep                               DGIGKHALAVVFNGVELFGLVHTVFVFAGLVN
                                     |||:| |||||:|:|:|:|:|:|:|
g550      DGFFVHRVQHFRQQVCAGEAQEDVFAPNRIGKYAPAVVFNGVEFFGFVHAVFVFAGLVN
               190      200      210      220      230      240

               40      50      60      70      80      90
m550.pep      HAFGVANGHVFAFQAQIQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDGRA
               |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g550      HAFGVANGYVFTFQAQIQLVQAGNRGGTCAGAHQSRFFDFTAGITQGVQYGGGGNDGRA
               250      260      270      280      290      300

               100
m550.pep      VLVVVEYGDFAAFAX
               |||:|:|:|:|:|:|
g550      VLVIMKYGDFAAFAX

```

310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTCAC TTGGTTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTTCGC
451 CAGCGGCGGC AGGATTTCCG GATTTCGGGT GGCCATAGCG AACACGATGG
501 GTTTTTCGTT CATGGTGTTC AGTATTTTCA GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTTG TCTTCAATGG CGTAGAAGTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTCGC GTTTCAGGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTCGTCGTG GAATACGGGG ATTTTGCAGC GTTTGCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FGGSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQRTAE DEREAYIVH LVREVGAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGVEL FGLVHTVFEV AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYGS GG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```

                                     10      20      30
m550.pep                               DGIGKHALAVVFNGVELFGLVHTVFEVFAGL
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVFEVFAGL
           170      180      190      200      210      220

                                     40      50      60      70      80      90
m550.pep      VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGNDG
a550      VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYGS GGNDG
           230      240      250      260      270      280

                                     100
m550.pep      RAVLVVVEYGDFAAFAX
a550      RAVLVVVEYGDFAAFAX
           290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttggt attgcccttc gccgcactgg cattgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttggca cgttggtctg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcagggcg cagaagcctt taatcggtat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcgggtc gtccgtcggt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaaa tagcgggtatc ttggactgca
```

830

451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt
501 acggcgcatc atctgcggcg gtatagtga ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep
1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIARHHL PEFTEELRRI ICGGIVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)
1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA
201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAG TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAACG
551 CCGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)
1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	: : : : : :					
g552	MKLKTLLLPFAALALCANAF AAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	: : : : :					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
m552.pep	YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
	: : : : :					
g552	YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq
1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA

831

```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 CCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLL PFATLALCTNAF AAPPDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEIEDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

	10	20	30	40	50	60
m552.pep	IKLKTLLL PFATLALCTNAFAAPPDASLARWLD	TQNFDRDIEKNMIEGFNAGFKPYADK				
a552	IKLKTLLL PFATLALCTNAFAAPPDASLARWLD	TQNFDRDIEKNMIEGFNAGFKPYADK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEIEDGMIAF					
a552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEIEDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTTEELRRIICGGKNPDAG					
a552	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTTEELRRIICGGKNPDAG					
	130	140	150	160	170	180
	190					
m552.pep	CKQAGQVGKRHQKX					
a552	CKQAGQVGKRHQKX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCCG CCCGCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLTLLL PFATLALCTN AFAAPPDAS LARWLDQNF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEFN RYRENVKDL ITPEVKQAVR
101 NTLKNAREI YQEIEDGMI AFYGSPVGQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

832

```

1   TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTT GAAAGATTTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1   LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLKLNAREI YTQEEIDGMI AFYGSFVGQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

a552-1.pep	10	20	30	40	50	60
	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
m552-1	10	20	30	40	50	60
	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
a552-1.pep	70	80	90	100	110	120
	DKALAEMPEAKKDQAAEAFNRYRENVKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMI					
m552-1	70	80	90	100	110	120
	DKALAEMPEAKKDQAAEAFNRYRENVKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMI					
a552-1.pep	130	140	150	160	170	180
	AFYGSFVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGKNPD					
m552-1	130	140	150	160	170	180
	AFYGSFVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGKNPD					
a552-1.pep	190					
	AGCKQAGQVGKRHQKX					
m552-1	190					
	AGCKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1   atggattatc tgcaaacct gtctttgggc ttgacaaaaa agctgcccgt
51  tatactgcaa acagaagtag cggagtgtgg cttggcatgt ctacgagctg
101 tggccggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatg gggctgacgg gacgggctgt gaggtggat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcggatatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgcaaagtca agacggagga aatatcgcg aagtttacgg
401 gaattgcttt ggaactgtgg ccaaacacgc gtttcgaggc aggggaagaa
451 aagcaggaaa tccgcatacct acccatgttg cgcgggattt ctgggctggg
501 gcggacattg tttcagcttt tggctttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgtttgcg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaagt catgataaat gggcacgaca
701 tttacagctt accgccacct tttattccgc aatttgagtg cgatggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

833

```

1 MDYLQNLISLG LTKKLPVILQ TEVAECGLAC LAAVAGFYGF YTDLRALRSK
51 YCLSLKGENL ADIVRFADDM GLTGRALRLD LDELGSLRLP CILHWDNLNHF
101 VVLESVSSDG AAVMDPASGR RKVKTEEISR KFTGIALELW PNTRFEAGEE
151 KQEIRILPML RGISGLGRTL FOLLALAAAM EVFAFLQNV FKIGRGESLA
201 LIGRSGCGKS TLLDILSGNL PPESGKVMIN GHDIYSLPPP FIPQFECDDQ
251 GRTMFYSGLN LNR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1621>:

m553.seq (partial)

```

1 ATGGATTATT TATCAAGACT GTCCTTTGGA TTTAACAAAA AGCTACCTGT
51 CATTCTGCAA ACAGAAGTTG CTGAATGTGG TTTAGCATGC CTGACATCCA
101 TCTTGCTCTA TTATGGCTTT CACACTGATT TAAGAACGTT ACGCCAAAAA
151 TACACCTGT CATTAAAGGG CGCAAATCTT GCAGACATCA TGAGATTTGG
201 CAATGAAATG AATTTAACGC CACGAGCTTT GCGTTTAGAG TTAGATGAGC
251 TGTCAAATTT ACAACTACCC TGCATTCTCC ATTGGAACCT AAACCATTTT
301 GTTGTACTTT GTTCCATTTC CAAAGACAGT ATCGTCATTA TGGACCCTGC
351 TGTGCGTATG CGAAAAATCA AAATGGACGA AGTTTCACAA AAATTCACAG
401 GGATTGCCCT AGAATTATTC CCCAATACCC ATTTTGAAGA GAAAAAAGAA
451 ACAAAGAAAA TCAAATATT ATCTCTATTA AGGGGGGG.T CAGGCTTAAA
501 ACGCTCTTTA ATTCAAATGC TTATATTAGC TATTTCTTTG GAAGTCTTTG
551 CATTG...

```

This corresponds to the amino acid sequence <SEQ ID 1622; ORF 553>:

m553.pep (partial)

```

1 MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYGFG HTDLRTLROK
51 YTLSLKGANL ADIMRFGNEM NLTPRALRLE LDELSNLQLP CILHWNLNHF
101 VVLCISISKDS IVIMDPAVGM RKIKMDEVSQ KFTGIALELF PNTHFEKKKE
151 TKKIKILSLL RGXSGLKRSI IQMLILAISL EVFAL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

m553/g553

	10	20	30	40	50	60
g553.pep	MDYLQNLISLGLTKKLPVILQTEVAECGLAC	LAAVAGFYGFYTDLRALRSKYCLSLKGENL				
m553	MDYLSRLSFGFNKKLPVILQTEVAECGLAC	LTSILSYGFGHTDLRTLROKYTLKGANL				
	10	20	30	40	50	60
	70	80	90	100	110	120
g553.pep	ADIVRFADDMGLTGRALRLDLDELGSLRLP	CILHWDNLNHFVVLESVSSDGA	AAVMDPASGR			
m553	ADIMRFGNEMNLTPRALRLELDELSNLQLP	CILHWNLNHFVVLCISISKDS	IVIMDPAVGM			
	70	80	90	100	110	120
	130	140	150	160	170	180
g553.pep	RKVKTEEISRKFTGIALELWPNTRFEAGEE	KQEIRILPMLRGISGLGRTL	FOLLALAAAM			
m553	RKIKMDEVSQKFTGIALELFPNTHFEKKET	KKIKILSLLRGXSGLKRSI	IQMLILAI	SL		
	130	140	150	160	170	180
	190	200	210	220	230	240
g553.pep	EVFAFLQNV	FKIGRGESLALIGRSGCGKSTLLDILSGNL	PPESGKVMINGHDIYSLPPP			
m553	EVFAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1623>:

a553.seq

```

1 ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT
51 TATCTGCAA ACAGAAATAT CAGAATGCGG CTTGGCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

```


m553/a553 62.7% identity in 51 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

m554.seq.

1	ATGACAGCAC	ATAAAATCCT	GCCCGTCTCTG	CTTTCCATCA	TCTTAGGCGT
51	TTCTCACGCA	ACGGCTGCAT	CGCCCGCGCC	CAACAGACCG	ACGGTACACG
101	CCGCCCCCA	GTTCCAAACA	CCCGAAACCC	TCACAGCGGC	ACACATCGTT
151	ATCGACCTTC	AAAGCAAACA	GATTTTATCC	GCCAAAACA	TCAATACCC
201	TGTTGAACCG	CGCGCACTAA	CCCAACTGAT	GACCGCATAT	CTGGTTTTC
251	AAAACATGAA	ATCGGGCAAT	ATCCAATCTG	AAGAAAACCT	AAAAATACCC

```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCTATC
751 TCCGGCAACG GCAGGCACAT CCTTGTCTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCTTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCCGACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IQSEENLKIP
101 ESAWASEGSR MFVRPGDVS TDKLLKGMIA LSANDAALT AGRLGNGSIE
151 NFVQQMKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFNIEQNN RNILLYRDN VNGLKAGHTE SGGYNLAVSY
251 SGNRHILVI TLGSESAETR ASDNSKLLN ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPKKEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554 . pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSKQILS					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSRQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m554 . pep	AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDVS					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m554 . pep	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMKEARRLGMKNTVFNPTGLSREG					
g554	TDKLLKGMIALCANDAALTADRLGNGSIENFVQQMKEARRLGMKNTVFNPTGLGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m554 . pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFNIEQNNRNILLYRDNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFNIEQNNRNILLYRDNVNGLKAGHTE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m554 . pep	SGGYNLAVSYSGNHRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					

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```

g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554.pep  QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY
           |||||||||||||||||||||||||||||||||||||||||||||||||||||:
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGH
           310      320      330      340      350      360

           370      380      390
m554.pep  TIAEKEIVALENVKKRSRWQRLWACLTGQX
           |||||||||||||:|||||||:|||||
g554      TIAEKEIVALENVKKRSRWQRLWTRLTGQX
           370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```

a554.seq
1  ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCACGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
201 TGTCGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTCA
251 AAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAAACCT AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCAG CTGTCTGAAG CATTGATGCG CGACTTTCGG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTCA AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAGCCCG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCTATC
751 TCCGGCAACG GCAGGCACAT CTTGTCTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAAGTGG GCATTGCAAG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAACCGT TGCCCAAATG
901 CAAATTTCCG GAGGCAGCAA AAAAACCCTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```

a554.pep
1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IRSEENLKIP
101 ESAWASEGSR MFVRPGDTSV TDKLLKGMIA LSANDAALT AGRLNGSIE
151 NFVQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SNGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

m554/a554 99.2% identity in 389 aa overlap

```

           10      20      30      40      50      60
m554.pep  MTAHKILPVL LSIILGVSHATAASPAPNRPVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a554      MTAHKILPVL LSIILGVSHATAASPAPNRPVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554.pep  AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTSV
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a554      AKNINTPVEPAALTQLMTAYLVFKNMKSNGIRSEENLKIPESAWASEGSRMFVRPGDTSV

```

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	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
a554	TDKLLKGMIALSANDAALTLAGRLNGS	IEFVQQMNKEARRLG	MKNTVFKNPTGLS	SREG		
	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
a554	QVSTAKDLALLSEALMRDFPEYYPLFS	IKSFKFKNIEQNNRN	ILLYRDNNVNLKAG	HT		
	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
a554	SGGYNLAVSYSGNGRHILVITLGSESA	ETRASDNSKLLN	WALQAFDTPKI	YPKGKTVAQI		
	250	260	270	280	290	300
m554.pep	310	320	330	340	350	360
a554	QISGGSKKTVRAGFLKEAYITLPHKEA	KMAEQILETIQIP	PAPVKKGQILGK	IKIRQNGY		
	310	320	330	340	350	360
m554.pep	370	380	390			
a554	TIAEKEIVALENVKKRSRWQRLWACLT	GQX				
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatacctgct tgccgccgtc atcgtcgccg ccgctgcggg cggctttggt
151 tggacatccc gccgacagca acgccagttt atcgaacgtc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggg ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKRPT RQEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC TCGCTTGGGC GGCCTGATTT TACTGACCAC
51  CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTGCGCAA AATGTTCGGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

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101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKT KLRLGGLILLTTAVLSLIIVLIVDSWPLA ILLAAVIVAAAAGGFVWTSRRQQRQF					
g556	MDNKT KLRLGGLILLTTAVLSLIIVLIVDSWPLA ILLAAVIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKR PTR					
g556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKR PTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
g556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAA	ACT	GCGCTTGGGC	GGCCTGATTT	TACTGACCAC
51	CGCCGTTTTA	AGCCTCATTA	TCGTATTGAT	TGTCGATTCC	TGGCCGCTTG	
101	CCATCCTGCT	TGCCGCCGTC	ATCGTCGCCG	CCGCTGCGGG	CGGCTTTGTT	
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT	
201	CGACATCGAT	CCCGAAAAAG	GCAGAAATCAA	CGAGGCAAAC	CTGCGCCGTA	
251	TGTACCACAG	CGGCGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC	
301	CTGTCGCAAA	AATGTTTCGGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG	
351	CCCGACACGT	CAGGAAATCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC	
401	AGAAACGTCC	GCACCGTTAA				

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKT KLRLG	GLILLTTAVL	SLIIVLIVDS	WPLAILLAAV	IVAAAAGGFV
51	WTSRRQQRQF	IERLKKFDID	PEKGRINEAN	LRRMYHSGGQ	HQKDAITLIC
101	LSQKCSVDEA	HAMFKKRPTR	QEINQMAAKQ	SRGQKRPHR*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKT KLRLGGLILLTTAVLSLIIVLIVDSWPLA ILLAAVIVAAAAGGFVWTSRRQQRQF					
a556	MDNKT KLRLGGLILLTTAVLSLIIVLIVDSWPLA ILLAAVIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKR PTR					
a556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKR PTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
a556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

g557.seq
 1 atgaacaaaa tattccttac tgccgcagcc ttggtgctgg gcgcgtgcgg
 51 tttccacctg aaaggtgcag acggcatttc tccgccgctg acctaccgga
 101 gctggcacat cgaaggcgga caggcattgc aatttccttt ggaaaccgcg
 151 ctgtatcagg cttcgggcag ggtggacgat gctgccggcg cgcagatgac
 201 cctgcgtata gacagcgttt cccaaaacaa ggaaacctat accgttacct
 251 gtgcggcagt catcaacgaa tatcttttga tattgacggt tgaagcgcag
 301 gtattgaaac gcggcgagcc ggtcggcaaa ccgatgaccg tgtccgtccg
 351 ccgcatcttg gattatgccg acaacgaaat tttgggcaaa caggaagaag
 401 aagaaacctt gtgggcggaa atgcggcagg atgttgccga acagattgtc
 451 cgcgcctga ctttctgaa ggcggaatga

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..
 1 MNKIFLTAAA LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
 51 LYQASGRVDD AAGAQMTRLI DSVSQNKETY TVTRA AVINE YLLILTVEAQ
 101 VLKRGE PVGK PMTVSVRRIL DYADNEILGK QEEEELWAE MRQDVAEQIV
 151 RRLTFLKAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..
 1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
 51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
 101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC GGTTCCTTT GGAAACCGCG
 151 CTGTATCAGG CTTCGGGCAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
 201 CCTGCGTATA GACAGCGTTT CCAAAAACAA GGAAACCTAC ACCGTTACCC
 251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
 301 GTATTGAAAC GCGGCGAGCC GGTCCGTAAA CCGATGACCG TGTCCGTCCG
 351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
 401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
 451 CGCCGCTGA CTTTCTGAA GCGGGAATGA

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pep..
 1 MNKLFLTAAV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA
 51 LYQASGRVDD AAGAQMTRLI DSVSQNKETY TVTRA AVINE YLLILTVEAQ
 101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
 151 RRLTFLKAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

	10	20	30	40	50	60
m557.pep	MNKLFLTAAV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA LYQASGRVDD					
g557	MNKIFLTAAALVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA LYQASGRVDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTRLIDSVSQNKETY TVTRA AVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
g557	AAGAQMTRLIDSVSQNKETY TVTRA AVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRIL					
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEILGK QEEEAALWAE MRQDAAEQIV RRLTFLKAE X					
g557	DYADNEILGK QEEETLWAE MRQDVAEQIV RRLTFLKAE X					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

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```

a557.seq
  1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGC GG
  51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
 101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
 151 CTGTATCAGG CTTCGGGTAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
 201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
 251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
 301 GTATTGAAAC GCGGCGAGCC GGTCCGCAAA CCGATGACCG TGTCCGTCGG
 351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
 401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
 451 CGCCGCCTGA CCTTCTGAA GCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

```

a557.pep
  1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
  51 LYQASGRVDD AAGAQMTRLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
 101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
 151 RRLTFLKAE*

```

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHLKGADGISPPLTYRSWHIEGGQALRFPLETA LYQASGRVDD					
a557	MNKLFLTA AV LMLGACGFHLKGADGISPPLTYRSWHIEGGQALQFPLETA LYQASGRVDD					
	10	20	30	40	50	60
m557.pep	AAGAQMTRLRIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGE PVGK PMTVSVRRVL					
a557	AAGAQMTRLRIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGE PVGK PMTVSVRRVL					
	70	80	90	100	110	120
m557.pep	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAE X					
a557	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAE X					
	130	140	150	160		
m557.pep	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAE X					
a557	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAE X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

```

g558.seq..
  1 ATGGATGCTT GTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT
  51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
 101 TGCCCTTATA TACTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG
 201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
 251 AGTCCATTTT CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
 301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

```

g558.pep..
  1 MDACFFVIPA QAGIRRFIV FKRSGRILAG AGMMPYTFE ELYMLQQGTA
  51 HQAPHCVLPE RGCPPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP
 101 LSDGIV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

```

m558.seq..
  1 ATGAATGCTT GTTTTTCGT CATTCCACA CAGGCGGGAA TTCGGAGATT
  51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
 101 TGCCCTTATA TACTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG
 201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
 251 AGTCCATTTT CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
 301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m558/g558

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

m558/a558 70.2% identity in 141 aa overlap

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1649>:

q560.seq

1 atgctcatca tccgcaacct gatttactgg ctgatactct gttccagcct

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```

51  gattttcctc tttcccttta tgctgctcgc ctgcgcttcc cgggacgggg
101 cgcacaagat ggcgcgggtc tgggtcggca tcctcaactg gtcgctcaaa
151 cacatcgtcg ggctcaaata ccgcatcatc ggcgcggaac acattccgga
201 ccgccccctc gtcattctgcg ccaaacacca aagcggctgg gaaacgctcg
251 cgctccaaga gatttttccg ccgcagggtt acgttgccaa gcgcgagttg
301 ttcaaaatcc cctttttcgg ctggggcttg aaactgggtc aaaccatagg
351 catagaccgc aacaaccgcc gcgaagccaa cgaacagctc ataaaacagg
401 gtttggcgcg caaaaacgaa ggttattgga ttaccatttt ccccgaggcg
451 acgcgccttg cgcccggaac acgcggcaaa tacaaactcg gcggcgcgcg
501 catggcgaaa atgtttgaga tggacatcgt ccccgctgcc ctcaacagcg
551 gcgaattttg gccgaaaaat tcctttctga aatatccggg ggaaatcacc
601 gtcattcatc gtccgaccat cccgcacgca agcggcagcg aagccgaatt
651 gatggaaaaa tgcgaacacc tcattgaaac gcaacaaccg cttatttccg
701 gcgcaggccc gtttgccgcc gaaatgccgt ctgaaaccgc atga

```

This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:

g560.pep..

```

1  MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAEHIPDRPS VICAKHSGW ETLALQEIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRK GYKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VIICPTIPHA SGSEAELEMEK CEHLIETQOP LISGAGPFAA EMPSET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1651>:

m560.seq

```

1  ATGCTCATCA TCCGCAACCT GATTTACTGG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGGGACGGGG
101 CGCACAAGAT GGC GCGGGTTC TGGGTCGGCA TTCTCAACTG GTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGC GCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCGG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCGG CTGGGGCTTG AAACCTGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAAACAGG
401 GGTGGTGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCC GAAGGC
451 ACGCGCCTTG CGCCCGGAAA ACGCGGCAAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCC GTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCGGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGAAAAA TGCGAACATC TCATCGAAAC GCAACAACCG CTTATTTCGG
701 GCGCAGGCCC GTTGTCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:

m560.pep

```

1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAENIPDRPA VICAKHSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLVRKNE GYWITIFPEG
151 TRLAPGKRK GYKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMEK CEHLIETQOP LISGAGPFAA KMPSETA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng)

from *N. gonorrhoeae*:

m560/g560

```

              10      20      30      40      50      60
m560.pep    MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK HIVGLKYRII
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g560         MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK HIVGLKYRII
              10      20      30      40      50      60

              70      80      90      100     110     120
m560.pep    GAENIPDRPA VICAKHSGW ETLALQDIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g560         GAEHIPDRPS VICAKHSGW ETLALQEIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITTVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	:					
g560	LNSGEFWPKNSFLKYPGEITVIICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```

a560.seq
1  ATGCTCATCA TCCGCAACCT GATTACTGCG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGAGACGGGG
101 CGCACAAAGAT GGCGCGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCCG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAATCC CTTTTTTCGG CTGGGGCTTG AAACGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAACAGG
401 GGTGGCGCG CAAAACGAA GGCTATTGGA TTACCATTTT CCCCAGAGGC
451 ACACGCCTTG CGCCCGGAAA ACGCGGCAAA TACAAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCGCGTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAAA TGCGAACACC TCATCGAAAC GCAGCAGCCG CTCATTCCG
701 GCGCAGGCCC GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```

a560.pep
1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAKHQSGW ETALAQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGARMAM MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQQP LISGAGPFAA KMPSETA*

```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK HIVGLKYRII					
	:					
a560	MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK HIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	:					
a560	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAEKMEKCEHLIETQQPLISGAGPFAA					
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAEKMGKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

m561.seq.

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCCCT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAACA	TCGAACTGTT	TTTGCAGGCA
451	TTGGAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCAATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCTGC	TGTACTGATG	CTGTTTTGGC
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTCGGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCTG	CTGTACCAAA	CTACACGGGA
801	CCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTTCATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCGGATTTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCCATT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCCTG	CTTGCAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCCTTTGC
1251	CGAAAACAAA	CGGGAGGAAG	CCGCAGAAAA	CATCAGCTTT	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTCCGT
1351	ACCAAAATCA	GCAATAAAGA	ATTTCCCGAA	GCCGTTGCCG	ACCTATTCGC
1401	CCGCTTTACG	CAACAAACCG	GGATAACGGT	CGAAACCGCC	TGGGAAAACG
1451	GTTCGTTCCCT	GCCGCCTCAG	GAAGCGCAGC	TCCAAATGAT	TTTATCCTG
1501	CAGGAAAGCC	TGTCCAACAT	CCGCAAAAC	GCCCGCGCCA	CCCATGTAAA
1551	ATTCACCCTT	TCCGAACACG	GCGGACGCTT	TACCATGACC	ATCCAAGACA
1601	ACGGACAAGG	TTTCGACACG	GAGAAAATAG	GAGAACCCAC	GGGCAGCCAT
1651	GTCGGACTGC	ACATCATGCA	GGAGCGTGCC	AAACGCATCC	ATGCCGTTTT
1701	AGAAATCCGT	TCCCAAGCTC	AACAGGGAAC	CACCGTCTCA	TTGACGGTTG
1751	CATCTGAAGA	AAGCTTGAAA	TGA		

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

m561.pep

1	MILPARFSDG	ISLSRLRLKL	TGLWVGLAAL	SVVLTLLLSL	RLENAASVIE
51	EAGNLRMQAY	RLAYMAGEGS	PRAQIDNQVA	EFEKSLKRIA	QSDAIHPLIP
101	SDTPLAYDLI	QSMLIIDWQA	HILPPLQSYR	RPTQVDLYRF	AGNIELFLQA
151	LENANEKNTW	WLRRFQWAIM	LMTLVSSVLM	LFWHQIWVIR	PLQALREGAE
201	RIGRRCFDIP	VPEGGTPEFK	QVGRCFNQMG	GRLKILYDDL	EGQVAEQTRS
251	LEKQNQNLT	LYQTRDLHQ	SYIPQAAEH	FLNRILPAVG	ADSGRVCLDG
301	GSDVYVSIH	ADCGTAASDL	GKYHEEIFPI	EYQNETLGR	LLSFPNGISL
351	DEDDRILLQT	LGRQLGVSLA	GAKEEEKRL	LAVLQERNLI	AQGLHDSIAQ
401	ALTFLNLQVQ	MLETAFANENK	REEAENISF	IKTGVQECYE	DVRELLLNFR
451	TKISNKEFPE	AVADLFARFT	QQTGITVETA	WENGSLFPQ	EAQLQMIFIL

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501 QESLSNIRKH ARATHVKFTL SEHGGRFTMT IQDNGQGFDT EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS	SVVLTLLLSRL	LENAASVIEE	EAGNLR	MQAY	
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALS	SVVLTLLLSFR	LENAASVIEE	EAGNLK	MQAY	
	10	20	30	40	50	60
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAE	FEKSLKRIAQSDAIHPLIPSDT	PLAYDLIQSMLIIDWQA			
g561	RLAYMAGEGSPRAQIDNQIAE	FEKSLKRISQSDAIHPLIPSDN	PLAYDLIQSMLIIDWQA			
	70	80	90	100	110	120
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIE	LFLOALENANEKNTWWLRRFQWAIM	MLTLVSSVLM			
g561	NILPPLQAYRRPTQIELYRFAGNIE	LFLOALENAGEKNTWWLRRFQWVIM	MLTLVSSVLM			
	130	140	150	160	170	180
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIGRRC	FDPVPEGGTPEFKQVGRCFNQMG	GRKLKILYDDL			
g561	LFWHQIWVIRPLQALREGAERIGQRH	FDPVPEDVRPNSNRSGGVSTKWR	SGX			
	190	200	210	220	230	
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQNQNLTLLYQT	TRDLHQSYIPQQA	AHFLNRILPAVGADSGR	VC	LDG	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCCCT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCTTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAACA	TCGAACGTGT	TTTGCAGGCA
451	TTGGAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCAATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCTGC	TGTACTGATG	CTGTTTTGCG
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTGCGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTTCATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCGGATTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCCATT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCCTCT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCCTG	CTTGCAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCCTTTGC
1251	CGAAAACAAA	CGGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	CGGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCCGAA	GCCGTTGCCG	ACCTATTCTC

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```

1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCAATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCACGCCA CCCATATCAA
1551 ATTCAAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
  1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
  51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
 101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
 151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
 201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
 251 LEKQNQNLTLYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
 301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGRLLSFPNGISL
 351 DEDDRILLQT LGRQLGVSLA GAKQEEERLL LAVLQERNLIAQGLHDSIAQ
 401 ALTFLNLQVQ MLETAFENK REEAENIGF IKTGVQECYE DVRELLLNFR
 451 TKISNKEFPE AVADLFSRET QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
 501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQGFDI ENIGEPSGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

m561/a561 96.9% identity in 590 aa overlap

      10      20      30      40      50      60
m561.pep MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSLRLLENAASVIEEAGNLRMQAY
|||||
a561      MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSLRLLENAASVIEEAGNLRMQAY
      10      20      30      40      50      60

      70      80      90     100     110     120
m561.pep RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA
|||||
a561      RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA
      70      80      90     100     110     120

      130     140     150     160     170     180
m561.pep HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
|||||
a561      HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
      130     140     150     160     170     180

      190     200     210     220     230     240
m561.pep LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGRLKILYDDL
|||||
a561      LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGRLKILYDDL
      190     200     210     220     230     240

      250     260     270     280     290     300
m561.pep EGQVAEQTRSLEKQNQNLTLYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
|||||
a561      EGQVAEQTRSLEKQNQNLTLYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
      250     260     270     280     290     300

      310     320     330     340     350     360
m561.pep GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT
|||||
a561      GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT
      310     320     330     340     350     360

      370     380     390     400     410     420
m561.pep LGRQLGVSLAGAKQEEERLLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK
|||||
a561      LGRQLGVSLAGAKQEEERLLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK

```

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	370	380	390	400	410	420
	430	440	450	460	470	480
m561.pep	REEAAENISFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFARFTQQTGITVETA					
a561	REEAAENIGFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m561.pep	WENG SFLPPQEAQLQMIFILQESLSNIRKHARATHVKFTLSEHGGRFTMTIQDNGQGFD T					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRKHAHATHIKFRLKQDGSFTMTIQDNGQGFD T					
	490	500	510	520	530	540
	550	560	570	580	590	
m561.pep	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKX					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKX					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

```

g562.seq..
1  atggcaagcc cgtcgagtct gcctttcaat tcgggcaaga ccaaaccgac
51  ggcttttgcc gcgccggttt tggtcggaat catgttttcc acgccgctgc
101 gggcgcggcg caggtctttg tggcgcacgt cggtaacggt ttggtcgttg
151 gtcagtgcgt ggatggtggt cattgcgcct ttgacgatgc cgacgctttc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251 tggaaacgac ggtcatgtcg gcggtcagga cgctgtcgtt caccgcttac
301 acgacggttg catcgacatc gtcgccgccc ggtgcggaaa tgaggacttt
351 tttcgcgcgc ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggc tgcgggtcga gaagaagggg attttgcgcg cgttgacgat
501 gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggtcagatgg gcgttggttt caaggctgcc gctggcgttg
601 acggcgacga tttggagttg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

```

g562.pep
1  MASPSLFPN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNLT LATGERQLVV QEAL ETVMS AVRTLSFTPY
101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM T KSTPSSFHGS
151 SAGLRVEKKG ILSPLTMR L PWDTSASKR PCTVSNLVRW ALVSR LPLAL
201 TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

```

m562.seq
1  ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
101 GGGCGCGCGC CAGGTCTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGT CATGTCG GCGGTCAGGA CGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCGCGCCG CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401 TGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TCGGGTCTGA GAAGAAGGGG ATTTTGTGCG CGTTGACGAT
501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG
551 TGTCGAATTT GGT CAGATGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA GTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

```

m562.pep
1  MASPSLFPN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNLT LATGERQLVV QEAL ETVMS AVRTLSFTPY

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101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
 151 SAGLRVEKKG ILSPLTMLRP PSWDTASASKR PCTVSNLVRW ALVSRLPLAL
 201 TATSWWS*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP					
g562	MASPSSLPFNSGSKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALTTVMSAVRTLSTPYTTVASTSSPPGAEMRTFFAP					
g562	LTMPTLSLNTLATGERQLVVQEALTTVMSAVRTLSTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPSPWDTASASKR					
g562	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPSPWDTASASKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
g562	PCTVSNLVRWALVSRLPLALTATIWSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq
 1 ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC
 51 GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
 101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
 151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
 201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
 251 TGGAAACGAC GGTCATGTCG GCGGTCAGGA TGCTGTCGTT CACGCCGTAC
 301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
 351 TTTCCGCGCG CTTTCAGAT GAACCTTTGGC TTTTCTTTG CTGGTGAACG
 401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
 451 TCGGCAGGGT TCGGGGTCNA GAAGAANGG ATTTTGTGCG CGTTGACGAT
 501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG
 551 TGTCGAATTT GGTGAGGTGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
 601 ACGGCGACGA TTTGGAGTTG GTCTTGA

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep
 1 MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
 51 VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALTTVMS AVRMLSTFPY
 101 TTVASTSSPP GAEMRTFFAP LSR*TLAFSL LVNAPVHSMT KSTPSSFHGS
 151 SAGLRVXKXG ILSPLTMLRP PSWDTASASKR PCTVSNLVRW ALVSRLPLAL
 201 TATIWSWS*

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP					
a562	MASPSSLSFNSGSKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP					
	10	20	30	40	50	60

849

	70	80	90	100	110	120
m562 . pep	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R T L S F T P Y T T V A S T S S P P G A E M R T F F A P					
a562	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R M L S F T P Y T T V A S T S S P P G A E M R T F F A P					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562 . pep	L S R W I L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V E K K G I L S P L T M R L P P S W D T S A S K R					
a562	L S R X T L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V X K X G I L S P L T M R L P P S W D T S A S K R					
	130	140	150	160	170	180
	190	200	209			
m562 . pep	P C T V S N L V R W A L V S R L P L A L T A T S W S W S X					
a562	P C T V S N L V R W A L V S R L P L A L T A T I W S W S X					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563 . seq

```

1  ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGGTTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTTAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTTCTTTAT GTTTGGCTTT
201 GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCcc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCCAAGTTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GGCGGTTGGA TTCAAGGCAA TCCTTGGTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTGAAAC CAAATCAACA GCAGCCATCC
501 TTCACAACCT AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAAAGTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTAAAGATAA GGCAAGGCAA TGCTGTAATC GCCCGACACG
701 GTTTGGATGC CCGTGATACC GATTTACACAC GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTC GTAATCAAGG
801 GCAGTTGTTT GCTTCTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCACGATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAGTCAA TATCCGCAGT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACACTGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCTAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTCAGG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATTT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACCTTGC AAGCAGGAAA ACGCATTCCG
1351 ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CGGTACGACA GACATTGGCA CGCAGCACAA TTAAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAACCAA ATCCAAGCCG GGCAAAATGAA TAATATCGGT
1501 ACAGGTCGGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAACG ATATGGCGGT TGGCGGGCGA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACACAATGC CGGCGCAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1801 TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1851 AGCATTTGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGGTTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAAGTG CGCTTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

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2101 GGGCGCCAAT TGCTTGTGCA AACAGAAAAA GACGGTTTGC ATAACGAGCA
2151 AACCTTTTGGC GAGAAGAAAAG TCTTCAGCGA AAATGGTAAG TTGCACAACCT
2201 ACTGGCGTGC GCGTCGTAAA GGACATGATG AAACAGGGCA TCGTGAACAA
2251 AATTATACCT TGCCGGAGGA AATCACACGC GACATTTTAC TGGGTTTATT
2301 TGCCTATGAA TCGCATAGCA AAGCATTAAAG CCGTCATGCG CCCAGCCAAG
2351 GCACTGAGTT GCCACAAAGT AACCGGGATA ATATCCGTAC TCGCAAAAAGC
2401 AACGGTATTT CGCTACCCTA TACGCCCAAT TCTTTTACCC CATTACCCGG
2451 CAGCAGCTTA TACATTATCA ATCTTGCCAA TAAAGGCTAT CTGTTGAAA
2501 CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGGGTAG TGAATATATG
2551 CTGGGCAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC GTTTGGGTGA
2601 TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA GAGCTGACAG
2651 GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA ATTTAAAGCC
2701 TTAATGGATA ATGGCGCGAC TGGCGCACGT TCGATGAATC TCAGCGTTGG
2751 CATTGCATTA AGTGCCGAGC AAGCAGCGCA ACTGACCAGC GATATTGTTT
2801 GGTGGGTACA AAAAGAAGTT AAACCTTCTG ATGGCGGCAC ACAAACCGTA
2851 TTGATGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGGCA TAGACGGTAA
2901 AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT TCAGGCAGCC
2951 TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT TATCAATACC
3001 GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA AATCAGCGGT
3051 TACGGCCACA CAAGACATCA ATAATATTGG CGGCATTCTT TCTGCCGAAC
3101 AGACATTATT GCTCAATGCG GGTAACAACA TCAACAACCA AAGCACGGCC
3151 AAGAGCAGTC AAAATGCACA AGGTAGCAGC ACCTACCTAG ACCGAATGGC
3201 AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA GCGCAGGCAG
3251 GCAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA ATCAGATCAA
3301 GGGCAAAACC GGTGCGAGGC AGGACGCGAC ATTAACCTGG ATACGGTACA
3351 AACCGGCAAA TATCAAGAAA TCCATTTTGA TGCCGATAAC CATACCATCC
3401 GAGGTTCACG GAACGAAGTC GGCAGCAGCA TTCAAACAAA AGGCGATGTT
3451 ACCCTatTGT CAGGGAATAA TCTCAATGCC AAAGCTGCCG AAGTCGGCAG
3501 CGCAAAAGGC ACACTTGCCG TGTATGCTAA AAATGACATT ACTATCAGCT
3551 CAGGCATCCA TGCCGGCCAA GTTGATGATG CGTCCAAACA TACAGGCAGA
3601 AGCGGCGGCG GTAATAAATT AGTCATTACC GATAAAGCCC AAAGTCATCA
3651 CGAAACTGCT CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT GTATTGCAGG
3701 CAGGAAACGA TGCCAACATC CTTGGCAGTA ATGTTATTTT CGATAATGGC
3751 ACCCGGATTC AAGCAGGCAA TCATGTTGCG ATTGGTACAA CCCAAACTCA
3801 AAGCCAAAGC GAAACCTATC ATCAAACCCA AAAATCAGGA TTGATGAGTG
3851 CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA AGAAAAACCA
3901 TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCGAGC TGAAAGGCGA
3951 TACCACCATT GTTGCAAGCA AACACTACGA ACAAACCGGC AGCAACGTTT
4001 CCAGCCCTGA GGGCAACAAC CTTATCAGCA CGCAAAGTAT GGATATTGGC
4051 GCAGCACAAA ACCAATTAAA CAGCAAAACC ACCCAAACCT ACGAACAAAA
4101 AGGCTTAACG GTGGGCATTG AGTTCGCCCC TTACCGATTT GGCACAACAA
4151 GCGATTGCCG TAGCACACAA AGCAGCAAAC AAGTCGGACA AAGCAAAAAC
4201 GACCGCGTTA ATGCCATGGC GGCTGCCAAT GCAGGTGGC AGGCCTATCA
4251 AACAGGCAAA GGCGCACAAA ACTTAGCCAA TGGTACAACC AATGCCAAAC
4301 AAGTCAGCAT CTCATAACC TACGGCGAAC AGCAAAACCG ACAAAACCAC
4351 CAAGTTCAAG CCAATCAAGC CCAAGCGAGT CAAATTCAAG CAGGCGGCAA
4401 AACTACCCCT TATTGCCGAA GGTGCGGCGA ACAATCCAAT ATCAACATCA
4451 CAGGCTCAGG TGTTTCAGGC AGAGCAGGAA CCGGCCTGAT TGCCGATAAG
4501 CAAATCCATC TGCAATCAGC CGAGCAAAGC AATACCGAAC GCAGCCAAAA
4551 CAAATCAGCA GGCTGGAACG CAGGTGCTGC CGTATCATTC GGACAAGGAG
4601 GCTGGTCATT AGGCGTTGCC GCAGGCGGCA ATGTCGGCAA AGGCTACGGC
4651 TATGGCGATA GCGTAACCCA CCGCCATAGC CATATTGGCG ACAAAGGCAG
4701 CCAAACCCCT ATCCAAAGTG GTGGCGATAC CATCATCAAA GGCAGCGCAAG
4751 TACGCGGCAA AGGCGTACAA GTCAATGCCA AAAACCTAAG CATTCAAAGT
4801 GTACAAGATA GAGAACTTA TCAAAGCAAA CAACAAAACG CCGGTGCACA
4851 AGTTACCGTA GGTATGGCT TCAGTGCCAG TGGCGATTAC AGCCAAAGCA
4901 AAATCCGAGC CGACCATGCT TCGGTAACCG AGCAAAGCGG TATTTATGCC
4951 GGAGAAGACG GCTATCAAAAT CAAGGTCGGA AACCATACAG GCCTCAAAGG
5001 CGGCATCATC ACCAGCAGCC AAAGCGCAAA AGACAAGGGT AAAAAACCAT
5051 TCAGCAAGAG CACACTCGCC GGCAGTGATA TTCAAATTA CAGCCAATAC
5101 GAAGGAAAAA GTTTTGGATT GGGTGCCAGC GTTGCCGTAA GCGGCAAAAC
5151 ACTGGGACAG GGCGCAAAAA ATAAACCTCA AGACAAACAC CTGACAAGCA

5201 TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
 5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CCAAAAACAT
 5301 TCAAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
 5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
 5401 CGACATTCGG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG
 5451 TGAAGTGGAT TTACAAAGaa CCGTCAGCCA AGATTTTAGT AAAAATGTTT
 5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC
 5551 AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
 5601 GGAAACTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAAG
 5651 CAGATAATTG GCAACAAGGC AAAGTCATT CTAACATGTT AGCCTCAGGT
 5701 TTAGCTGAGC CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC
 5751 GCCagacGTA TCGTATGCGA TTGGACAGCA CTTTAAagaT TTAGCCGGTC
 5801 AAAACGCGAA TGGCAAATA ACCGCCAGTC AagaAACCGC TCACGTTCTT
 5851 CCCCACGCGG TATTAGGAGC AGCGGTTGCC GCAGCATGAG GCAACAATGC
 5901 CCCGGCAGGA GCATTGGGTG CGGGCGGGTc ggAagcggCC GCCCAATCA
 5951 TCGGCAAATG GCTGTACGGC AAAGGAGAcg gcggcagccT GAATgaggag
 6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggtta cGgctGCCGG
 6051 AGCAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGGT TGTTTTcaaa
 6101 cggctTCaga TTTTCGTTCC TCTTTTTCAT ATCCTATAAA CATGTGA

This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pep..

1 MNKTLRYVIF NRKRGAUVAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
 51 SKAFCF~~S~~ALG FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTGNIP
 101 QVNIQTPTSA GVSVNQYAF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
 151 TRGEARVVVN QINSSHPSQL NGYIEVGRR AEVVIANPAG IAVNGGGFIN
 201 ASRATLTGQ PQYQAGDFSG FKIRQGNVAV AGHGLDARDT DFTRILLYAN
 251 KITLISTAEQ AGIRNQGLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN
 301 TAEHKVNIRS QAFENSGTAV SQQGTQIHSQ SIQNTGKLLS AGTEDLAVSG
 351 SLNNQNGEIA TNQQLIIHDG QQSTVVIDNT NGTIQSGRDV AIQAKSLNN
 401 GTLAADNKL DIALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR
 451 IKANNLDNAV QGNIQSGGTT DIGTQHNLTN RGLIDGQQTQ IQAGQMNNIG
 501 TGRIYGDNIA IAATRLDNQD ENGTGAAIAA RENLNLGIEQ LNNRENSLIY
 551 SGNDMAVCGA LDTNDQATGK AQRIHNAGAI IEAAGKMRLG VEKLHNTNEH
 601 LKTQLVETGR ERIVDYEAFG RHELLREGTQ HELGWVFNYN ESDHLRTPDG
 651 VAHENWHKYD YEKVTQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
 701 GGQLLVQTEK DGLHNEQTFG EKKVFSENGK LHNRYWRARRK GHDETGHREQ
 751 NYTLPEEITR DISLGSFAYE SHSKALSRHA PSQGTLPQS NRDNIRTAKS
 801 NGISLPYTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YRQWLGSYDM
 851 LGSLKLDPN LHKRLGDGYE EORLINEQIA ELTGHRRLDG YQNDEEQFKA
 901 LMDNGATAAR SMNLSVGIAL SAEQAAQLTS DIVVLVQKEV KLPDGGTQTV
 951 LMPQVYVRVK NGGIDGKGAL LSGSNTQINV SGSLKNSGTI AGRNALIINT
 1001 DTLDNIGGRI HAQKSAVTAT QDINNIGGIL SAEQTLILLNA GNNINNQSTA
 1051 KSSQNAQGS TYLDRMAGIY ITGKEKGVLA AQAGKDINII AGQISNQSDQ
 1101 GQTRLQAGRD INLDTVQTGK YQEIHFADN HTIRGSTNEV GSSIQTKGDV
 1151 TLLSGNNLNA KAAEVGSAKG TLAVYAKNDI TISSGIHAGQ VDDASKHTGR
 1201 SGGGNKLVI DKAQSHHETA QSSTFEGKQV VLQAGNDANI LGSNVISDNG
 1251 TRIQAGNHVR IGTQTQTSQS ETYHQTQKSG LMSAGIGFTI GSKTNTQENQ
 1301 SQSNEHTGST VGSLLKGDITI VASKHYEQTG SNVSSPEGNN LISTQSMDIG
 1351 AAQNQLNSKT TQTYEQKGLT VGIQFARYRF GTTSDCRSTQ SSKQVQSKN
 1401 DRVNAMAAN AGWQAYQTGK GAQNLANGTT NAKQVSISIT YGEQONRQTT
 1451 QVQANQAQAS QIQAGGKTTL YCRRCEQSN INITGSGVSG RAGTGLIADK
 1501 QIHLQSAEQS NTERSQNKSA GWNAGAAVSF GQGGWSLGVA AGGNVKGKYG
 1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTIHK GAQVRGKGVQ VNAKNLSIQS
 1601 VQDRETYQSK QQNAGAQTIV GYGFASGDY SQSKIRADHA SVTEQSGIYA
 1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFSTGTLA GSDIQNYSQY
 1701 EGKSFGLGAS VAVSGKTLGQ GAKNKPQDKH LSTIADKNGA SSSVGYGSDS
 1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVTDTAE
 1801 RHSGSLKNIF DKDRVQSELD LQRTVSQDFS KNVQQTNTETI NQHLDKLLAD
 1851 KEAAETA~~A~~AE ALANGDMETA KRKAHEAQDA AAKADNWQQG KVILNMLASG
 1901 LAEPTQSGAG IAAATASPDV SYAIGQHFKD LAGQNANGKL TASQETAHVL
 1951 AHAVLGA~~A~~VA AAXGNNAPAG ALGAGGSEAA APIIGKWLYG KGDGGS~~L~~NAE
 2001 EKETVSAITR MLGTAAGAAE GNSSADAVWG CFQTASDFAS SFSYPINM*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

```

1   ATGAATAAAA CTCTCTATCG TGTAATTTTC AACCGCAAAC GTGGGGCTGT
51  GGTAGCCGTT GCTGAACTA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGATTCAGG CAGCGCTCAT GTGAAATCTG TTCCTTTTGG TACTACTCAT
151 GCACCTGTTT GTCGTTCAAA TATCTTTTCT TTTTCTTTAT TGGGCTTTTC
201 TTTATGTTTG GCTGTAGGTA CGGCCAATAT TGCTTTTGCT GATGGCATTAA
251 TTGCTGATAA AGCTGCTCCT AAAACTCAAC AAGCCACGAT TCTGCAAACA
301 GGTAACGGCA TACCGCAAGT CAATATTCAA ACCCCTACTT CGGCAGGGGT
351 TTCTGTTAAT CAATACGCCC AGTTTGATGT GGGTAATCGC GGGGCGATTT
401 TAAACAACAG CCGCAGCAAC ACCCAAACAC AGCTAGGCGG TTGGATTCAA
451 GGTAATCCTT GGTGGCAAG GGGCGAAGCA CGTGTGGTTG TAAACCAAAT
501 CAACAGCAGC CATTCTTCAC AAATGAATGG CTATATTGAA GTGGGCGGAC
551 GACGTGCAGA AGTCGTTATT GCCAATCCGG CAGGGATTGC AGTCAATGGT
601 GGTGGTTTTA TCAATGCTTC CCGTGCCACT TTGACGACAG GCCAACCGCA
651 ATATCAAGCA GGAGACCTTA GCGGCTTTAA GATAAGGCAA GGCAATGTTG
701 TAATCGCCGG ACACGGTTTG GATGCCCCTG ATACCGATT CACACGTATT
751 CTCAGTTATC ATTCCAAAAT TGATGCACCC GTATGGGGAC AAGATGTTCTG
801 TGTCGTCGCG GGACAAAACG ATGTGGTCGC AACAGGTAAT GCACATTCTGC
851 CTATTCTCAA TAATGCTGCT GCCAATACGT CAAACAATAC AGCCAACAAC
901 GGCACACATA TCCCTTTTAT TGCGATTGAT ACAGGCAAAT TAGGAGGTAT
951 GTATGCCAAC AAAATCACCT TGATCAGTAC GGCCGAGCAA GCAGGCATTG
1001 GTAATCAAGG GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA
1051 AATGGCCGTT TAGTCAATAG TGGCACGATG GCTGCCGCCA ATGCGAAAGA
1101 TACGGATAAT ACAGCGGAAC ACAAAGTCAA TATCCGCGAGT CAGGGCGTTG
1151 AAAACAGCGG TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAG
1201 TCGATTCAAA ACACTGGCAC ATTATTGTCC TCAGGCGAAA TATTGATTCA
1251 CAATTCCGGC AGCCTGAAAA ATGAAACATC AGGCACCATT GAAGCCGCTC
1301 GTTTGGCTAT TGATACCGAC AACTTAATA ATCAAGGCAA ACTCTCTCAA
1351 ACAGGTTTCA AAAAATCCA TATTGATGCA CAAGGCAAAA TGGATAACCG
1401 TGGCCGCATG GGTTTACAAG ATACCGCACC AACCGCGTCA AATGGTTCAA
1451 GCAATCAAAC CGGCAATAGT TACAATGCAT CTTTCCATT CACTACTACC
1501 ACACCAACAA CGGCAACAGG TACGGGTACT GCAACCGTTT CTATATCAAA
1551 CATAACTGCG CCTACCTTTG CTGATGGGAC AATTCGCACT CATGGTGCAC
1601 TGGATAATTC AGGCAGTATT ATTGCCAATG GTCAAACAGA TGTTAGTGCG
1651 CAACAAGGTT TAAATAATGC AGGACAAATA GACATTCATC AGTTAAATGC
1701 AAAAGGTTCT GCGTTTGACA ATCACAATGG AACAATTATC AGTGATGCGG
1751 TCCACATTCA AGCCGGCAGC CTGAATAATC AAAATGGCAA CATCACAACA
1801 CGCCAACAGT TAGAGATTGA AACCGATCAA CTGGATAACG CTCATGGCAA
1851 GTTATTATCA GCAGAAATAG CGGATTTAGC CGTTTCAGGC AGCCTGAACA
1901 ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT TCACGATGGT
1951 CAGCAATCTA CCGCTGTCAT TGATAATACG AATGGCACGA TACAATCAGG
2001 CCGTGATGTT GCTATTCAGG CAAAATCGTT ATCCAACAAC GGCACACTTG
2051 CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATTT TTATGTAGAA
2101 CGCAATATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC GAGGCAGCCT
2151 GAAAAATTCA CATACTTTCG AAGCAGGAAA ACGCATTTCG ATTAAAGCAA
2201 ATAACCTTGA TAATGCAGCA CAAGGCAACA TTCAATCCGG CGGTACGACA
2251 GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA TTGACGGACA
2301 ACAAACCAAA ATCCAAGCCG GGCAATGAA TAATATCGGT ACAGGTCGGA
2351 TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA CAATCAAGAT
2401 GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGTGAAAACC TGAATTTAGG
2451 CATCGGACAA TTAAACAACC GTGAAAACAG TCTGATTTAC AGCGGTAACG
2501 ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGGCCAAGC CACAGGCAAA
2551 GCCCAAAGGA TACACAATGC CGGCGCAACC ATTGAAGCTG CAGGCAAAAT
2601 GCGTTTAGGT GTAGAAAAGC TGCAACAATC CAATGAGCAT TTGAAAACGC
2651 AGTTGGTAGA AACAGGGCGC GAGCATATTG TTGATTACGA AGCATTTGGA
2701 CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG GCTGGTCTGT
2751 CTATAACGAT GAATCAGACC ACTTACGCAC CCCTGATGGA GCGGCGCATG
2801 AAAATTGGCA TAAATACGAT TATGAAAAAG TCACCCAAAA AACCCAAGTT
2851 ACCCAAATCG CGCCAGCCAA AATCATTTCA GGTAATGATT TAACCATTTGA
2901 TGGTAAAGAA GTATTTAATA CCGATAGCCA AATCATTGCT GGTGGCAATC
2951 TCATTGTACA AACAGAAAAA GACGGTTTGC ATAACGAGCA AACCTTTGGC

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3201 GCCGCAAAGC AACGGTATTT CGCTACCCTA TACGTCCAAT TCTTTTACCC
3251 CATTACCCAG CAGCAGCTTA TACATTATCA ATCCTGTCAA TAAAGGCTAT
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4251 AGGCGATGTT ACCCTATTGT CAGGGAATAA CCTCAATGCC AAAGTGCCG
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4601 CCCAAACTCA AAGCCAAAGC GAAACCTATC ATCAAACCCA GAAATCAGGA
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4701 AGAAAACCAA TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCT
4751 TGAAAGGCGA TACCACCATT GTTGACAGGCA AACACTACGA ACAAATCGGC
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5101 GCCAAACAAG TCAGCATCTC CATAACCTAC GGCGAACAGC AAAACCGACA
5151 AACCACCCAA GTTCAAGCCA ATCAAGCCCA AGCGAGTCAA ATTCAGCAG
5201 GTGGTAAAAA CACATTAATC GCCACAGGCG CAGCAGAAACA ATCCAATATC
5251 AACATCGCAG GCTCAGATGT TGCCGGCAAA GCAGGCACAA TCCTGATTGC
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6051 CGACAGCGAC AGTCAAAGCA GCATCACAAA AAGCGGCATC AACACCCGCA

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6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
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6251 AAAGTGAAC TGGATTACAA AGAACCGTCA GCCAAGATT TAGTAAAAAT
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6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTTAGCC
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6701 ATGCTCTAGC AGGAGCATTG AGTGCGGGCG GGTGGAAGC GGCTGCGCCT
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6851 CGGGTGCGGC AGTCGGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
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6951 TGCTCTTAGG CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
7001 ATCCTGGCTC TACATTAGAG CCTAATATT CAACAATTGC TTCAACTTTT
7051 CAATTAAAT TATTTCTTAA TAGTGAATT GGTGGTGAAG GTGGAGTTGG
7101 CAATGCATTC AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTG
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7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAAATACCA
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7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
7401 TGTAAGAAAA AGATTATCTG AAAAAGATTA CCAGAATACA AGCAATATAT
7451 TGATTCACCT AGATAATACT GGTGCCGGAT TAAAATTCA GCAGAGGAGA
7501 AAACAAATCA GAGCACAAAT TTCAGCCAGA CAATGGAGAA GATAA

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This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

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1 MNKTLRYRVIF NRKRGAUVAV AETTKREGKS CADSDSGSAH VKSVFPGTTH
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101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TQTQLGGWIO
151 GNPWLARGEA RVVVNQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
201 GGFINASRAT LTTGQPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
251 LSYHSKIDAP VWGQDVRVVA QONDVVATGN AHSPILNNA ANTSNNTANN
301 GTHIPLFAID TGKLGGMNAN KITLISTAEQ AGIRNQGOLF ASSGNVAIDA
351 NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QVENSQTAV SQQTQIHSQ
401 SIQNTGTLLS SGEILIHNSG SLKNETSGTI EAARLAIDTD TLNNQKLSQ
451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSSTT
501 TPTTATGTGT ATVSISNITA PTFADGTIRT HGALDNSGSI IANGQTDVSA
551 QOGLNNAQOI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
601 RQQLIETDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIHDG
651 QQSTAVIDNT NGTIQSGRDV AIQAKSLSNN GTLAADNKLD IALQDDFYVE
701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
751 DIGTQHNLTN RGLIDGQOTK IQAGQMNNIG TGRIYGDNIA IAATRLDNQD
801 ENGTGAAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGGA LDITNGQATGK
851 AQRHINAGAT IEAAGKMRLG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
901 RHELLREGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSFAYE
1051 SHRKALSHHA PSQGTELPQS NGISLPYTSN SFTPLPSSSL YIINPVNKGY
1101 LVETDPRFAN YRQWLGS DYM LDSLKLDPNN LHKRLGDGY EORLINEQIA
1151 ELTGHRRLDG YQNDEEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
1201 DIVVLVQKEV KLPDGGTQTV LVPQVYVRVK NGDIDGKGAL LSGSNTQINV
1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQKSAVTAT QDINNIGGML
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1351 AQAGKDINII AGQISNQSEQ GQTRLQAGRD INLDTVQTSK HQATHFDADN
1401 HVIRGSTNEV GSSIQTGQDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
1451 NISAGINTTH VDDASKHTGR SGGGNKLIVIT DKAQSHHETA QSSTFEGKQV
1501 VLQAGNDANI LGSNVISDNG TQIQAGNHVR IGTTQTQSQS ETYHQTQKSG

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Homology with a predicted ORF from *N.gonorrhoeae*

m563/g563

[illegible]

856

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m563.pep	370 380 390 400 410 420	AAANAKDNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG
g563.pep		-----
m563.pep	430 440 450 460 470 480	SLKNETSGTIEAARLAIDTDTLNNQKLSQTSQKLHIDAQGMKNRGRMGLQDTAPTAS
g563.pep		-----
m563.pep	490 500 510 520 530 540	NGSSNQTGNSYNASFHSSTTTPTTATGTGTATVSIENITAPTTFADGTIRTHGALDNSGSI
g563.pep		-----
m563.pep	550 560 570 580 590 600	IANGQTDVSAQQGLNAGQIDIHQLNAKGSAFDNHNGTIIISDAVHIQAGSLNNQNGNITT
g563.pep	350 360 370 380	-----EDLAVSGSLNNQNGEIATNQQLIIHDGQQSTVVIDNT
m563.pep	610 620 630 640 650 660	RQQLIEIETDQLDNAHGKLLSAEIALAVSGSLNNQNGEIATNQQLIIHDGQQSTAVIDNT
g563.pep	390 400 410 420 430 440	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS
m563.pep	670 680 690 700 710 720	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS
g563.pep	450 460 470 480 490 500	HTLQAGKRIRIKANNLDNAVQGNISGGTTDIGTQHNLNTRGLIDGQQTQKIAGQMNNIG
m563.pep	730 740 750 760 770 780	HTLQAGKRIRIKANNLDNAAQGNISGGTTDIGTQHNLNTRGLIDGQQTQKIAGQMNNIG
g563.pep	510 520 530 540 550 560	TGRIYGDNIAIAATRLDNQDENGTTGAAIAARENLNLGIEQLNNRENSLIYSGNDMAVGGA
m563.pep	790 800 810 820 830 840	TGRIYGDNIAIAATRLDNQDENGTTGAAIAARENLNLGIGQLNNRENSLIYSGNDMAVGGA
g563.pep	570 580 590 600 610 620	LDTNDQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGRERIVDYEAFF
m563.pep	850 860 870 880 890 900	LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGREHIVDYEAFF
g563.pep	630 640 650 660 670 680	RHELLREGTQHELGFVYNNESEDHLRTPDGAHENVHKKYDYKVTQETQVTGTAPAKIIA
m563.pep	910 920 930 940 950 960	RHELLREGTQHELGWSVYNNESEDHLRTPDGAHENVHKKYDYKVTQKTQVTGTAPAKIIS
	690 700 710 720 730 740	

857

g563 . pep	GSDLIIDSKAVFNSDSRIIAGGQLLVQTEKDGLHNEQTFGEKKVFSENGKLHNYWRARRK
m563 . pep	GNDLTIDGKEVFNTDSQIIAGGNLIVQTEKDGLHNEQTFGEKKVFSENGKLHSYWREKHK
	970 980 990 1000 1010 1020
g563 . pep	GHDETGHREQNYTLPEEITRDISLGSFAYESHKALSRHAPSQGTLPQSNRDNIRTAKS
m563 . pep	GRDSTGHSEQNYTLPEEITRNISLGSFAYESHKALSHHAPSQGTLPQSN-----
	750 760 770 780 790 800
	1030 1040 1050 1060 1070
g563 . pep	NGISLPYTPNSFTPLPGSSLYIINPANKGYLVETDPRFANYRQWLGS DYMLGSLKLDPNN
m563 . pep	-GISLPYTPNSFTPLPSSSLYIINPVNKG YLVETDPRFANYRQWLGS DYMLDSLKLDPNN
	810 820 830 840 850 860
	1080 1090 1100 1110 1120 1130
g563 . pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
m563 . pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
	870 880 890 900 910 920
	1140 1150 1160 1170 1180 1190
g563 . pep	SAEQAAQLTSDIVWL VQKEVKLPDGGTQTVLMPQVYVRVKNGGIDGKGALLSGSNTQINV
m563 . pep	SAEQVAQLTSDIVWL VQKEVKLPDGGTQTVLVPQVYVRVKNGDIDGKGALLSGSNTQINV
	930 940 950 960 970 980
	1200 1210 1220 1230 1240 1250
g563 . pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGILSAEQTLLLNA
m563 . pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGMLSAEQTLLLNA
	990 1000 1010 1020 1030 1040
	1260 1270 1280 1290 1300 1310
g563 . pep	GNNINNQSTAKSSQNAQGSSTYLDRMAGIYITGKEKGVLAQAQKDINIIAGQISNQSDQ
m563 . pep	GNNINSQSTTASSQNTQGSSTYLDRMAGIYITGKEKGVLAQAQKDINIIAGQISNQSEQ
	1050 1060 1070 1080 1090 1100
	1320 1330 1340 1350 1360 1370
g563 . pep	GQTRLQAGRDINLDTVQTGKYQEIHFADNHTIRGSTNEVGSSIQTGKDVTL LSGNNLNA
m563 . pep	GQTRLQAGRDINLDTVQTSKHQATHFDADNHVIRGSTNEVGSSIQTGKDVTL LSGNNLNA
	1110 1120 1130 1140 1150 1160
	1380 1390 1400 1410 1420 1430
g563 . pep	KAAEVGSAKGT LAVYAKNDITISSGIHAGQVDDASKHTGRSGGGNKLVI TDKAQSHHETA
m563 . pep	KAAEVSSANGT LAVSAKNDINISAGINTTHVDDASKHTGRSGGGNKLVI TDKAQSHHETA
	1170 1180 1190 1200 1210 1220
	1440 1450 1460 1470 1480 1490
g563 . pep	QSSTFEGKQVVLQAGNDANILGSNVISDNGTRIQA GNHVRIGTTQTQSQSETYHOTQKSG
m563 . pep	QSSTFEGKQVVLQAGNDANILGSNVISDNGTQIQAGNHVRIGTTQTQSQSETYHOTQKSG
	1230 1240 1250 1260 1270 1280
	1500 1510 1520 1530 1540 1550
g563 . pep	LMSAGIGFTIGSKTNTQENQSQSNEHTGSTVGS LKGDTTIVASKHYEQTGSNVSSPEGNN
	1290 1300 1310 1320 1330 1340

	1950	1960	1970	1980	1990	2000
g563 . pep	TASQETAHVLAHAVLGA AVAAAXGNNAPAGALGAGGSEAAAPIIGKWLYGKGDGGSLSNAE					
m563 . pep	TASQETAHVLAHAVLGA AVAAVGDNNALAGALSAGGSEAAAPYISKWLYGKEKGSDLTAE					
	2210	2220	2230	2240	2250	2260

	2010	2020	2030	2040	2049	
g563 . pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFTASDFASSFSYPINMX					
m563 . pep	EKETVTAITNVLTATGA AVGNSATDAAQGSLSNAQSAVENNDTVEQVKFALRHPRIAIAI					
	2270	2280	2290	2300	2310	2320

m563 . pep	GSVHKDPGSTLEPNISTIASTFQLNLFNSEFGGEGGVGNAFRHVLWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

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m564 . seq
1   ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51  GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAAC ACAGCCGACA
101 CCCAAGCTGT AGGTATTTTG CCAAATGATA TTGCGGGCTT TGCGGGTTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTC
201 TGCCCTTATC CTGACTTCTT CTTCTGCTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CTTGGTTGG CAAGGGGCGA AGCACGTGTG GTTGTAACC AAATCAACAG
501 CAGCCATTCT TCACAACTGA ATGGCTATAT TGAAGTGGG GACGACGTG
551 CAGAAGTCGT TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCTGTC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAATCG
701 CCGGACACGG TTGGATGCA CGTGATACCG ATTACACACG TATTCTCAGT
751 TATCATTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCGT
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATT
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTGCGAT TGATACAGGC AAATTAGGAG GTATGTATGC
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 2451 AAAAGGCCGT CTGAAAAATA CCCATACCCT ACAAGCAGGC CATACGCTCA
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 2601 GATCAACAGC GACGGTTTGA CCCACATCGG TGCAGGTCAA ACCCTGACCA
 2651 ACACCGGGAC AGGCAAAATC TATGGCAACC ATATTGCCCT GGACGCGCAA
 2701 ATACTGCTTA ACCGGGAAGA AACGACGGAA GGCAGTACCA AAGCGGGGGC
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 2901 CAGTGCCGGT TTGGAAGTAC AAGGTGATGC ATTGATGTCC GTTCGGAATA
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 3251 AAAATTGGCT GAACAAAGAC AGCCGGATTG TAGTAGGCGG GCGTATTATC
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 3351 AGGTCGCACA GATGCTGTGC GCACACAGTG GGATTGAGTT AAAAAAAG
 3401 GATGGTACAG CGGTAGAAAA AGACAACGCC GACTGAAAG AAACCATACT
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 3551 CAATCAAACT GATTGACGGA GTATCCACGG CAGCCGTCAA TGGTCAGCGC
 3601 ATCCATACCG GTAATGTGGT CTCGTAAAT AACGCTACTG TTACTCTGCC
 3651 TAACAGCAGC CTCTATACCA CCCATCCTGA CAATAAAGGC TGTTGGTTG
 3701 AAACCGATCC TCAATTTGCA GACTACCGCC GCTGGTTGGG CAGCGACTAC
 3751 ATGTTGCAAC AACTGCAATT GGACACCAAT CATCTACACA AACGGCTTGG
 3801 CGACGGCTAC TACGAACAAA AACTTGTTAA TGAACAAATC CATCAGTTAA
 3851 CAGGCTACCG CCGACTCGAC GGCTACAGGA GTGATGAAGA ACAATTCAAA
 3901 GCTCTGATGG ACAACGGCCT TACTGCTGCC AAAACATTCTG GTCTCACCCC
 3951 AGGTATCGCC TTGAGTGCAG AGCAAGTTGC CCGCTAACT TCAGATATCG
 4001 TTTGGATGGA AAATCAAACC GTCACCTGT CTGACGGTTC GACTCAAAACC
 4051 GTACTGGTTC CTAAAGTCTA TGCCCTGGCG CGCAAAGGTG ATCTCAATAC
 4101 CTCGGTGCG CTGATTAGTG CCGAACAAGT CTTACTTAAA CTGCAAAACG
 4151 GCACCTGAC TAACAGCGGT ACCATTGCGG GGCGACAGGC CGTACTCATC
 4201 CAGGCACGGA ATATTAACAG CAACGGTAAC ATTCAAGCCG ACCAAATCGG
 4251 CTTAAAAGCT GAAAAAAGTA TCAATATCGA CGGCGGGCAG GTACAAGCAG
 4301 GCAGACTGCT GACTGCCCAA GCGCAAAATA TCAACCTTAA CGGTACAACC
 4351 CAAACTTCCG GTAATGAACG TAACGGCAAT ACCGCCATCG ATCGTATGGC
 4401 CGGCATTAAC GTGGTCGGAA GCCATACTGA ACAAGTAGAT AACAGAATT
 4451 CAGACGGCAT CCTATCCCTG CATGCCAGCA ACGATATCAA CCTCAATGCG
 4501 GCCACCGTCT CTAACCAAGT TAAAGACGGC ACTACCCAAA TTACCGCCGG
 4551 CAATAATCTC AACCTCGGCA CCATCCGTAC CGAACATCGC GAAGCCTATG
 4601 GTACATTAGA TGACGAGAAC CATCGCCATG TCCGCCAAAG TACCGAAGTC
 4651 GGCAGCAGTA TCCGCACGCA AAACGGCGCA CTGCTTAGAG CCGGTAACGA
 4701 CTTAAAAATC CGCCAAGCGC AACTGGAGGC CGAAGAAGGC AAAACCGTCC
 4751 TTGCCGCAGG ACGTGATGTC ACTATCAGCG AAGGACGCCA AATAACCGAA
 4801 CTGGATACCT CGGTAAGCGG AAAAAGCAAA GGCATCCTTT CCAGTACCAA
 4851 AACACACGAC CGCTACCGCT TCAGTCATGA TGAAGCAGTC GGCAGCAACA
 4901 TCGGCGGCGG CAAAATGATT GTTGACGCGG GGCAGGATAT CAATGTACGC
 4951 GCGAGCAACC TTATTCTGA TAAGGGCATT GTTTTAAAAG CAGGACACGA
 5001 CATCGATATT TCTACTGCCC ATAATCGCTA TACCGGCAAT GAATACCACG
 5051 AGAGCAAAAA ATCAGGCGTC ATGGGTACTG GCGGATTGGG CTTTACTATC
 5101 GGTAACCGGA AAATACCGA TGACACTGAT CGTACCAATA TTGTCCATAC
 5151 AGGCAGCATT ATAGGCAGCC TGAATGGAGA CACCGTTACA GTTGCAGGAA
 5201 ACCGCTACCG ACAAAACGGC AGTACCGTCT CCAGCCCGA GGGGCGCAAT
 5251 ACCGTCACAG CCAAAAGCAT AGATGTAGAG TTCGCAACA ACCGGTATGC
 5301 CACTGACTAC GCCCATACCC AGGAACAAAA AGGCCTTACC GTCGCCCTCA
 5351 ATGTCCCGGT TGTCCAAGCT GCACAAAAT TCATACAAGC AGCCCAAAAT
 5401 TTGGGCAAAA GTAAAAATA ACGCGTTAAT GCCATGGCTG CAGCCAATGC
 5451 TGCATGGCAG AGTTATCAAG CAACCAACA AATGCAACAA TTTGCTCCAA
 5501 GCAGCAGTGC GGGACAAGGT CAAAACAACA ATCAAAGCCC CAGTATCAGT

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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CGGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAAG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
5851 GGAATTACCG CCGGAGGAAA TATCGGTAAA GGTAAAGAGC AAGGGGGAAG
5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGCG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
6051 TGAACCTAT CAGAGCAAAC AGCAAAACGG CAATGTCCAA GTTACTGTCG
6101 GTTACGGATT CAGTGCAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACCAC AGCCGCTACG AAGGCAGAAG
6351 CTTCGGCATA GGCGGCAGTT TCGACCTGAA CGGCGGCTGG GACGGCACGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAAACAGC ACCACCCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCGG CATCGACACC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAACAGCT TCGACAAAGA
6651 CGCGGTGCGC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCC
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCG TGGAGGCCGA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAA AGCCGCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCTAT CTTGCCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCCGGCGGC GGCCTTCCC
7001 TTGCCGCACC GTATTTGGAC AAAGCGGCGG AAAACCTCGG TCCGGCGGGC
7051 AAAGCGGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAACTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAAGATTG AACAAATAGGC
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAATATGC CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGGTGGAC AAAGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGAATGACGA GCCTTGTCAG CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA CCCGACAGTT
7651 ACCGGCAGCG ATCCCTTATT GGCGGGTGCG GGAATATCC GTATCCCTGC
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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1 MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51 IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QQPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPQYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW GQDVRRVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGMYANKI TLISTVEQAG IRNQGWFFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNSVIPQ IPSTATSGS STVSVSKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLNCSGL
551 NAAKLRVSGD SFNNTVKGKL QAHD LAVNTQ TAKNSGHLIT QTGKIDNREL
601 HNAGEIAANN LTLHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNNLRN TGKVSVARLN TEGQTLDNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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901	ILLNREETTE	GSTKAGATAA	RKRLDIGAKE	IHNQEGALLS	SEGI FAVGNR
951	LDEQHHAAGM	ADTFVNGSAG	LEVQGDALMS	VRNMQNINNH	FKTETYLAKE
1001	EKQVRDYTVL	GQNTYYQAGK	DGLFDNSQCG	KDQTTATFHL	KNGSRIEANQ
1051	WHVRDYHIET	YKERIENRPT	AHITVGGDLT	ASGQNWLNKD	SRIVVVGGRII
1101	TDDLNQKEIT	NQSTTGKGRF	DAVGTOQWDSV	TKKGWYSGRK	RQRRTERNHT
1151	PYHDTQLFTH	DFDTPVSVIQ	QNAASPSFQP	AASAIKLIDG	VSTA AVNGQF
1201	IHTGNVVSLN	NATVTLPNSS	LYTTHPDNKG	WLVEDTPQFA	DYRRWLGS DY
1251	MLQQLQLDTN	HLHKRLGDGY	YEQKLVNEQI	HQLTGYRRLD	GYRSDEEQFK
1301	ALMDNGLATA	KTFGLTPGIA	LSAEQVARLT	SDIVWMENQT	VTLSDGSTQT
1351	VLVPKVVALA	RKGLDLNTSGG	LISAEQVLLK	LDNGNLNTSG	TIAGRQAVLI
1401	QARNINSNGN	IQADQIGLKA	EKSINIDGGQ	VQAGRLLTAQ	AQNINLNGTT
1451	QTSGNERNGN	TAIDRMAGIN	VVGSHTEQVD	NRTSDGILSL	HASNDINLNA
1501	ATVSNQVKDG	TTQITAGNNL	NLGTIRTEHR	EAYGTLDDEN	HRHVRQSTEV
1551	GSSIRTQNGA	LLRAGNDLKI	RQGELEAAEG	KTVLAAGRDV	TI SEGRQITE
1601	LDTSVSGSKS	GILSSTKTHD	RYRFSHDEAV	GSNIGGGKMI	VAAQGDINVR
1651	GSNLISDKGI	VLKAGHDIDI	STAHNRYTGN	EYHESKKSGV	MGTGGLGFTI
1701	GNRKTTDDTD	RTNIVHTGSI	IGSLNGDVT	VAGNRYRQTG	STVSSPEGRN
1751	TVTAKSIDVE	FANNRYATDY	AHTQEQQKLT	VALNVPPVQA	AQNFIQAQAN
1801	VGKSKNKRVN	AMAAANAAWQ	SYQATQGMQQ	FAPSSSAGQG	QNNNQSPSIS
1851	VSITYGEQKS	RNEQKRHYTE	AAASQIIGKG	QTTLAATGSG	EQSNINITGS
1901	DVIGHAGTAL	IADNHIRLQS	AKQDGESEQS	NKSSGWNAGV	AVKIGNGIRF
1951	GITAGGNI GK	GKEQGGSTTH	RHTHVGSTTG	KTTIRSGGSDT	TLKG VQLIGK
2001	GIQADTRNLH	IESVQDTEY	QSKQONGNVQ	VTVGYGFSAS	GSYRQSKVKA
2051	DHASVTGQSG	IYAGEDGYQI	KVRDNTDLKG	GIITSSQSAE	DKGNLFTQTA
2101	TLTASDIQNH	SRYEGRSFGI	GGSF DLNGGW	DGTVTDKQGR	PTDRISPAAG
2151	YGS DGD SKNS	TTRSGVNTHN	IHITDEAGQL	ARTGRTAKET	EAR IYTGIDT
2201	ETADQHSGLH	KNSFDKDAVA	KEINLQREVT	KEFGRNAAQA	VAAVADKLGN
2251	TQSYERYQEA	RTLLEAELQN	TSDEAEKAAF	RASLGQVNA	LAENQSRYDT
2301	WKEGGIGRSI	LHGAAGGLTT	GLSGEILAGG	GTSLAAPYLD	KAAENLGPAG
2351	KAAVNALGGA	AIGYATGGSG	GAVVGANVDW	NNRQLHPKEM	ALADKYAEAL
2401	KREVEKREGR	KISSQEAA MR	IRRQILRWVD	KGSQDGYTDQ	SVISLIGMKG
2451	EDKALGYTDW	YRDY GARNPQ	TYNDPKLFEE	YRRQDKPEYR	NLTWLHSGTK
2501	DTKIRQGERK	NEEFALNVAE	VLTSVNPNP	RIKQVPILAGI	RNLNKIKPTV
2551	TGSDPLLAGA	GNIRIPANGN	VAKGDRIPDT	ALASKGIKHK	DRKDQLEKK*

Homology with fha

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m564/fha
ID   FHAB_BORPE          STANDARD;          PRT;   3591 AA.
AC   P12255;
DT   01-OCT-1989 (REL. 12, CREATED)
DI   01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DI   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE   FILAMENTOUS HEMAGGLUTININ. . . .
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SCORES Init1: 190 Initn: 524 Opt: 594
Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

		10	20	30	40	50	60	
m564	.pep	MNRTLYKVVF	NKHRNCMIAVA	ENAKREGKNTAD	TQAVGILPNDI	AGFAGFIHSIS	VISVIFS	
		: : : :	: : :	: :	: :	: :	: : : :	
fhfab_borpe		MNTNLYRLVF	SHVRGMLVPV	SEHCTV-G-NT	FCGRTRG---	QARSGARATSL	SVAPNALA	
		10	20	30	40	50		
		70	80	90	100	110	119	
m564	.pep	LSLLLG-SAL	ILTSSSATAQ	GIVADKSAPA	QQQPTILQT	GNGIQPVNI	QTPTSAGVSVNQ	
		: : : :	: : :	:	: :	: :	: :	
fhfab_borpe		WALMLACTGL	PLLVTH---	AQGLV-----	P-QGQTQVLQ	GGNKVPVVNI	ADPNSSGGVSHNK	
		60	70	80	90	100		
		120	130	140	150	160	170	179
m564	.pep	YAQFDVGNR	GAILNNSRS	NTQTQLGGW	IQGNPWLARGE	ARVVVNQINSS	HSSQLNGYIEV	
		: : :	: : :	: : : :	: :	: : : : :	: : :	
fhfab_borpe		FQQFNVANP	GVVFNNG	LTLDGVSRI	GGALTKNP	NLTR-QASAIL	AEVTDTS	SPSRLAGTLEV
		110	120	130	140	150	160	

864

m564	.pep	760	770	780	790	800	810
		TLALNNADGTIQSAGNVSLQAKSLANNGLTAGNKLDIALTDDFVVERDLTAGKQL-NLS					
fhab_borpe		RL-----DGA-HAGGQLRVSSDQAALGSLAAKGELTVSAARAATVA-EL---KSLDNIS					
			720	730	740	750	760
m564	.pep	820	830	840	850	860	870
		IKGRLK-NTHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLNSDGLT					
fhab_borpe		VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE---GWGAVGADSL-					
		770	780	790	800	810	
m564	.pep	880	890	900	910	920	930
		HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETEGSTKAGAIAARKRLDI-GAKEIHN					
fhab_borpe		--GSDGAISVSGRDAVRVDQARSLADISLG---AEGGATLGAVEAAGSIDVRGGSTV--					
		820	830	840	850	860	
m564	.pep	940	950	960	970	980	990
		QEGALLSSEGIFAVGNRLDEQHHAAGMADTFVNGSAGLEVQGDALMSVRNMQINNHFKT					
fhab_borpe		AANSLHANRDVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV					
		870	880	890	900	910	920
m564	.pep	1000	1010	1020	1030	1040	1050
		ETYLAKAEK--QVRDYTVLGQNTYYQAGKDGLFDNSQGQKQDQTATFHLKNGSRLEANQ-					
fhab_borpe		ALQSAKASGTLHVQGGHELDLGTLAAVGAVDV---NGTGDVRVAKLVSDAGADLQAGRS					
		930	940	950	960	970	
m564	.pep	1060	1070	1080	1090	1100	
		--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNWLNKDSRIVVGGRIITDDLNQKE					
fhab_borpe		MTLGIVDTTGDQLQARAQQKLELGSVKSDDGGLQAAAGGALSAAAEEVAGALELS---GQGV					
		980	990	1000	1010	1020	1030
m564	.pep	1110	1120	1130	1140	1150	1160
		ITNQSTTGKGRDVAVGTDQWDSVTKKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV					
fhab_borpe		TVDRASASRARIDSTGSGVIGALKAGAVEAASPRRARRALR-----QDFFTPG					
		1040	1050	1060	1070	1080	
m564	.pep	1170	1180	1190	1200	1210	1220
		SVI---QQNAASPSFQPAASAIKLIDGVSTAANVGQRIHTGNVVSNNATVTLPNSSLYT					
fhab_borpe		SVVVRAGQGNVTVGRGDPHQVLAQGDIIIMDA--KGGTLLLRNDALTENGTVTISADSAVL					
		1090	1100	1110	1120	1130	1140
m564	.pep	1230	1240	1250	1260	1270	1280
		THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQLDTNHLHKRLGDGYEQLVNEQIHQ					
fhab_borpe		EHSTIESKISQSVLAAKGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRQIDV					
		1150	1160	1170	1180	1190	
m564	.pep	1290	1300	1310	1320	1330	1340
		LTGYRRLDGYSDEEQFKALMDNGLTAAKTFGLTPG-IALSAEQVARLTSDIVWMENQTV					
fhab_borpe		VDGRPQI----TDAVTGEARKDES SVSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--					
		1200	1210	1220	1230	1240	1250

865

m564	.pep	1350	1360	1370	1380	1390	1400
		TLSDGSTQTVLVPKVYALARKGDLNTSSGLISAEQVLLKLQNGNLNLSGTIAGRQAVLIQ					
fhab_borpe		--ENGASVTVRTT-----GNLVNKGYSAGKQGVLEV-GGALTNEFLVGSDDGTQRIE					
		1260	1270	1280	1290	1300	
m564	.pep	1410	1420	1430	1440	1450	
		ARNINSNGNIQ-----ADQIGLKAESINIDGGQVQAGRLLTAQ----AQNINLNGTT					
fhab_borpe		AQRIENRGTFQSQAAGTAGALVVKAAEAIIVHDGVMATKGEMQIAGKGGGSPTVTAGAKA					
		1310	1320	1330	1340	1350	1360
m564	.pep	1460	1470	1480	1490	1500	
		QTSGNERNGNTAI-DRMAGINVV-GSHTEQVDNRTSD-GILSLHASNDINLNAATVSNQV					
fhab_borpe		TTSANKLSVDVASWDNAGSLDIKKGAQVTVAGRYAEHGEVSIQGDYTVSADAIALAAQV					
		1370	1380	1390	1400	1410	1420
m564	.pep	1510	1520	1530	1540	1550	
		--KDGTQTITAGNNLNLGT-IRTE---HREAYGTLDENHRHVRQST-----EVGS					
fhab_borpe		TQRGGAANLTSRHDTRFSNKIRLMGPLQVNAGGPVSNLTGNLKVREGVTVTAASFDNETGA					
		1430	1440	1450	1460	1470	1480
m564	.pep	1560	1570	1580	1590	1600	
		SIRTQNGALLRAGNDLKIRQGELEAEEGKTVLAAGRDV--TISEGRQITELDTS---VSG					
fhab_borpe		EVMAKSATLTTSGAARN--AGKMVQKEAATIVAASVSNPGTFTAGKDITVTSRGGFDNEG					
		1490	1500	1510	1520	1530	
m564	.pep	1610	1620	1630	1640	1650	1660
		K---SKGILSSTKTHDRYRF---SHDEAV-GSNIGGGKMIVAAGQDINVRGSLNLSKGI					
fhab_borpe		KMESNKDIVIKTEQFSNGRVLDKAKHDLTVTASGQADNRGSLKAGHDFTVQAQRI--DNSG					
		1540	1550	1560	1570	1580	1590
m564	.pep	1670	1680	1690	1700	1710	
		VLKAGHDIDISTAHNRYTG-----NEYHESKKSVMGTGGLGFTIGNRKTTDDTDRTNIV					
fhab_borpe		TMAAGHDATLKAPHLRNTGQVVAGHDIHIINSAKLENTGRV--DARNIDALDVADFTN--					
		1600	1610	1620	1630	1640	1650
m564	.pep	1720	1730	1740	1750	1760	1770
		HTGSIIGSLNGDVTVAGNRYRQT---GSTVSSPEGRNTVTAKSIDVEFANNRYATDYA					
fhab_borpe		-TGSLEYAEHDA-TLTLAQGTQRDLVVDQDHILPVAEGTLRVKAKSLTEIETGNPGSLIA					
		1660	1670	1680	1690	1700	1710
m564	.pep	1780	1790	1800	1810	1820	1830
		HTQEQKGLTVALNVPVQAAQNFIAQAQNVGKSKNKRNVNAMAANAA-WQSYQATQMQQ					
fhab_borpe		EVQE-----NIDNKQA-----IVVGKDLTSL-SAHGNVANEANALLWAAGELTVKAQN					
		1720	1730	1740	1750		
m564	.pep	1840	1850	1860	1870	1880	1890
		FAPSSSAGQGQNNNQSPSISVSITYGEQKSRNEQKRHYTEAAASQIIGKGQTTLAATGSG					
fhab_borpe		ITNKRAALIEAGGNARLTAAVALLNKLGRIRAGEDMHLN---APRI-----ENTAKLSGEV					
		1760	1770	1780	1790	1800	1810
m564	.pep	1900	1910	1920	1930	1940	1950
		EQSNINITGSDVIGHAGTALIADNHIRLQSAKQDGEQSKNKSSGWNAGVAVKIGNGIRF					
fhab_borpe		QRKGVQDVGGGEHGRWSGIGYVNYWLRAGNGKKAGT-----IAAPWYGGDLTAEQSLIEV					
		1820	1830	1840	1850	1860	

866

		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGKEQGGSTTHRHVHVGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
				::		::	::::
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGHIIG-----DVDNRSV-					
		1870	1880	1890		1900	
		2020	2030	2040	2050	2060	
m564	.pep	IESVQDTETYQSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE					
		::::	::	::	::	::	::
fhab_borpe		VRTVSAMEYFKTFLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY					
		1910	1920	1930	1940	1950	1960
		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGKNLFTATLTASDIQNHS--RYEGRSFGIGGS					
		:::::				:::::	
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----PELDRGHTLESAGRKI-FGEY					
		1970	1980	1990		2000	2010
		2130	2140	2150	2160	2170	
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYSGDGSKNSTTRSGVNTNHIHITDEAG					
				:	:	:	:
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRVRVDQLG-----QRYGKALGGMDAETKEVDGIIQ					
		2020	2030	2040	2050	2060	2070
		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTKEFGRNAA					
		::	::	:		::::	:
fhab_borpe		EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGRV--LAKALS					
		2080	2090	2100	2110	2120	
		2240	2250	2260	2270	2280	2290
m564	.pep	QAAVAADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
		:::	:::	:::	:	:	:
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQTVLAAGAGLTLSNGAIHNGENA					
		2130	2140	2150	2160	2170	2180
		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYDTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK					
		:::	:		:	:	:
fhab_borpe		AQNRGRPEGLKIGAHSAHSVSGSFDALRDVGLEKRLDIDDALA AVLNPHIFTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1   atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accggcggct tccaatactt
101 ccctgcgttt cgcacgcgcg aacgacaccg gctcgcctgc acttctggct
151 acctgcacgc gtgcgatgtc caagtcgagc gcgaaatacg gaatacctc
201 tttgggcgaa gacgcgtccg accgtctgcc cgccccgcc gaagccgaca
251 atcagcacat gatcagactt gctcatcgtc tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1   MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1   ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

```

867

```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTGCG CGCCTGTTC CATTCTGGCG AAACCATATC AAGCTGCCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTGCG CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRТААVААCС HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSSIANSIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

              10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
              |||
g565           MDSTLSKTCCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
              10      20      30      40      50      60

              70      80      90      100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
              |||
g565           AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
 51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA
251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTGCG CGCCTGTTC CATTCTAGCG AAACCATATC AAGCTGCCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTGCG CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRТААVААCС HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSSIANSIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

              10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
              |||

```

868

```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
m565.pep  PKRKGAIIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
a565      PKRKGAIIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
m565.pep  KAMANTTSAFNTSSSIANSINTCRQPPINAX
           190     200     210
a565      KAMANTTSAFNTSSSIANSINTCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct ttccagacgg cattttgtat ggggggtaac
51 ggttggtcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 ttaccctaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggct
151 gccggccttg tgggtgattt ccacgcgttc gccgtcggtg gcgaagaggg
201 cggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgcggcg gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTCAG CCCGAGTAGC TCCTGCATAT CGTACAAACC CGTTTTGCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACCG GCGGCAAAGG TCATGCGCGT
151 GCTGGCCTTG TGGGTGATT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51  AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAHSA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m566/g566  93.1% identity in 116 aa overlap
           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||

```

```
a566.seq
1  ATGCCGCTCTG  AACAATATCT  TTTCAGACGG  CATTTTGTAT  GGGGGTTAAC
51  GGTGTGTTACG  CCCGAGTACG  TCCTGCATAT  CGTACAAACC  CGTTTTACCG
101 TTTACCCAAA  TCGCGGCGCG  GACGGCAAAGG  TCATGCGGCT
151 GCTTGCTTTG  TGGGTGATTT  CCACGCGCTC  GCCGTCGGTG  GCGAAGAGGG
201 CGGTGTGGTC  GCCGACGATG  TCGCCCGCGC  GGACGGTGGC  AAAGCCGATG
251 GTGGACGGAT  CGCGCGGGCC  GGTGTGGCCT  TCGCGGCCGT  AAACGGCGCA
301 TTGTTTGAGG  TCTCTGCCGA  GCGCGCCGGC  GATGACTTCG  CCCATGCGTA
351 A
```

a566.pep

1	MPSEQYLFR	HFVWGLTVVQ	PEYVLHIVQT	RFTVYPNCGA	DGAGGKGHAA
51	ACLVGDFHAL	AVGGEEGGVV	ADDVARADGG	KADGGRIARA	GVAFAAVNGA
101	LFEVSAERAG	DDFAHA*			

	10	20	30	40	50	60
m566.pep	MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL					
a566	MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL					
	10	20	30	40	50	60
	70	80	90	100	110	
m566.pep	AVGGEEGGVVADDVACADGGKADGRRIRARTGVAFAAVNGALFEVSAERAGDDFAHAX					
a566	AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX					
	70	80	90	100	110	

```
g567.seq..
1  atgcgacgac  gggcagcggc  atcgacaagg  cgggtttgca  gtcggcggtt
51  tatcaggtct  tattgggcga  tgcggacgtg  cagtcggcgg  cggtacgcag
101 caaagagggc  ggatacggcg  tgttggtgct  gaacgcgcgc  gcttcgcggc
151 gcggaaatcg  agctggtgca  ggaaatcgcc  cggsaagtgc  gtttgaaaaa
201 cgcgctcaag  gcagtgggcg  aagattacga  ctttatcctg  atcgactgtc
251 cgcttctgct  gacgctgttg  acgcttaacg  gcttggtggc  ggcgggcggc
301 gtgattgtgc  cgatgttgtg  cgaatatatt  gcgctggaag  ggatttccga
351 tttgattgcy  accgtgcgca  aaatcgcgtc  gcgggtcaat  cccgatttgg
401 acatcacggg  catcgtgcgt  acgatgtacg  acagccgcag  caggctggtt
451 gccgaagtca  gcgaacagtt  gcgcagccat  ttcggggatt  tgctttttga
501 aaccgccatc  ccgcgcaata  tccgccttgc  ggaagcgccg  agccacggta
551 tgccggtgat  ggcttaacga  gccgaggcaa  aggggtgcca  ggcgtatctt
601 qccttgccga  acgaattagc  qccgaagggt  tcggggaaat  ag
```

```
g367.pep
  1  MRRRAAATR  RVCSPAFIRS  YWAMRTCSRR  RYAAKRADTA  CWVRTRALAG
  51  AEIELVQEIA  REVRLKNALK  AVAEDYDFIL  IDCPPSLTLL  TLNGLVAAGG
101  VIVPMLCEYY  ALEGISDLIA  TVRKIRQAVN  PDLDTGIVR  TMYDSRSRLV
151  AEVSEQLRSH  FGDLFFETAI  ERNIRLAEAP  SHGMPVMAYD  AQAKGAKAYL
201  ALADELAARV  SGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
  1  ATGAGTGCGA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
 51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101  GCGTGCTGGT GGTTCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151  GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201  CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
251  CTGTGTTGGG TGCGAACC GCCTGGCCG GCGCGGAAAT CGAACTGGTG
301  CAGGAAATCG CCCGGAAGT GCGTTTGAAG AACGCGCTCA AGGCAGTGGA
351  AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401  TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451  TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501  CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGACATCAGG GGCATCGTGC
551  GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601  TTGCGCAGCC ATTTGCGGGA TTTGCTTTTT GAAACCGTCA TCCCGCGCAA
651  TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701  ACGCGCAGGC AAAGGTACC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751  GCGGCGAGGG TGTCGGGGAA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
  1  MSANILAIAN QKGGVGKTTT TVNLAASLAS RGRVLLVVDL DPQGNATTGS
 51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101  QEIAREVRLK NALKA VEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151  CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201  LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGT KAYLALADEL
251  AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

      60      70      80      90      100      110      119
m567.pep  GYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKA VEED
g567      AFIRSYWAMRTCSRRYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKA VEED
           20      30      40      50      60      70

      120     130     140     150     160     170     179
m567.pep  YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
g567      YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
           80      90      100     110     120     130

      180     190     200     210     220     230     239
m567.pep  TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKG
g567      TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKG
           140     150     160     170     180     190

      240     250
m567.pep  TKAYLALADELAARVSGKX
g567      AKAYLALADELAARVSGKX
           200     210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
  1  ATGAGTGCGA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
 51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101  GCGTGCTGGT GGTTCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151  GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201  CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
```

871

```

251 GCGTGTGGG TGCGAACCGC GCGCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCCTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTT GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCTGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
  1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
  51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYGVLGANR ALAGAEIELV
 101 QEIAREVRLK NALKAVAEDY DFILDCPPS LTLTLNGLV AAGGVIVPML
 151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
 201 LRSHEGDLDF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
 251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

              10      20      30      40      50      60
m567.pep    MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKAGLQSG
a567        MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              10      20      30      40      50      60

              70      80      90     100     110     120
m567.pep    VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
a567        VYQVLLGDADVKSAAVRSKEGGYGVLGANRALAGAEIELVQEIAREVRLKNALKAVAEDY
              70      80      90     100     110     120

              130     140     150     160     170     180
m567.pep    DFILDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
a567        DFILDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
              130     140     150     160     170     180

              190     200     210     220     230     240
m567.pep    GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAGT
a567        GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
              190     200     210     220     230     240

              250
m567.pep    KAYLALADELAARVSGKX
a567        KAYLALADELMARVSGKX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
  1 atgctcaggg tcagaccggt attatttgcc gtcaaggcct ccgcctcttc
  51 gataccttgc agaatctgcc gattaaagcg ttcgcggctg cccaatatat
 101 tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
 151 tgtaaaaaca gcccatcag gaacgaaact tcgtcttcg ggcgacgcca
 201 gttttcgggt gaaaaggcaa acacggctcag atattgcacg cccagtttgg
 251 cgcaatgctt caccatatat tccaacgcgt ccaagccgcg tttgtgtccc
 301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
 351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```

```
g568.pep
  1  MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCKA
 51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101  IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSFAFKRL
151  NAAP*
```

```
m568.seq
1  ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC
51  GATGCCCTGC AGAATCTGCC GGTGAAGCG TTCCGCGGCT CCCAATATCT
101 TCAGGCCGAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TCGCAAGACC
151 TGTAAAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTTCGCC CAACGGCCGT TTGCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTGCGGGT CGGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAAGTT AAATTGCCAT CAAATCTTCT TCTTTTGGAC
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCCGTGAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTT ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATAGAGA
651 CGCGGCCCTT TTCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA
```

```
m568.pep..
1  MLRVRPVLFA  VNASASSMPC  RICRLKRSRL  PNIFRRILFS  CRRRTCFCKA
51  CKNSPIRNET  SSSGRRQFSV  EKANTVRYCT  PSLAQCFITF  SNASKPRLCP
101 IMRGRKRFFA  QRPLPSIITA  ICLGMAVCSK  TACVLLFMSA  FRGSAFKCRL
151 NAEPCRLNCH  QIFFFGSQEF  VGFGNVFVGQ  FLNRFFAATC  LVFGNFFVFE
201 EFFDVVVGIA  AHVADRDAAF  FRFAAYDFNQ  VFAAFLGQHG  HRHADQVADS
251 CRVOSQ*
```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	: :					
g568	MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	:					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIIRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLGMAVCSKTACVLLFMFAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGENVFVGQ					
	: :					
g568	MCLGMAVCSKMVCVLLFISAFRGSAFKCRLNAAPX					
	130	140	150			
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVEEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
  1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
 51 GATGCCCTTC AGGATTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTAGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CGGCATTCAA ATGCCGTCGT
451 AACGCCGAAC CGTGCAGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTT TTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCCTCG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
  1 MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
 51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCLRNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIKRLKRSRLPSIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
	130	140	150	160	170	180
m568.pep	ICLMAVCSKTACVLLFMSAFRGSFAFKCRLNAEPCLRNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLMAVCSKTACVLLFMSAFRGSFAFKCRLNAEPCLRNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADGDAAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADGDAAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	HRHADQVADSCRVSQVX					
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
  1 atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
 51 gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgccggc
101 tgattgcctt gaccgccttg tgggagatg cccgatggc cggtttgtgc
```


874

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa tttggtttgg tatgttggtt
251 tggcattttt gctcgccggt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgctcatgcc
351 gttttggttc gcgctcgat cctggcgcc cgcacccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNNGWQVYAV GWLLLMPEFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCT GATTGCCCTT TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGTTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTITG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGTTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CCGTATGCTG CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGCGCG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTGCA TACAGGCTGG
601 TCGATACCG TGTTAATCGG TTGGTGTGCG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGGACAC GCGGCGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCACGCTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNNGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAIKPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRDLSL
251 IAVISVYAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m569.pep	ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAIKPGKSWEGAIGGAVC					
g569	ALVSLAPASRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCT GATTGCCCTT TGGGAATATG CCCGTATGGG CGGTTTGTGC

```

875

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTG GTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCACGCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGCGGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

a569.pep

```

1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLI GLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRDTS
251 IAVISVYAAM MSVLN*

```

m569/a569 99.6% identity in 265 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
a569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
a569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m569.pep	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
a569	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
	130	140	150	160	170	180
	190	200	210	220	230	240
m569.pep	VAVYMTAVRSAGWLAFDTGWFDTVLI GLVL TVVSVCGDLL ESWLKRAAGI KDSSKLLPGH					
a569	VAVYMTAVRSAGWLAFDTGWFDTVLI GLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH					
	190	200	210	220	230	240
	250	260				
m569.pep	GGVFDRDTSLIAVISVYAAMMSVLNX					
a569	GGVFDRDTSLIAVISVYAAMMSVLNX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1  atgatccgtt tgaccgcgc gtttgccgcc gccctgatcg gtttatgctg
51  caccacaggc gcgcacgcgc acaccttcca aaaaatcggc tttatcaaca
101 cggagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gatttggaag ggcagctcgc cggcggcaaa ctaaggacg
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggt cgaagcgttc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaacgccaa ccgcgtcatc gtcaaaatcg

```

```

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
451 acccaatacg acgttaccga cagcgtcatt aaagaaatga acgcccgtcg
501 a

```

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

```

g570.pep..
  1 MIRLTRAFAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151 TQYDVTDSVI KEMNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

```

m570.seq..
  1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
 51 CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
501 A

```

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

```

m570.pep
  1 MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQNVYVN
151 TQYDVTDSVI KEMNAR*

```

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MIRLTRAFAAALIGLCCTTGAAHADTFQKIGFINTERIYLESKQARNIQKTLDGEFSARQD					
	10	20	30	40	50	60
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLDKAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLDKAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
m570.pep	SLQQNANRVIKIAKQEGYDVILQNVYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

```

a570.seq
  1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
 51 CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

```

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101  RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIIYVN
151  TQYDVTDSVI KEMNAR*

m570/a570  97.6% identity in 166 aa overlap

              10      20      30      40      50      60
m570.pep    MTRLTRAFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD
a570         MTRLTRAFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD
              10      20      30      40      50      60

              70      80      90     100     110     120
m570.pep    ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
a570         ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              70      80      90     100     110     120

              130     140     150     160
m570.pep    SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX
a570         SLQQNANRVIVKIAKQEGYDVILQDVIIYVNTQYDVTDSVIKEMNARX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttggt gttaccgttt tcggcgcgcg
 51  tataggttct gccgtccac acgctgcctg cgtcgcaaaa caggctcagg
101  cggacggtgc gtgcgtcttt cgcaccgggc atcggaaga gcagctcggc
151  ggagacgttg gcttttttgt tgcgcgcta gctgattttt tcgccgtatt
201  cgtcatacac ttccgggccc agcgtgccgc ttctgtagcc gcgcaccgaa
251  cccaggccgc cgcgtagaaa gttttcaaa aaggggattt ctttggttct
301  gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351  ttttgc...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRFV VTVEGGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG
 51  GDVGFFVAAV ADFFAVFVIH FRAERAAVFA AHRTQAAAVE VFKEGDFFGS
101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCCG CCGGTCGCGG
 51  AACTGCTGTT GTCGTCGTAG GTTTGCCGT CCCACACGCT GCCTGCGTCG
101  GCAAACAGGC TCAGGCGGAC GGTGCGCGC TCTTTCGCGC CGGGCATCGG
151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201  TTTTTCGCC GTATTCGTCA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
251  TATCCGCGCA CCGAACCCAG GCCGCGCGC TAGAAGTTT CAAAGAAGGG
301  GATTTCCTTG GTTCTGCCGT AGCCGCCGC AATGCCGACT TCGCCGCCGA
351  GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAGGT TTGGTTGTGG
401  GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTCGGCGTT
451  CACGCCCGTC AGGTAGCCGC GCGTCGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTA VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
 51  EEQLGGDVGF FVAAVADFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101  EFFGSAVAAR NADFAAEHQR EGFAQGEEPG LVVGGGVVLQ FAARQGDFGV
151  HARQVAARRP *

```

878

m571/g571 93.1% identity in 102 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLNPAAGRGTAVVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
g571      MRVFRVNRFFVTVFGGGIGSAVPHAACVKGQAQADGACVFRTGHREEQLGGDVGF
           10      20      30      40      50

      70      80      90      100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQR
g571      FVAAVADFFAVFVIHFRAERAAAFVAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQR
           60      70      80      90      100     110

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGGVVLQFAARQGDFGVHARQVAARRPX
g571      EGFA
           119

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCCG CCGGTCGCGG
51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTGCCG CCGTAGCTGA
201 TTTTTCGCC GTATTCGTCA TACACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCCAG GCCGCCGCCG TAGAAGTTT CAAAGAAGGG
301 GATTCTTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGGTTTTG CTTAAGGGGA AGAACCAGGT TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCG GGCAGGGCGA TTTCGGCGTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```

a571.pep
1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVKGQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQR EGFA*GEEPG LVVGGGVVLQ FAAGQGDFGV
151 HARQVAARRP *

```

m571/a571 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLNPAAGRGTAVVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
a571      MGIAGAVNVLNPAAGRGTAVVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           10      20      30      40      50      60

      70      80      90      100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQR
a571      FVAAVADFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQR
           70      80      90      100     110     120

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGGVVLQFAARQGDFGVHARQVAARRPX
a571      EGFAXGEEPLVVGGGVVLQFAAGQGDFGVHARQVAARRPX
           130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq..

g572.pep..

m572.seq.

m572.pap..

m572/g572 92.9% identity in 295 aa overlap

```

              10      20      30      40      50      60
m572.pep      MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVPVDSHNAVF
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572           MCAIVGAAGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVPVDSHNAIF
              10      20      30      40      50      60

              70      80      90      100     110     120
m572.pep      QVLPRDYAGRLNEHGIASIIILTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572           QVLPRDYDTRLNEHGIDSIIILTASGGPFLTDLSTFDSITPEOAVKHPNWRMGRKISVDS

```

880

	70	80	90	100	110	120
	130	140	150	160	170	180
m572 . pep	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
g572	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572 . pep	CLGLPERIDSGVGLDFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGLDFGALSALTFOKPDFGRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572 . pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGQIKFTDIAKTVAHCLAQDFSNGMGDIEGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```
a572 . seq
1   ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGCGGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCCGTG CAAACGGCGC GGCACTGCTG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTT CAAGTTTTGC CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGGCC GTTCTTGACC GCCGATTTAA ACACGTTCTG CAGCATTACG
301 CCCGACCAAG CGGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGAGAGCT ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGC
501 GCAACTGGGC AATCCCGATA TGCGAACGCC TATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCT GGTGTCGGCG ACCTGGATTT CGACGCATTG
601 TCCGCGCTGA CCTTCCAAAA GCCCGACTTT GACCGCTTCC CCTGCCTGAA
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TGCCTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCGCCCT TTTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTTC
801 AGACGCATA GCGACATAG GGGGGCTCTT GCGCAAGAT GCCCGACAC
851 GCGACAAGC GCGGCATTT ATCGGCACAC TGCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```
a572 . pep
1   MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPRDYTGR LNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFOKPDF DRFPCLKLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*
```

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572 . pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572 . pep	QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	QVLPRDYTGRLNEHGIASII LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120

881

	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDPKLEVVIIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDPKLEVVIIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1   atgccctggt  tgtgccgcct  taatcgcaat  atcggcagtt  tccaaatcac
51  gaatctcacc  gaccataatg  atgtccgggt  cctgacgcag  gaaagacttc
101 aaagcagcgg  caaaagtcag  accctgctta  tcattgacgt  taacctgatt
151 gatgcccgcc  aggttaatct  cggcagggtc  ttccgccgtt  gcaatattta
201 ccgactccgt  attcaaaata  ttcaaacagg  tatagagcga  caccgtctta
251 cccgaacccg  tcggaccggt  taccagcacc  atcccgttaag  gacggtgaat
301 cgcttccaac  aacaattttt  tctggaacgg  ctcaaaaccg  agctggtcga
351 tgttcaaaga  cgccgcatcg  gaattcaaaa  tccgcatcac  gaccttttcg
401 ccaaacagcg  tcggcaatgt  gctgacacgg  aaatcgacag  gcttgccgcc
451 cttttgaaag  gtcagctgca  tcctaccgtc  ctgccgtatc  cgtttttcgg
501 aaatgtccaa  acgcgacatt  accttaatcc  gggaagcaag  ctgccccctt
551 accgcaatgg  cgggctgaac  cacctcgagg  agctgcccgt  ccacacggaa
601 accgatacgc  gcatttgtgt  cgtaaaactc  gaaatggatg  tcggatgccc
651 cgctacgcaa  ggcattccgc  aaagttttat  ggataaacct  cggaacaggg
701 ccgtctctcg  cctcctcgtc  gtcgatatac  aggggtgtgc  ttctctcttc
751 ctcttgcccc  tccccaaagt  cctgaagcag  cgatgtcgaa  cggaaccca
801 cccaatcgag  caaacccgcc  aactgggtcat  cctcgacaat  gaccaactca
851 accgcaatcc  ctgcggcaga  aaccgttttc  tgaatttgcg  gcattctggg
901 cggatcggaa  accgcaaaaa  atactttgtc  gccccacgg  aaaaccggca
951 cacagtggaa  ctccaccatc  tgctctctcg  tcaacacccc  catcagcacc
1001 ctgtggcgcg  gataatgacg  caaatcaaga  atcgaataac  tgaacaccct
1051 cgcaatcaat  gccgcaagcg  acttgggcga  aatgacaccg  tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1   MPCLRLNRN  IGSFQITNLT  DHNDVRVLTQ  ERLQSSGKSQ  TLLIIDVNLI
51  DARQVNLGRV  FRCNIYRLR  IQNIQTGIER  HRLTRTRRTG  YQHPVTRTVN
101 RFQQQFFLER  LKTELVDVQR  RGIGIQNPHH  DLFAKQRRQC  ADTEIDRLAA
151 LLKGQLHPTV  LRYPPFGNVQ  TRHYLNPGSK  LPPYRNGRLN  HLAELPVHTE
201 TDTRIVFVKL  EMDVGCPATQ  GIRQSFMDKP  RNRAVFCLLV  VDIQGVAFLE
251 LLPLPKLLKQ  RCRTTRTHPI  E  QTRQLVILDN  DQLNRNPGCR  NRFLNLRHLG
301 RIGNRKKYFV  APTENRHTVE  LHHLLLRQHP  HQHPVARIMT  QIKNRITEHP
351 RNQCRKRLGR  NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1   ATGCCCTGTT  TGTGCCGCCT  TAATCGCAAT  ATCGGCAGTT  TCCAAATCAC
51  GAATCTCACC  GACCATAATG  ATGTCCGGGT  CCTGACGCAG  GAAAGACTTC
101 AAAGCAGCGG  CAAAAGTCAG  GCCCTGCTTA  TCATTGACGT  TAACCTGATT
151 GATGCCCGGC  AGGTAAATCT  CGGCAGGGTC  TTCCGCCGTT  GCAATATTTA
201 CCGACTCCGT  ATTCAAAATA  TTCAAACAGG  TATAGAGCGA  CACCGTCTTA
251 CCCGAACCCG  TCGGACCGGT  TACCAGCACC  ATCCCGTAGG  GACCGTGAAT
301 CCTACCAAC  aCaw.TTTT  TCTGAAACGG  CTCAAAACCG  AGCTGGTCGA
351 TGTTCAAAGA  CGCGGCATCG  GAATTCAAAA  TCCGCATCAC  GACCTTTTCG
401 CCAAACAGCG  TCGGCAATGT  GCTGACACGG  AAATCGACAG  GCTTGCCGCC
451 CTTTGTAAAG  GTCAGCTGCA  TCCTGCCGTC  CTGCGGTATC  CGTTTTTCGG
501 AAATGTCCAA  ACGCGACATT  ACCTTAATCC  GTGAAGCAAG  CTGCCCCCTT

```



```

551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCCG CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCAC
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

m573.pep..

```

1  MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51  DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXFLLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

m573.pep	10	20	30	40	50	60
	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV					
g573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV					
m573.pep	70	80	90	100	110	120
	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRYQHXFLLKRLKTELVDVQR					
g573	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRYQHXFLLKRLKTELVDVQR					
m573.pep	130	140	150	160	170	180
	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
g573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPPFGNVQTRHYLNPGSK					
m573.pep	190	200	210	220	230	240
	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
g573	LPPYRNGRLNHLAELPVHTETDTRIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
m573.pep	250	260	270	280	290	300
	VDIQGVAFLELLPLPKLLKQRCRTTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	VDIQGVAFLELLPLPKLLKQRCRTTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
m573.pep	310	320	330	340	350	360
	RIGNRKKYFVAPTENRHTVELHHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

883

a573.seq

```

1   ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAAATTTT TCTGAAACGG CTCAAACCCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGTAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GCGAAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCTGCCCC TCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTT TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCACCATC TGCTCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCTT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1   MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51  DARQVNLGRV FRRCNIRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPFEGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAQ GIROSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQTLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m573.pep	FRRCNIRLR IQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXXFFLKR LKTELVDVQR					
a573	FRRCNIRLR IQNIQTGIERHRLTRTRRTGYQHHPVGTVNRFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFEGNVQTRHYLNXPXSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFEGNVQTRHYLNPGSK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAQGIRQSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAQGIRQSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

884

	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
a573	NDTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1  atgtctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51  attgtggatt atcctgctgc cgattatcct ttgcccgcgc ttcttcacga
101 tgggctgggt tggcgccgcg gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc cttcgggatt ttataaaagc ctggacgctt tggcgaccg
201 caacagcggg cgcgcggcaa gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaatctta ccgtcagcgc
301 ggcgaaaacg acaaaagccat caacatacac cggacaatgc tgcattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaa
401 actaccaaag cgcgggtttg gtcgatcgtg ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaagcc agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcggtt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgcgcgcgtc
751 gaagcctatg ccgccatcga gcagcaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaccg tctgacagga tatatgcaga cgtttcccga acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg ctttaagggcg agaagaagc
951 cgcgcaaacg gccgtcgagc ttgtccgcgc caagcccgac cttaacggcg
1001 tgtaccgcct gctcggtttg aaactcagcg atttggatcc ggcttggaaa
1051 gccgatgccg acatgatgcg ttcggttatc ggacggcagc tccagcgcag
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagtttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1  MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEAREQA RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQAAALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQGK PEEGLNRLTG YMQTFPELDL
301 INVVEKSLLL LKGEKEAAQT AVELVRRKPD LNGVYRLLGL KLSLDLPAWK
351 ADADMMSRVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1  ATGCGCCCGA ATCTACCAAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCCGGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGTGAAC CTCACCTCGC GCAAACTTTA CCGCCAGCGT
301 GGCGAAAACG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351 CGATACGGTC GCGGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGGG
451 CTGCAAGACG GTAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTCGATG TCGCGCGTTT

```

```

651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAACTCAGCG ATATGAATCC GGCTTGGAAA
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCT
1151 GGCCTGCCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```

1 MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGMAREAR RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQAAALFES NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQKG PEEGLNRLTG YMQTFPELDL
301 INVVEKSLLL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSMDNPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFESQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

m573/g573 97.8% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA KSIPSGFYKS					
g574	MLPNLPNSLK KADMDNELWI ILLPIILLPV FFMGWFAAR VDMKTVLKQA KSIPSGFYKS					
	10	20	30	40	50	60
m574.pep	LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR GENDKAINIH RTMLDSPDTV					
g574	LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR GENDKAINIH RTMLDSPDTV					
	70	80	90	100	110	120
m574.pep	LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR GENDKAINIH RTMLDSPDTV					
g574	LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR GENDKAINIH RTMLDSPDTV					
	70	80	90	100	110	120
m574.pep	GEKRARVLFE LAQNYQSAGL VDRAEQIFLG LQDGMAREAR RQHLLNIYQQ DRDWEKAVET					
g574	GEKRARVLFE LAQNYQSAGL VDRAEQIFLG LQDGMAREAR RQHLLNIYQQ DRDWEKAVET					
	130	140	150	160	170	180
m574.pep	GEKRARVLFE LAQNYQSAGL VDRAEQIFLG LQDGMAREAR RQHLLNIYQQ DRDWEKAVET					
g574	GEKRARVLFE LAQNYQSAGL VDRAEQIFLG LQDGMAREAR RQHLLNIYQQ DRDWEKAVET					
	130	140	150	160	170	180
m574.pep	ARLLSHDDQT YQFEIAQFYCE LAQAALFES NFDVARFNVG KALEANKKCT RANMILGDIE					
g574	AQLLSHDEQT YQFEIAQFYCE LAQAALFES NFDVARFNVG KALEANKKCT RANMILGDIE					
	190	200	210	220	230	240
m574.pep	ARLLSHDDQT YQFEIAQFYCE LAQAALFES NFDVARFNVG KALEANKKCT RANMILGDIE					
g574	AQLLSHDEQT YQFEIAQFYCE LAQAALFES NFDVARFNVG KALEANKKCT RANMILGDIE					
	190	200	210	220	230	240
m574.pep	HRQGNFPAAV EAYAAIEQQN HAYLSMVGEK LYEAYAAQKG PEEGLNRLTG YMQTFPELDL					
g574	HRQGNFPAAV EAYAAIEQQN HAYLSMVGEK LYEAYAAQKG PEEGLNRLTG YMQTFPELDL					
	250	260	270	280	290	300
m574.pep	HRQGNFPAAV EAYAAIEQQN HAYLSMVGEK LYEAYAAQKG PEEGLNRLTG YMQTFPELDL					
g574	HRQGNFPAAV EAYAAIEQQN HAYLSMVGEK LYEAYAAQKG PEEGLNRLTG YMQTFPELDL					
	250	260	270	280	290	300
m574.pep	INVVEKSLLL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSMDNPAWK ADADMMRSVI					
g574	INVVEKSLLL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSMDNPAWK ADADMMRSVI					
	310	320	330	340	350	360
m574.pep	INVVEKSLLL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSMDNPAWK ADADMMRSVI					
g574	INVVEKSLLL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSMDNPAWK ADADMMRSVI					
	310	320	330	340	350	360
m574.pep	GRQLQRSVMY RCRNCHFESQ VFFWHCPACN KWQTFTPNKI EVX					
g574	GRQLQRSVMY RCRNCHFESQ VFFWHCPACN KWQTFTPNKI EVX					
	370	380	390	400		
m574.pep	GRQLQRSVMY RCRNCHFESQ VFFWHCPACN KWQTFTPNKI EVX					
g574	GRQLQRSVMY RCRNCHFESQ VFFWHCPACN KWQTFTPNKI EVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1  ATGCGCCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTTGGATT ATCCTGCTGC CGATTATCCT TTGCCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCTCG GCAAACCTTA CCGCCAGCGT
301 GGCAGAAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TCGGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTTGAAACC GCCCGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG CCGCGCGTTT
651 CAATGTGCGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCGCTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTGCG GTTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTCAACGCGC
1001 TGTACCGCCT GCTTGGTTTG AAACTCAGCG ATTTGGATCC GGCTTGAAAA
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTCT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1  MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLTDSPTT GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQAALEFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDLDPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFESQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m574/a574 97.5% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
a574	MRPNLPNSLEKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINMHQTLLDSPDTT					
	70	80	90	100	110	120
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINMHQTLLDSPDTT					
	70	80	90	100	110	120
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET					
a574	GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE					
	190	200	210	220	230	240
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE					

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	190	200	210	220	230	240
	250	260	270	280	290	300
m574 . pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGVMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGVMQTFPELDL					
	310	320	330	340	350	360
m574 . pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLGVYRLLGLKLSDMNPAWKADADMMRSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLGVYRLLGLKLSDLPAWKADADMMRSVI					
	370	380	390	400		
m574 . pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575 . seq      (partial)
1  ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51  ccgtaacaaca gtccgctttc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggaacttc actggctgtt tccgcaacag
151 gttcggaaac ggtgttaccg gtttcgtcgg tcggcgtgtc gatggcagaa
201 gcgccggcctt cttggggggg cggtattcggc agcgggttcc gatgcggcag
251 tatttgcagc gggtaacagg cgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggttcgggt cgaacggccg gttttccgc
351 ttttgcttcg ggcgcggcaa cttttgttc aggtttttca accggtttt
401 cgacagggtt ctctatcggg ttctccacag ttgcctgttt ggacgggtta
451 gacggcatgg atgcagtttc ggctttgggt ttcgccgttt gcggtttggg
501 ttgttccgct ttgatttttt tgggtgtgtc cgctttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575 . pep      (partial)
1  ..MPCLRRQAAR CTNRRTDRQT VRFRLLLRQK FVRQVRQVR RQLHWLFPPQ
51  VRKRCYRFRR SACRWQKRRL LGGADSAAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGSG RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACL DGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAAALI LFRFGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575 . seq .
1  ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCCC GTTTTGCGCG GCTGCCAGGC TGTGCAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGT
401 TTGCCGATAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAAATGCC GCGCCTCCG CGGCAAGCAG
651 CAAGGTGTAC GAACGCCGA ACAGACCGTC AAACAGTCCG CTTTCGGTTT
701 CTTCTTCGGC AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTGATG GGCAGAAGCG GCGGCTTCTT GGGGGGCGGA
801 TTCGGCAGCG GTTTCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 GTCGAACGGC GGGTTTTCCT GCTTTTGCTT CGGGCGCGGC AACTTTTGCT
901 TCAGGTTTTT CAACCGGTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTCGGGTT
1001 GTTCCGCTTT GATCCTGTTC AGATTCGGAA TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

```
m575.pep
  1  MVSGEAEFRK PASPEGEAGF AEAUVSSVPIW LFEGRLSEKS VSTVSGLFSA
 51  VWATDSGSGV SMTISTGLYG LKVSQSYTSL VDSMAFQSAS ARFWVSSSCV
101  SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
151  TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201  RKSSSRINA APPPASSKVY EPPNRPNSNP LSVSSSAETC STGSETALPV
251  SSVGVSMAEA AASWGADSAA VSDAAVFAAG TGSGRTAGFS AFASGAATFA
301  SGFSTGFSTV ACLDGS DMD AVSALGFAVC GLGCSALILF RFGM*

m575/g575 70.2% identity in 114 aa overlap

      240      250      260      270      280
m575.pep  SSAETCTGSETALPVSSVGVSMEEAAASWGADSAVSDAAVFAAGT-----
              |||||
g575      LHWLFPPQVRKRCYFRRSACRWQKRRLGGADSAVSDAAVFAAGTGPWRSVAEAGVS
              50      60      70      80      90     100

      290      300      309      310      320
m575.pep  -----SGRTAGFSAFASGAATFASGFSTGFST-----VACLDGSDGMDAVSALGFA
              |||||
g575      DTAGLGGRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA
              110     120     130     140     150     160

      330      340
m575.pep  VCGLGCSALI-----LFRFGMX
              |||||
g575      VCGLGCSALIFLGAAALILFRFGMX
              170     180
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

```
a575.seq
  1  ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
 51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101  GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCGGGTTT GTTTTCGGCA
151  GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201  GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251  TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301  AGTGCGCCGG ATAAATGCC GTTTGCGCG GCTGCCAGGC TGTCGAAATC
351  CAAGTCGATG CGGTTGGAAG GCGTATCGGT TCGACATCG AACGTTTGTT
401  TTGCCGACAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTTT
451  ACATCGTTTT TCGAGCGGG TTCGGGCGTT GCCGAGTTT CGACTTCGGC
501  AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551  CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601  CGCAAAGCA GCAGCAGGGC GATCAATGCC GCGCCTCCGC CGGCAAGCAG
651  CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG
701  AAACCTGTTT GACAGGTTTC GAAACGCGCT TACCGGTTTC GTCGGTCGGC
751  GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT
801  TTCCGATGCG GCAGTATTTG CAGCGGTAC AGGTTGCGGT CGAACGCGCG
851  GTTTTCCGC TTTTGCTTCG GGCGCGGCAA CTTTGTCTTC AGGTTTTTCA
901  ACCGTTTCT CTACCGTTGC CTGTTTGGAC GGTTCGGACG GCATGGATGC
951  GGTTTCGGCT TTGGGTTTCG CCGTTTGGCG TTTGGGTTGT TCCGCTTGA
1001 TCCTGTTTCA ATTCCGAATG TGA
```

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

```
a575.pep
  1  MVSGEAEFRK PASPEGEAGF AEAUVSSVPIW LFEGRLSEKS VSTVSGLFSA
 51  VWATDSGSGV SMTISTGLYG LKVSQSYTSL VDSMAFQSAS ARFWVSSSCV
101  SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
151  TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201  RKSSSRINA APPPASSKVY EPPNPLSVS SSAETCTSGS ETALPVSSVG
251  VSMEEAAASW GADSAVSDA AVFAAGTSGS RTAGFSAFAS GAATFASGFS
301  TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *
```

889

m575/a575 98.8% identity in 344 aa overlap

m575.pep	10	20	30	40	50	60
	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVSTV	SGLFS	SAVWATDSGSGV
a575	10	20	30	40	50	60
	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVSTV	SGLFS	SAVWATDSGSGV
m575.pep	70	80	90	100	110	120
	SMTISTGLYGLK	VGSGSYT	LSVDSMAFQ	SASARFWSS	SCVSAPDKMPF	CAARLSKSKSM
a575	70	80	90	100	110	120
	SMTISTGLYGLK	VGSGSYT	LSVDSMAFQ	SASARFWSS	SCVSAPDKMPF	CAARLSKSKSM
m575.pep	130	140	150	160	170	180
	RLEGVSVSTSNVC	FADNSSSD	SPSKASVS	FTSFFGAGSGV	AGVSTSAKVIS	IMPSSAASSR
a575	130	140	150	160	170	180
	RLEGVSVSTSNVC	FADNSSSD	SPSKASVS	FTSFFGAGSGV	AGVSTSAKVIS	IMPSSAASSR
m575.pep	190	200	210	220	230	240
	SGSSSGTDSSVRR	ARLDWARRKSS	SRAINAAPPP	PASSKVYEPPN	RPSNSPLSVSS	SAETC
a575	190	200	210	220	230	240
	SGSSSGTDSSVRR	ARLDWARRKSS	SRAINAAPPP	PASSKVYEPPN	----SPLSVSS	SAETC
m575.pep	250	260	270	280	290	300
	STGSETALPVSSV	GVSMAEAAAS	SWGADSAAVS	DAVFAAGTGS	GRTAGFSAFAS	GAATFA
a575	240	250	260	270	280	290
	STGSETALPVSSV	GVSMAEAAAS	SWGADSAAVS	DAVFAAGTGS	GRTAGFSAFAS	GAATFA
m575.pep	310	320	330	340		
	SGFSTGFSTVAC	LDGSDGMDA	VSALGFAVCG	LGCSALILFR	FGMX	
a575	300	310	320	330	340	
	SGFSTGFSTVAC	LDGSDGMDA	VSALGFAVCG	LGCSALILFR	FGMX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1  ..atgggctggtg acatcggacg ctccctgaaa caaatgaagg aacagggcgc
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttctctgcagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcggtt ccgtggaata
351 cgaagccgcg ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccttccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactggtca aaatcggcgc acccgaaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1  ..MGVDIGRSLK QMKEQGA EID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGAEFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```


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```

51   GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCCGG GTTGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCGA
501  AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTGATGT GAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  A QEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 L QYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 V IPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
201 K IGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

	10	20	30	40	50	60
m576.pep	MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ A QEVMMKFLQ					
	:					
g576	MGVDIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ A QEVMMKFLQ					
	10	20	30	40	50	
	70	80	90	100	110	120
m576.pep	EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQEG GKQPTKDDIV					
	:					
g576	EQQAKAVEKH KADAKANKEK GEAFLENAA EDGVKTTASGLQYKITKQEG GKQPTKDDIV					
	60	70	80	90	100	110
	130	140	150	160	170	180
m576.pep	TVEYEGRLID GTVFDSSKAN GGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE					
	:					
g576	TVEYEGRLID GTVFDSSKAN GGPVTFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE					
	120	130	140	150	160	170
	190	200	210	220		
m576.pep	QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	:					
g576	QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
	180	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGC GGCAAAA AAGAAGCCGC CCCC GCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA

```

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```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

m576.pep
10 20 30
MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
|||||
a576
CGKKEAAPAS ASEPAASSA QGDTSSIGSTM MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
30 40 50 60 70 80

m576.pep
40 50 60 70 80 90
FTEAMQAVYDG KEIKMTEEQAQ EVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
|||||
a576
FTEAMQAVYDG KEIKMTEEQAQ EVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
90 100 110 120 130 140

m576.pep
100 110 120 130 140 150
KDGVKTTASGLQYKITKQ EGKGQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
|||||
a576
KDGVKTTASGLQYKITKQ EGKGQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
150 160 170 180 190 200

m576.pep
160 170 180 190 200 210
VIPGWTEGVQLLKEGGEATFYIPSNLAYRE QGAGDKIGPNATLVFDVKLV KIGAPENAPA
|||
a576
VILGWTEGVQLLKEGGEATFYIPSNLAYRE QGAGDKIGPNATLVFDVKLV KIGAPENAPA
210 220 230 240 250 260

m576.pep
220
KQPAQVDIKKVN
|||||
a576
KQPAQVDIKKVN
270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

g576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCGC TTCTGCCGCG CAGGGCGACA CCTTTCAAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCTGTCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAGTACA AAATCACCAC ACAGGGTGAA GGCAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCGCCGG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep

```

1  MNTIFKISAL  TLSAALALSA  CGKKEAAPAS  ASEPAAASAA  QGDTSSIGST
51  MQQASYAMGV  DIGRSLKQMK  EQGAEIDLKV  FTDAMQAVYD  GKEIKMTEEQ
101 AQEVMMKFLQ  EQQAKAVEKH  KADAKANKEK  GEAFLENAA   KDGVKTTASG
151 LQYKITKQGE  GKOPTKDDIV  TVEYEGRLID  GTVFDSSKAN  GGPATFPLSQ
201 VIPGWTEGVR  LLKEGGEATF  YIPSNLAYRE  QGAGEKIGPN  ATLVDVKLV
251 KIGAPENAPA  KQPDQVDIKK  VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq

```

1  ATGAACACCA  TTTTCAAAAT  CAGCGCACTG  ACCCTTTCCG  CCGCTTTGGC
51  ACTTTTCGCC  TGC GGCAAAA  AAGAAGCCGC  CCCC GCATCT  GCATCCGAAC
101 CTGCCGCGCG  TTCTTCCGCG  CAGGGCGACA  CCTCTTCGAT  CGGCAGCAGC
151 ATGCAGCAGG  CAAGCTATGC  GATGGGCGTG  GACATCGGAC  GCTCCCTGAA
201 GCAAATGAAG  GAACAGGGCG  CGGAAATCGA  TTTGAAAGTC  TTTACCGAAG
251 CCATGCAGGC  AGTGTATGAC  GGCAAAGAAA  TCAAATGAC   CGAAGAGCAG
301 GCTCAGGAAG  TCATGATGAA  ATTCTTCAG  GAACAACAGG  CTAAAGCCGT
351 AGAAAAACAC  AAGGCGGACG  CGAAGGCCAA  TAAAGAAAAA  GGCGAAGCCT
401 TTCTGAAAGA  AAATGCCGCC  AAAGACGGCG  TGAAGACCAC  TGCTTCCGGC
451 CTGCAATACA  AAATCACCAC  ACAGGGCGAA  GGCAAAACAG  CGACCAAAGA
501 CGACATCGTT  ACCGTGGAAT  ACGAAGGCCG  CCTGATTGAC  GGTACGGTAT
551 TCGACAGCAG  CAAAGCCAAC  GGCGGCCCGG  TCACCTTCCC  TTTGAGCCAA
601 GTGATTCCGG  GTTGGACCGA  AGGCGTACAG  CTTCTGAAAG  AAGGCGGCGA
651 AGCCACGTT  TACATCCCGT  CCAACCTTGC  CTACCGCGAA  CAGGGTGCGG
701 GCGACAAAT  CCGTCCGAAC  GCCACTTGG  TATTTGATGT  GAAACTGGTC
751 AAAATCGGCG  CACCCGAAAA  CGCGCCCGCC  AAGCAGCCGG  CTAAGTCGA
801 CATCAAAAAA  GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL  TLSAALALSA  CGKKEAAPAS  ASEPAAASSA  QGDTSSIGST
51  MQQASYAMGV  DIGRSLKQMK  EQGAEIDLKV  FTEAMQAVYD  GKEIKMTEEQ
101 AQEVMMKFLQ  EQQAKAVEKH  KADAKANKEK  GEAFLENAA   KDGVKTTASG
151 LQYKITKQGE  GKOPTKDDIV  TVEYEGRLID  GTVFDSSKAN  GGPVTFPLSQ
201 VIPGWTEGVQ  LLKEGGEATF  YIPSNLAYRE  QGAGDKIGPN  ATLVDVKLV
251 KIGAPENAPA  KQPAQVDIKK  VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TL	SAA	LALS	SACGKKEAAPAS	ASEPAAASAAQ
m576-1	MNTIFKISAL	TL	SAA	LALS	SACGKKEAAPAS	ASEPAAASSAQ
	10	20	30	40	50	60
g576-1.pep	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	QAQEVMMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ	QAQEVMMKFLQ	EQQAKAVEKH
	70	80	90	100	110	120
g576-1.pep	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITKQGE	GKOPTKDDIV	TVEYEGRLID
m576-1	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITKQGE	GKOPTKDDIV	TVEYEGRLID
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF	YIPSNLAYRE	QGAGEKIGPN
m576-1	GTVFDSSKAN	GGPVTFPLSQ	VIPGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
m576-1	ATLVFDVKLV	KIGAPENAPA	KQPAQVDIKK	VN		
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGGCGCAAAA AAGAAGCCGC CCCC GCATCTCT GCATCCGAAC
101 CTGCCGCGCG TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAG ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGC GG
701 GCGACAAATQ CGGCCCGAAC GCCACTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

a576-1.pep	10	20	30	40	50	60
	MNTIFKISAL <u>TL</u> SAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISAL <u>TL</u> SAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pep	70	80	90	100	110	120
	DIGRSLKQMKEQGAEIDLKVTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	130	140	150	160	170	180
	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	190	200	210	220	230	240
	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	250	260	270			
	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

q577.seq..

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

q577.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

m577.seq..

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

m577.pcp..

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m577/q577 88.1% identity in 160 aa overlap

```

              10      20      30      40      50      60
m577.pep    MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGGVFIYGANMKLI
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g577        MERSGVFGKIVGNRILRMPSEHAAAFYPKPCKSFKLTQSWFRVRSCTCGVFIYGANMKLI
              10      20      30      40      50      60
              70      80      90     100     110     120
m577.pep    YTVIKIIILLFLLLAVINTDAVTFSYLPGQKFDLPLIVVLFGAFFVVGIIIFGMFALFGRLL

```

```

g577      |||||
          YTVIKIIILLFLLAVINMDAVTFSYLPQSVNLPPLIVVLFGAFFVVGIVFGMFALFGRL
          70          80          90          100          110          120

m577.pep      130          140          150          160
          LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:||||:|:|:|
g577      LSLRGENSRLRAEVKK SARLSGQKLTAPPIQNAAESAKQPX
          130          140          150          160

```

a577.seq

1	ATGGAAGGA	ACGGTGTATT	TGGTAAATT	GTCGGCAATC	GCATACTCCG
51	TATGTCGTCC	GAACACGCTG	CCGCATCCTA	TCCGAAACCG	TGCAAATCGT
101	TTAAACTAGC	GCAATCTTGG	TTCAGAGTGC	GAAGCTGTCC	GGGCGGCGAT
151	TTTATTTCAG	GAGCAACAT	GAACTTATC	TATACCGTCA	TCAAATCAT
201	TATCCTGCTG	CTCTTCTGTC	TGCTTGCTGT	CATTAATACG	GATGCCGTTA
251	CCTTTTCCTA	CCTGCCGGGG	CAAAAATTCTG	ATTTGCCGCT	GATTGTCGTA
301	TTGTTGGGCG	CGTTTGTCTG	CGGCATCGTG	TTCGGAATGT	TTGCCTTGTT
351	CGGACGGTTG	TTGTCGTTAC	GTGGCGAGAA	CGGCAGGTTG	CGTGCCGAAG
401	TAAAGAAAAA	TGCGCGTTTG	ACGGGGAAGG	AGCTGACCGC	ACCACCGGCG
451	CAAAATGCGC	CCGAATCTGC	CAACACGCCT	TGA	

a577.pep

1	MERNGVFGKI	VGNRIILRMSS	EHAAASYPKP	CKSFKLAQSW	FRVRSPPGGV
51	FIYGANMKLI	YTVIKIIL	LFLLLAVINT	DAVTFSYLPG	QKFDLPLIVV
101	<u>LFGAFVVGIV</u>	<u>FGMFALFGRL</u>	<u>LSLRGENGL</u>	<u>RAEVKKNARL</u>	<u>TGKELTAPPA</u>
151	ONAPESAKOP	*			

	10	20	30	40	50	60
m577.pep	MERNGVFGKIVGNRI	LRMSSEHAAASY	PKPCKSF	KLQAQSWFRV	RSC	LGGVFIYGANMKLI
a577	MERNGVFGKIVGNRI	LRMSSEHAAASY	PKPCKSF	KLQAQSWFRV	RSC	PGGVFIYGANMKLI
	10	20	30	40	50	60
	70	80	90	100	110	120
m577.pep	YTVIKIIILLFLL	LAVINTDAV	TFSYLP	GQKFDLPL	IVVLF	GAFVVGIIFGMFALFGRL
a577	YTVIKIIILLFLL	LAVINTDAV	TFSYLP	GQKFDLPL	IVVLF	GAFVVGIVFGMFALFGRL
	70	80	90	100	110	120
	130	140	150	160		
m577.pep	LSLRGENGLRAEV	KKNARLTG	KELTAPPA	QNAPESTK	Q	PX
a577	LSLRGENGLRAEV	KKNARLTG	KELTAPPA	QNAPE	SAK	Q
	130	140	150	160		

g578.seq. .

```
1  atgggaaagc tgcacatcgg gatattgttt gccgattttc tcaaagattt
51  cgcgccacag ttcgggtggt tccaaaacgt tggctttgcc tacggagcag
101 acttttttgc tgcgtttttg gccggaattg aaggccacgt gggcgatcgc
151 gcggatttcg ctttcgctgt atttcatggt gtgtagcct tcgtgttcgc
201 cgttttccaa aacacggatg ccgcgcggtt cgcgaaata aatatcgcgc
251 gtaagttcgc gcacaatcaa aatatccaaa ccggcaacga tttcaggett
301 gacgcgtgga gcqtttgcta a
```

g578.pep

1	MGKLDIGILF	ADFFKDFAPQ	FGGFQNVGFA	YGADFFAAFL	GGLEGHVGDA
51	ADFAFAVFGH	VVAFVFAVFG	NTDAAARFAEI	NIAGKFAHNO	NIOTGNDERL

101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

```
m578.seq..
1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTTGC TCGTTTTTGC GCGGATTGG AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACCGGATG CCGCGCGGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGGCAACGA TTTCAGGCTT
```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

```
m578.pep..
1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMGNT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGGVG*
```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	:					
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGHVGDADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQNADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	:					
g578	VVAFVFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

```
a578.seq
1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTTGC TCGTTTTTGC GCGGATTGG AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G
```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

```
a578.pep
1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGNT
51  ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*
```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	:					
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGDVGNTADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQNADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	:					
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

```
g579.seq..
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
```

897

```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCTTA AAAGACCAGC TGCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCGTTCAAA GTCGGCGACT
251 TTATCCGTGT CCGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

```

g579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

```

m579.seq..
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCG CCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CCGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCCACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

```

m579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGV DYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
g579	GNSIVNRSSLPLCRAQVIVGV DYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWT LQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
g579	DNAIEITLWAWANEADRWT LQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```

a579.seq
1   ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCTTGG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCGG CCCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGTGATG GGCAACAGCA TCGTCAACCG TTCCACTG CCGCTGTGCC
401 GCGCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT TAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCCGCCG OCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAACG AAGCAGACCG CTGGACGCTG
601 CAATCGGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```

a579.pep
1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSLRITDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWT L
201 QCDLNEQVVE NLRKVNINIP FPQORDIHIIN S*

m579/a579 100.0% identity in 231 aa overlap

10 20 30 40 50 60
m579.pep MRAAMTRAQVDATLISFLCNVANIGLLILV IIAALGRLGVSTTSVTALIGGAGLAVALSL
a579 MRAAMTRAQVDATLISFLCNVANIGLLILV IIAALGRLGVSTTSVTALIGGAGLAVALSL
10 20 30 40 50 60

70 80 90 100 110 120
m579.pep KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRITDNEEVVLPNSVVM
a579 KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRITDNEEVVLPNSVVM
70 80 90 100 110 120

130 140 150 160 170 180
m579.pep GNSIVNRSTLPLCRAQVIVGV DYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
a579 GNSIVNRSTLPLCRAQVIVGV DYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
130 140 150 160 170 180

190 200 210 220 230
m579.pep DNAIEITLWAWANEADRWT LQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
a579 DNAIEITLWAWANEADRWT LQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
190 200 210 220 230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:
g579-1.seq

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```

1  ATGGACTTCA AACAAATTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGGGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG ACGGTTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGGG GTTTGGCGGT GCGGTTGTCC TTAAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ACTTTATCCG TGTCGGCGGT TTTGAAGGAT ATGTCCGGGA AATCAAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCAGC CTGCCGCTTT
551 GCCGCGCCCA AGTGATAGTC GCGGTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CCGTGTTGAA AGCGCGCGCC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGCCCG CCGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQDFDLH LISVSGWGLH AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVVLPSNVV MGNSIVNRSS LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAA EHPLSVQNEE RQPAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGACTTCA AACAAATTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCT
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGGG GTTTGGCGGT GCGGTTGTCC CTGAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGGCACTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAATAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGCAACA GCATCGTCAA CCGTTCCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GCGGTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CCGTGTTGAA AGCGCGCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCTG CCGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQDFDLH LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVVLPSNVV MGNSIVNRST LPLCRAQVIV GVDYNCDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
g579-1	MDFKQDFDLHLISVSGWGHLEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
	10	20	30	40	50	60
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	70	80	90	100	110	120
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	130	140	150	160	170	180
m579-1.pep	GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPSNVVMGNSIVNRST					

900

```

|||||
g579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180

          190      200      210      220      230      240
m579-1.ppep LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||||
g579-1  LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190      200      210      220      230      240

          250      260      270      280
m579-1.ppep AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX
          |||||||
g579-1  AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```

a579-1.seq
1  ATGGACTTCA  AACAAATTGA  TTTTITACAC  CTGATAAGTG  CTTCCGGCTG
51  GGAGCATCTG  GCTGAAAAGG  CGTGGGCGTT  CGGGCTGAAC  CTTGCCGCGG
101 CGCTGCTTAT  TTTTITGGTC  GGAAATGGG  CGGCGAAACG  CATGTGCGCC
151 GTGATGAGGG  CGCGCATGAC  GCGCGCGCAG  GTCGATGCCA  CGCTGATTAG
201 TTTTITGTGT  AATGTTGCCA  ATATCGGCTT  ATTGATTTTG  GTGATTATTG
251 CCGCATTGGG  CAGATTGGGC  GTTCCACAA  CATCCGTAA  CGCCTTAATC
301 GCGGCGCGCG  GTTGGCGGCT  GCGGTTGTCC  TTGAAAGACC  AGCTGTCCAA
351 TTTTGCCGCG  GCGCGCTGA  TTATCCTGTT  CCGCCGTTT  AAAGTCGGCG
401 ATTTATCCG  CGTCGGCGGT  TTTGAAGGAT  ATGTCCGAGA  GATTAAATG
451 GTGCAGACTT  CTTTGGCGAC  GACCGACAAC  GAAGAAGTCG  TGCTGCCCAA
501 CAGCGTGGTG  ATGGGCAACA  GCATCGTCAA  CCGTTCACA  CTGCCGCTGT
551 GCCGCGCCCA  AGTGATAGTC  GCGGTCGATT  ACAACTGCCA  TTTGAAAGTG
601 GCGAAAGAGG  CGGTGTTGAA  AGCCGCCGTC  GAACCCCT  TGAGCGTTCA
651 AAACGAAGAG  CGGCAGGCCG  CCGCTACAT  CACCGCCTT  GCGGACAAAT
701 CCATCGAAAT  CACATTATGG  GCTTGGGCAA  ACGAAGCAGA  CCGTGACG
751 CTGCAATGCG  ACTGAACGA  ACAAGTGGTC  GAAAACCTCC  GCAAAGTCAA
801 TATCAACATC  CCGTCCCGC  AACGCGACAT  ACACATCATC  AATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```

a579-1.ppep
1  MDFKQDFDLH  LISASGWEHL  AEKAWAFGLN  LAAALLIFLV  GKWAAKRIVA
51  VMRAAMTRAQ  VDATLISFLC  NVANIGLLIL  VIIAALGRLG  VSTTSVTALI
101 GGAGLAVALS  LKDQLSNFAA  GALIILFRPF  KVGDFIRVGG  FEGYVREIKM
151 VQTSRLRTDN  EEVLPNSVV  MGNSIVNRST  LPLCRAQVIV  GVDYNCDLKV
201 AKEAVLKAAV  EHPLSVQNEE  RQAAAYITAL  GDNAIEITLW  AWANEADRWT
251 LQCDLNEQVV  ENLRKVNINI  PFPQRDIHII  NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.ppep MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          |||||||
m579-1  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          10      20      30      40      50      60

          70      80      90      100     110     120
a579-1.ppep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||||
m579-1  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120

          130     140     150     160     170     180
a579-1.ppep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          |||||||
m579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          130     140     150     160     170     180

          190     200     210     220     230     240
a579-1.ppep LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||||
m579-1  LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240

          250     260     270     280
a579-1.ppep AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX

```

```

|||||
m579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

```

g580.seq
1  atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
51  cgcgtcgcag ccatttcga tggcaaggca gacttcgccg atcatgtcgc
101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
151 tcgaaaaatca gcttggtaaa gccgttgctg caaccgttgg caatcgcacg
201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
251 ctttggcaga caattcggtt tcaccgacct atgccacttc gggggaagtg
301 tag

```

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

```

g580.pep.
1  MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
101 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

```

m580.seq..
1  ATGGATTTCGC CCAAGGTTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCGGCA
151 TCAAAAATCA GCTTGGTAAA GCCGTGTGCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCC GCCACGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG
301 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

```

m580.pep..
1  MDSPKVGCGW MVLPMASASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
101 *

```

m580/g580 97.0% identity in 100 aa overlap

```

          10      20      30      40      50      60
m580.pep  MDSPKVGCGWMVLPMASASQPISMARQTSP IISPPFGPTM PPPMMRPVSASKISLVKPLS
          |||
g580       MDSPKVGCGWMVLPMASASQPISMARQTSP IMSPPFGPTM PPPMMRPVSASKISLVKPLS
          10      20      30      40      50      60

          70      80      90      100
m580.pep  QPLAIARPEAAHGKLALVILRPEALADSSVSPTHATSGEVX
          |||
g580       QPLAIARPEAAHGKLALVILRPDALADNSVSPTHATSGEVX
          70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

```

a580.seq
1  ATGGATTTCGC CCAAGGTTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCCG
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCAGCA
151 TCAAAAATCA GCTTGGTGAA ACCATTGTGCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCAGA CAATTCGGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG
301 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

```

a580.pep
1  MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

```

902

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX					
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1  atgcacttcg cccagcttgt gggcacaacc ggtatagaac aaaatacgtt
51  ctgtcgtcgt ggttttaccg gcatcgatat gggcggaaat accgatgttg
101 cggtacagggc tgatcggggg cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagtgagaga atgctttgtt ggcttcagcc atacggtgta
201 cttcttcacg ttttttcaac gcaccgccac ggccttcgga cgcacatc
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttcggggc
301 cgcgtcgcga acccaacgca ttgccaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG
101 RVANPTHQCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC
301 CGCATCGCGA ACCCAGCGCA TGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGGLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAQADRGGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLTTFAGRVANPTHQCSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

```

a581.seq
  1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
 51  CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101  CGGTACAGGC TGATCGGGGT CTACGAGCC ATTTTATAG CCTTCAAAA
151  TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201  CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251  AATTTCGCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC
301  CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
  1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTQADRG LTSHFISLSK
 51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101  RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGLTSHFISLSKLETEVRECFV					
	:					
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTQADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
a581	GFSHTVYFFTFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
  1  atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
 51  agagaccgcg ctgcaatgcg ccgctttgac ggacaatgtt acgcgtttgg
101  cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151  gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201  cagcttggat aagggcgagg cggtcattgt tgttgaaaaa ggcggggatg
251  cgcttcctgc cgacagtgcg ggcgaaaccg ccgatatcta tacgccttgc
301  agcctgatgt acgacttgga caaaaacgat ttgcgcgggc tgttgggcgt
351  acgcgaacac aatccgatgt accttatgcc gttttggtat aacaattcgc
401  ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451  ttcggacagc agaaacgtgc ggaaaccaa ttgcaggttt cgttcaaaag
501  caaaattgcc gaaaatttgc ttaaaacccg cgcggatctg tggttcggct
551  acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601  ccgttccgca atacggatta caaacctgaa atttctctga cccagcctgt
651  gaagggcagg ttgccgttcg gcggcaggct gcgtatgctc ggtgcggggt
701  ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttcgtggaac
751  aggatttatg ccatggcagg catggaatgg ggcaaattga cggtgattcc
801  gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851  ccgatattgc cgactatatg gggtatggcg acgtgaagct gcagtaccgc
901  ctgaacgaca ggcagaatgt gtattccgta ttgcgtaca accccaaac
951  gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep..
  1  MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
 51  EQQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101  SLMYDLKND LRGLLVREH NPMYLMPFY NNSPNYAPSS PTRGTTVQEK
151  FGQQRKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSDW QIYNQGRKSA
201  PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251  RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYD GYGDVKLQYR
301  LNDRQNVSYS LRYNPKTGYG AIEAAYTFPI GKGLKGVVRG FHGYGESLID
351  YNHKQNGIGI GLMFNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GGCGGGGATG
251 CGCTTCTGCG CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTGT
301 AGCCTGATGT ACGACTTGGG CAAAAACGAT TTGCGCGGGC TGTGGGCGGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCGGGGTTTC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTCAAAAAG
501 CAAAATTGCC GAAGATTTGT TTAACACCCG CCGGATCTCG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCGA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTTCCGATT AAGGGCAAAC
1001 TCAAAGCGGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKDND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNG QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYD GYGDVKLQYR
301 LNDRQNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKVVVR FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

m582.pep	10	20	30	40	50	60
	MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
g582	MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
	10	20	30	40	50	60
m582.pep	70	80	90	100	110	120
	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKDNDLRLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKDNDLRLLGVREH					
	70	80	90	100	110	120
m582.pep	130	140	150	160	170	180
	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAENLFKTRADL					
	130	140	150	160	170	180
m582.pep	190	200	210	220	230	240
	WFGYTQRSWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNG					
g582	WFGYTQRSWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNG					
	190	200	210	220	230	240
m582.pep	250	260	270	280	290	300
	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYDGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYDGYGDVKLQYR					
	250	260	270	280	290	300
	310	320	330	340	350	360

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```

m582.pep      LNDRONVYSVLRYNPKTGYGAIEAAAYTFPIKGLKGVVRGFGHYGESLIDYNHKQNGIGI
|||||
g582          LNDRONVYSVLRYNPKTGYGAIEAAAYTFPIKGLKGVVRGFGHYGESLIDYNHKQNGIGI
                310      320      330      340      350      360

                370
m582.pep      GLMFNDLDGIX
|||||
g582          GLMFNDWDGIX
                370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTTGAAAAA GGCGGGGATG
251 CGCTTCCTGC CGACAGTGC GCGGAAACCG CCGACATCTA TACGCCTTGT
301 AGCCTGATGT ACGACTTGA CAAAAACGAT TTGCGCGGGC TGTTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTGC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAAACCAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TTA AACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGCGGAT TTGCCGTTGC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CGGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAAATG GTATTCCGTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVRH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYD GYGDVKLQYR
301 LNDRONVYSV LRYNPKTGYG AIEAAAYTFPI KGLKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

m582/a582      100.0% identity in 370 aa overlap

                10      20      30      40      50      60
m582.pep      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
|||||
a582          MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
                10      20      30      40      50      60

                70      80      90      100     110     120
m582.pep      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
|||||
a582          LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
                70      80      90      100     110     120

                130     140     150     160     170     180

```


906

```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQKRAETKLQVSFKSKIAEDLFKTRADL
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQKRAETKLQVSFKSKIAEDLFKTRADL
              130      140      150      160      170      180

m582.pep      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
a582          WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
              190      200      210      220      230      240

m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADIADYMGYGDVKLQYR
a582          QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADIADYMGYGDVKLQYR
              250      260      270      280      290      300

m582.pep      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
a582          LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
              310      320      330      340      350      360

m582.pep      GLMFNDLDGIX
a582          GLMFNDLDGIX
              370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatttacc catcttgccct tctgtgcctt
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gccagcggtt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaaacga ctcaacgcat cgctcatcgc cgcgcccggt ttgtcggcgg
351 ttacgcgggt tactgcgacc aaccgcgacg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcggca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatttgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSQIFT HLAFCFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLLP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTCGGCGG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCGGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAGGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA

```

551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSLR LDP VGYGQCQNQG AQYCGNGEGY RFETQFHHD LRK KDRPEKS
201 EK*

m583 / g583 98.5% identity in 202 aa overlap

m583.pep	10	20	30	40	50	60
	MIVDQSQIFT	HLAFAFCGI	GAVTAGNRLH	NRMYNAAAAR	GIGRNGSQQ	QFGKSETVTD
g583	MIIDQSQIFT	HLAFAFCGI	GAVTAGNRLH	NRMYNAAAAR	GIGRNGSQQ	QFGKSETVTD
	10	20	30	40	50	60
m583.pep	70	80	90	100	110	120
	AQRFSKNGDK	KQISDTHPQP	CFEQTARNHN	CDGNQPNQRI	GERTQRIahr	RARFVGGYAG
g583	AQRFSKNGDK	KQISDTHPQP	CFEQTARNHN	CDGNQPNQRI	GERTQRIahr	RARFVGGYAG
	70	80	90	100	110	120
m583.pep	130	140	150	160	170	180
	YCDQPDGNNR	QRAQRHGLAD	NGGNHTDKHG	QQRPSLR LDP	VGYGQCQNQG	AQYCGNGEGY
g583	YCDQPDGNNR	QRAQRHGLAD	NGGNHTDKHG	QQRPSLR LDP	VGYGQCQNQG	AQYCGNGEGY
	130	140	150	160	170	180
m583.pep	190	200				
	RFETQFHHD	LRK KDRPEKSEKX				
g583	RFETQFHHD	LRK KDRPEKSEKX				
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTGCCT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGCGGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCGGCGG
351 TTACGCCGGT TACTGCGACC AACCAGACGG CAATAATCGA CAGCGCACCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA
551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RARFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSLR LDP VGYGQCQNQG AQYCGNGEGY RFETQFHHD LRK KDRPEKS
201 EK*

m583/a583 99.0% identity in 202 aa overlap

m583.pep	10	20	30	40	50	60
	MIVDQSQIFT	HLAFAFCGI	GAVTAGNRLH	NRMYNAAAAR	GIGRNGSQQ	QFGKSETVTD

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```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQQFGKSETVTD
           10      20      30      40      50      60

           70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
           |||||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
           70      80      90      100     110     120

           130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRRLDPVGYGQCQNQGAQYCGNGEGY
           |||||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRRLDPVGYGQCQNQGAQYCGNGEGY
           130     140     150     160     170     180

           190     200
m583.pep  RFETQFHHIDLRRKKDRPEKSEKX
           |||||
a583      RFETQFHHIDLRRKKDRPEKSEKX
           190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

```

g584.seq..
1  atgctgcgtt ctatcttggc ggcttcctg ctggcggtat cttttccggc
51  ggcggtgag gcattgaatt acaatattgt cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcggcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttgta aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggtat
251 cgcgcagtgc gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggagggca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgccgtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcggttctg ggtgcgtccg gttataaaat cgtcaaattg aattttgggc
551 aaatcggcag ccatattgcy ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc ccatattgcy ggcgatgggg ctgttcgggc aaaaatgctg
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

```

g584.pep Length:..
1  MLRSILAASL LAVSFPAAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNVANA EFVKKFNNFT RSKNNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK AEGRDFDALN RFIADVQTD SLEDTDFSVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLGLVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEEISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

```

m584.seq..
1  ATGTTGCGTC TTGTTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAATTCAA
201 CAAGTTCATC AGAAAAATCGA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTTAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTTATTG CCGATATTC AAGCAGATGC GCGTTGGMAT
401 ATACGGATTT CCATGTGTGC CGCGAACGCC GCAACGAGGT CATCATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCGG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

m584.pep..

```

1  MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNKFI RSKNGSFKT ELVSRSAMPR YQYTNGRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

	10	20	30	40	50	60
m584.pep	MLRLVLAASLSAVSFPAAAEALNYNIVEFS	ESAGVEVAQDTMSARFQVTA	EGRDKNVNA			
	:					
g584	MLRSILAASLLAVSFPAAAEALNYNIVEFS	ESAGIEVAQDTMSARFQVAAEGRDKNVNA				
	10	20	30	40	50	60
	70	80	90	100	110	120
m584.pep	EFVKKFNKFI	RSKNGSFKT	ELVSRSAMPR	YQYTNGRRIQ	TGWEERAEFK	VEGRDFDELN
		:				
g584	EFVKKFNNT	RSKNGSFKT	ELVSRSAMPR	YQYTNGRRIQ	TGWEERAEFK	AEGRDFDALN
	70	80	90	100	110	120
	130	140	150	160	170	180
m584.pep	RFIADIQADA	ALXYTDFHVS	RERRNEVIXQ	VSKDAVLRFK	KARAEKLAGVL	GASGYKIVKL
		:				
g584	RFIADVQTD	ASLEDTDFS	VSRERRNEVIDQ	VSKDAVLRFK	KARAEKLAGVL	GASGYKIVKL
	130	140	150	160	170	180
	190	200	210	220	230	
m584.pep	NLGHIGSHIAG	GGAAQAKML	RAMPMAASVN	MEGADSAAPG	VEEISISVNG	TVQFX
	:					
g584	NFGQIGSHIAG	DGAVRAKML	RAMPMAASVN	MGTD	SAAPGVEEISIS	INGTVQFX
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

a584.seq

```

1  ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51  .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTACAC AGAAAATCAA AAAATGGTAG CTTTAAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TCGGTTGAAC CGTTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGATTTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

a584.pep

```

1  MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNFT RSKNGSFKT ELVSRSAMPR YQYTNGRRIQ
101 TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

	10	20	30	40	50	60
m584.pep	MLRLVLAASLSAVSFPAAAEALNYNIVEFS	ESAGVEVAQDTMSARFQVTA	EGRDKNVNA			
	:					
a584	MLRSILAASLL-----	IVEFS	ESAGVEAVQDTMSARFQVTA	EGRDKNVNA		
	10	20	30	40		

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	70	80	90	100	110	120
m584.pep	EFVKKFNKFKIRKSKNGSFKTELVSRSAMPRIQYTNGRRITQGWEEERAEFKVEGRDFDELN					
a584	EFVKKFNFNTRKSKNGSFKTELVSRSAMPRIQYTNGRRITQGWEEERAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADALEYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt  tccaacgcat  tttcgccaca  ttttgcgcg  ttatcgctctg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctggtgcag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattattt  ccgcattcaa  gacacggggc  gacaacggcg  cgcgcgaaat
201  cctgaccgaa  tggaaaaaca  gccccgtctc  atccgccgtt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaacc  gctatatcga  caattacacc
301  atagaacgcg  cccggtgtgt  tgccgccaac  aacccccatt  ccaaccttgt
351  ccgcattcgaa  tacgaccgtt  tcggcggaaga  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggccctgcgc  ttgccccgat  ttggcacgaa  ttcattcatc  tctccttcat
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgcca
551  aaccctcag  aatcttaggc  aacggcatgg  acagggtggc  agaacgagaa
601  cttgaagacc  gcgtttgcca  acaggttcgc  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgcaattcg  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFQRI FAT  FCAVIVCAIF  VASFSFWLVQ  NTLAENQFNQ  RRTIETTLMG
51  SIISAFKTRG  DNGAREILTE  WKNSPVSSAV  YVIQGDDEKD  ILNRYIDNYT
101  IERARLFAAN  NPHSNLVRIE  YDRFGEEYLF  FIKGWDNHQA  QRLPSPLFIP
151  GLPLAPIWHE  FIILSFIIIV  GLLMAYILAG  NIAKPIRILG  NGMDRVAERE
201  LEDRVCQQVR  DRDELADVA  MQFDTMVEKL  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT  TCCAACGCAT  TTTCGCCACA  TTTTGC GCGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTTCTTTCTG  GCTGGTGCAG  AACACCCTTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATTCG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CTTGACGGA  TGGAAAGACA  GCCCCGTCTC  ATCGGCGGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAACGCG  CCGGCTTTT  CGCCGCCGGA  CACCCGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACCGCT  TCGGCGAAGA  ATACCTGTTT  TTCACCAAAG
401  ACTGGGACAA  ACTCCAAGCC  CGCCGCTGTC  CCAGCCCTCT  GTTGATCCCC
451  GGCCCTGCCG  TCGCCCCGAT  TTGGCAGGAA  CTCATCATAT  TGTCTTCAT
501  CATCATCGTC  GGAATGCTGA  TGGCATATAT  CCTCGCCGGC  AACATTGCCA
551  AACCCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGGTGGC  AACCGGAGAA
601  CTTGAAACCC  CTATCTCCCA  ACAGGTCGAC  GACCGCGACG  ACGAATTGTC
651  CCATCTTGCC  ATCCAATTCG  ACAAATGGT  GGAAAACTC  GAAAACTCG
701  TTGCCAAGA  ACGCCACCTG  CTCCATCAG  TCTCCCATGA  AATGCGTTCT
751  CCCCTTGCGC  GCATGCAGGC  AATTGTGCGA  CTGATTCAGG  CGCAGCCCCA
801  AAAACAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAAGTG  ACCCGCATGG
851  ATACGCTGGC  CGGGGAAGTG  TTAACCCTGT  CCCGTCTCGA  AACTTCCAAT
901  ATGGCTTTGG  AAAAAGAAAG  CCTGAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAGAAGAC  AATCAAAGCA  TTGCCAGAA  AAACGGACAA  ACGGTTACCC
1001  TGCTTGCCGA  CGGAAAAATC  CCCGAAAACA  CAACCATCCT  TGCCAACGAA

```

```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

```

1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKDD ILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQVVD DRDDELHSLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPQKQE QYLRLEGELE TRMDTLAGELE LTLRSLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNQO TVTLSADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNYSPG GSTILINIQO DHKHWIIDVT DNGPGVDEMO
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

```

          10      20      30      40      50      60
m585.pep  MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFRARG
          |||
g585      MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFKTRG
          10      20      30      40      50      60

          70      80      90      100     110     120
m585.pep  DAGAREILTEWKDSPVSSGVYVIQGDEKDDILNRYIDSYTIERARLFAAGHPHNSNLVHIE
          | |||
g585      DNGAREILTEWKNSPVSSAVYVIQGDEKDDILNRYIDNYTIERARLFAANNPHNSNLVRIE
          70      80      90      100     110     120

          130     140     150     160     170     180
m585.pep  YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
          |||
g585      YDRFGEEYLF FIKGWDNHQAQRLPSPLFI PGLPLAPIWHEFIILSFIIIVGLLMAYILAG
          130     140     150     160     170     180

          190     200     210     220     230     240
m585.pep  NIAKPIRILGNMMDRVANGELETRISQVVD DRDDELHSLAIQFDKMVEKLEKLVAKERHL
          |||
g585      NIAKPIRILGNMMDRVAERELED RVCQVDRDDELADVAMQFDTMVEKLEX
          190     200     210     220     230

          250     260     270     280     290     300
m585.pep  LHHVSHEMRSPLARMQAIVGLIQAQPQKQE QYLRLEGELETRMDTLAGELE LTLRSLRLETSN

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

```

1 ATGAAACTGT TCCAACGCAT CTTCGCCACA TTTTGCGCGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCCG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAGACA GCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTT TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCGAT TTGGCAGGAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GACTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCA ACAGGTCGAC GACCGCGACG ACGAATTGTC

```

```

651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAAGA ACGCCACCTG CTCCATCAG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTGAG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAACTG TTAACCCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAAGAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGCTGCGCGA CGGAAAAATC CCCGAAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAAGTGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

```

a585.pep
1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEK KD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLI
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDEL SHLA IQFDKMVEKL EKLVAKE RHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPOKQE QYLKRLEGE LTRMDTLAGE LTLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTLSADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNSPE GSTILINIQ DHKHWDVT DNGPGVDEM
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHC GKIIA ENIKP NGLRM
451 RFILPKKKTG SKTEKSAN*

m585/a585 99.8% identity in 468 aa overlap

10 20 30 40 50 60
m585.pep MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG
|||||
a585 MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG
10 20 30 40 50 60

70 80 90 100 110 120
m585.pep DAGAREILTEWKDSPVSSGVYVIQGDEKDIILNRYIDSYTIERARLFAAGHPHNSNLVHIE
|||||
a585 DAGAREILTEWKDSPVSSGVYVIQGDEKDIILHRYIDSYTIERARLFAAGHPHNSNLVHIE
70 80 90 100 110 120

130 140 150 160 170 180
m585.pep YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
|||||
a585 YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
130 140 150 160 170 180

190 200 210 220 230 240
m585.pep NIAKPIRILGNMMDRVANGELETRISQQVDDRDEL SHLA IQFDKMVEKLEKLVAKE RHL
|||||
a585 NIAKPIRILGNMMDRVANGELETRISQQVDDRDEL SHLA IQFDKMVEKLEKLVAKE RHL
190 200 210 220 230 240

250 260 270 280 290 300
m585.pep LHHVSHEMRSPLARMQAIVGLIQAQPOKQE QYLKRLEGE LTRMDTLAGE LTLRLETSN
|||||
a585 LHHVSHEMRSPLARMQAIVGLIQAQPOKQE QYLKRLEGE LTRMDTLAGE LTLRLETSN
250 260 270 280 290 300

310 320 330 340 350 360
m585.pep MALEKESLKL LPFLGNLVEDNQSIAQKNGQTVTLSADGKI PENTTILANESYLYRAFDNV
|||||
a585 MALEKESLKL LPFLGNLVEDNQSIAQKNGQTVTLSADGKI PENTTILANESYLYRAFDNV

```

913

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1  atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatattt
51  ttggaaaacc acgggcaaat ggctgtttgc cctgctgatt ttggcggcac
101 tcggtacttt gggatacacg gtttaccaaa accgtgctgc ttcccaaaat
151 caggaagcgg cgcggtgtct ggcaaacatc gtggaaaagg cgcaaaacaa
201 agccccgcga agcgaaatca atgccgaact gtccaaactc caacaaagct
251 acccccattc catttcgcgc gcccaagcca cgctgatggc ggcggaacc
301 gaatttgacg cgcagcggtt cgatgttgcc gaaggctcatt tgaatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttgccg gcgcagcgtc
401 tggcggttgt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctgcacacgc cggttgaggg ggacttcgcc cccctgctga tggaaactaa
501 aggcgatgtt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaact
551 acggacagcg tttggaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1  MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNR AASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAElskl QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHlKWVLSN QKDSLlQALA AQLGvvllQ QKKYDAALAA
151 LDTpVEADFA PLLMETKGDV YAAQEKsQEA LKNYGQALEK MPQDSVGREL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1  ATGGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAAC TTAATATTT
51  TTGGA AAAACC ACGGGCAAAT GGCTGTTTGC CTTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTAAAGT TTCCCAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTAGAAAAGG CGCAAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GACCAAATC CAACAAAGCT
251 ACCCGCATT CATTTCGCC GCCCAAGCCA CACTGATGGC GCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 GTTGTCCAAC CAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAT ACATGCCGC GCTTGCCGC
451 CTCGATACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGA AAAAG CCAGGAAGCC TTA AAAAAT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCG TCGCAATTG
601 GTTCAAATGA AACTTGATT CTTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1  MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNR KVSN
51  QEAAAVLANI VEKAQSKAPQ SEINAEltkl QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHlKWVLSN QKDSLlQALA AQLGvvllQ QKKYDAALAA
151 LDTpVEADFA PLLMETKGDV YAAQGKSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQELDNFKYFWKTTGKWL Falli LAALGYLGYTVYQNRKVSNQEAAAVLANI					

914

```

g586      MAAHLEEQQEELDNFKYFWKTTGKWLFAALLILAALGYLGTYVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      VEKAQNKAPQSEINAELSKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIALAQAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      QKDSLIALAQAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQEKSQEA
           130     140     150     160     170     180

           190     200     210
m586.pep  LKNYGQALEKMPQDSVGRELVQMKLDSLKX
           |||||:|||||
g586      LKNYGQALEKMPQDSVGRELLQMKLDSLKX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1   ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51  TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTGCGGC TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTGGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAGCT
251 ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 ATTGTCCAAC CAAAAAGACA GCCTGATCCA GCGTGTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAAT ACGATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TAAAAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCAATTG
601 GTTCAAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1   MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAELAKL QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLKWVLSN QKDSLIALQA AQLRGVVLLQ QKKYDAALAA
151 LDTPEADFA PLLMETKGDV YAAQGKSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

m586/a586  97.6% identity in 209 aa overlap

           10      20      30      40      50      60
m586.pep  MAAHLEEQQEELDNFKYFWKTTGKWLFAALLILAALGYLGTYVYQNRKVSQNQEAAAVLANI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      MAAHLEEQQEELDNFKYFWKTTGKWLFAVLI LAALGYLGTYVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      VEKAQNKAPQSEINAELAKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIALAQAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      QKDSLIALAQAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           130     140     150     160     170     180

```

915

```

                190      200      210
m586.pep      LKNYGQALEKMPQDSVGRVLQMKLDSLKX
                |||||
a586          LKNYGQALEKMPQDSVGRVLQMKLDSLKX
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
  1  atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
 51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101  aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151  gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201  ccccatctcg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251  ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301  ggacgaggca gctatctgtg gcacgaagaa cgcaaacctc acggcaacgg
351  caaaacccgc aacaaacgga tgtccgacat atccgccggc atcagccaca
401  ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451  acggttttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501  gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
  1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNSR
 51  AALAAPVYIQ TGATSFIPIP TEIQENGST DMLAGTLGLR YGLTGNTDIY
101  GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151  TVYEKSRNKA SLIKRGLCP FYNLRYNEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
  1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
 51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101  AATGGAAACT GGAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151  GCCGAACCTG CCGCACCAGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201  CCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251  TCGGCACGCT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301  GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTC ACGGCAACAG
351  CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401  CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451  ACGGTTTACG AAAAAATCGC CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501  CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551  CCGCCGCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601  TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGTGCTG
651  CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701  CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751  GCCCATTTCT GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801  ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851  GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
  1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
 51  AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGTGLR YGLTGNTDIY
101  GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151  TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201  YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251  AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10

20

30

40

50

60

916

```

m587.pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                ||||||||||||||||:|||||||||||||||||||||||||||||||
g587          MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587.pep      TGATSFIPTEIQENGSTNDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                ||||||||||||||||:|||||||||||||||||||||||||||||||
g587          TGATSFIPTEIQENGSTNDMLAGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

                130     140     150     160     170     180
m587.pep      NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
                |||||:| ||||||||| |||||||||||||||||||||
g587          NKRMSDISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKKRGLCPFYNLRINYEY
                130     140     150     160     170     180

                190     200     210     220     230     240
m587.pep      LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
g587          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1819>:

```

a587.seq
1   ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTAT
201 CCCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGGCG TACGGACTGA CCGGAATAC CGACATTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCACCG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCGGTCGTC CTCTCATGTA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCAATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1820; ORF 587.a>:

```

a587.pep
1   MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51  AELAAPVYIQ TGATSFIPTE IQENGSTND DMLVGTGLRL YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTE*

```

m587/a587 95.2% identity in 289 aa overlap

```

                10      20      30      40      50      60
m587.pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                ||||||||||||||||:|||||||||||||||||||||||||||||||
a587          MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587.pep      TGATSFIPTEIQENGSTNDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                ||||||||||||||||:|||||||||||||||||||||||||||||||
a587          TGATSFIPTEIQENGSTNDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

```

917

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLKGQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1  atgcttaaac atctcgcat cctactgccc gccatgatgt tcgccctccc
51  cgccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaaaagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgccgg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaacaag gcttggcaca cggcaggttc gccgcctcgc aaaacggcga
351 aaccctcttt tattatgaaa tgcgaaacac gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1  MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGCCG GCGTCCTGA CTTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAAGAC GGTAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTTCG TTTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAAG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAAC
401 TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1  MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAKGKTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FLEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMK EVKLPMKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

918

```

m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
g588        MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGKGLPSGKGIWRCRDGRGYTGS
              10      20      30      40      50      60

              70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
g588        FKNGKFDGQGVYTVAAGREVLFEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
              70      80      90      100     110     120

              130     139
m588.pep    IMKCENGMIKEVKLPKNKX
g588        YYEMRTRHDX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51 CGCCGCGTCC GCCGTTCTGA CTTCTATCA AGAACCCGGC TGCACCTACG
101 AAGGCGATGT CGGCAAAGAC GGTAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTG TTTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAAG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAA GAAGTGAAGC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1  MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPKAGKGTWR
51 CQDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKL PKNK*

m588/a588    96.4% identity in 138 aa overlap

              10      20      30      40      50      60
m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
a588        MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKDGKPKAGKGTWRCQDGRNYTGS
              10      20      30      40      50      60

              70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
a588        FKNGKFDGQGVYTVAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
              70      80      90      100     110     120

              130     139
m588.pep    IMKCENGMIKEVKLPKNKX
a588        IMKCENGMIKEVKLPKNKX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
1  atgcaacaaa aaatccgttt ccaaatcgag gcgatgacct gtcaggcatg
51 tgcttcgcgc attgaaaaag tgttgaacaa aaaagatttt gtcgaatcgg
101 cgggagtgaa ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcgaaaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atatcggtcg gcggttggtg cttttgctga ccatcaatat cccgttcctt

```

```

301 atcggatatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgaac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaaggc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgtcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggctgta tgggtgatcg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcaccaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgccgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttacc
751 cgcaccaacc acggcgaacg catcgctgcc gacggcatta tcgaaagcgg
801 cagcggtttg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggg gggcggcaaa gtgttggcgg gcgcgctgat gaccgaaggc
901 agcgtggtgt accgcgcgcg gcagctcggc agccaaaccc tgcctggcga
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcatc
1051 gcgcttctga cttttatcgt tgccttggctg attaagggcg attggacggg
1101 cgcactgatg cacgcggttg ccgttttggg gattgcctgc ccgtgcgcgc
1151 tcggtctggc gacccctgcc gcgattatgg tcggcatggg caaagcggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtatttg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc cgcggtttat tacgttcccg acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgccgtcgag caaaacgcgc cccaccgcgt
1401 cgccgcgcgc atcgtctccg ccgcacaagc gcgcggtttg gagattcccg
1451 ctgcacaaaa tgcgcaaac gttgtcggag caggcattac cgccgaagtg
1501 gaaggcgttg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacg atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccaagc cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccg tggcgatggg
1851 cggcgacggc atcaacgacg cgcccgcgct tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacgttgccg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgttcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttcttctaca
2051 atatatggg cattccgctc gccgcgctcg gctttttaaa tcccgtcata
2101 gcaggcgcgg caatggcggc aagctcggtt tcggtattgg gcaatgcctt
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE  AMTCQACASR  IEKVLNKKDF  VESAGVNFAS  EEAQVTFDGS
51  KTSVADIAKI  IEKTGYGAKE  KTEDTLQPPE  AEHHIGWRLW  LLLTINIPFL
101  IGMVGMMLKG  LNWTRHDWMI  PPVWQFVLAS  IVQLWLAIPF  YKSAWASIKG
151  GLANMDVLVT  IGTVSIYLYS  VYMLFFSSHA  AHGMAHVYFE  AGVMVIGFVS
201  LGKFLEHRTK  KSSLNSLGLL  LKLTPTQVNV  QRNGEWKQLP  IDQVQIGDLI
251  RTNHGERIAA  DGIIESGSWG  ADESHLTGES  NPEEKKAGGK  VLAGALMTEG
301  SVVYRAAQLG  SQTLLGDMMN  ALSEAQGSKA  PIARVADKAA  AVFVPTVVGI
351  ALLTFIVAWL  IKGDWTVAlM  HAVAVLVIAc  PCALGLATPA  AIMVGMGKAV
401  KHGIWFKDAA  AMEEAAHVDA  VVLDKTGTLT  EGRPQVAAYV  YVPDSGFDED
451  ALYRIAAAVE  QNAAHPLARA  IVSAAQARGL  EIPAAQNAQT  VVGAGITAEV
501  EGVGLVKSgK  AEFAELTLPK  FSDGVWEIAS  AVTVSVNGKP  IGAFALSDAL
551  KADTAEAIgR  LKKHNIDVYI  MSGDNQSTVE  YVAKQLGIAH  AFGNMSPCDK
601  AAEVQKLKAA  GKTVMVGDG  INDAPALAAA  NVSFAMKGGA  DVAETASAT
651  LMQHSVNQLA  DALLISQATL  ENIKQNLFFA  FFYNILGIPL  AALGFLNPVI
701  AGAAMAASSV  SVLGNALRLK  WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA  AAATCCGTTT  CCAAATCGAA  GGCATGACCT  GCCAGGCCTG
51  CGCTTCGCGC  ATTGAAAAAG  TGTTGAACAA  AAAAGATTTT  GTCGAATCGG
101  CGGGGGTAAA  CTTGCCCAGC  GAAGAGGCGC  AGGTAGTGTT  TGACGACAGC
151  AAAACCTCAG  TAGCCGACAT  TGCCAAAATC  ATTGAGAAAA  CCGGTTACGG
201  CGCGAAGGAA  AAAACGGAAG  ATACATTGCC  GCAACCCGAA  GCAGAACACC
251  ATATCGGCTG  GCGGCTGTGG  CTGCTGTTCa  CCATCAACGT  CCCGTTTCCT

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920

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301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTTACAA AAGCGCGTGG GCGAGCATTA AGGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGCTACTGGG TAAATTTTTG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGGCGGGCG
851 GCAAAGTGTT GGCGGCGCGG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AACCAGCTC GCGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TGCGCGCGTA GCCGATAAAG
1001 CGGCTGCGGT ATTCGTGCCT GCCGTCTGG GCATTGCGTT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CGCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CGGTTAAACA CGGTATTTGG
1201 TTTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCCAGCTCG ATGCCGTCGT
1251 GTTGACAAA ACCGGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCCG
1301 TTTATTGCGT TCCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCGCCGCCG TCGAACAAAA CGCCGCCCAT CCGCTCGCCC GTGCCATCGT
1401 CTCCGCCGCC CAAGCGCGCG GTTTGGACAT TCCCGCCGCA CAAAACGCAC
1451 AAACCGTTGT CGGCGCAGGC ATTACGCCG AAGTGGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TGCGGTCTCA GTCGATAACA
1601 AACCACATCG CGCATTGCGA CTTGCCGACG CGTTGAAAGC CGATACGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCTT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAACCTCAAAG CCGCCGGCAA AACCGTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCC
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTG
2051 CTCTCGCCGC GCTTGCTTTT TTAAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGGCAAGCT CGGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAAACGGGT
2151 AAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

```

m589.pep..
  1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
 51  KTSVADIANK IEKTGYGAKE KTEDTLPOPE AEHHIGWRLW LLFTINVPFLL
101  IGMAGMMIGR HDWMIPPLWQ FALASVVQLW LAIPFYKSAW ASIKGGLANMM
151  DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVYFEVGMV IGFBVSLGKFL
201  EHRTKKSSLN SLGLLLKLTP TQVNVQRNGE WKQLPIDQVQ IGDILIRANHG
251  ERIAADGIEE SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSSVYR
301  ATQLGSQTQL GDMMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLTF
351  IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401  FKDAAMEEEA AHVDAVVLDK TGTLTEGSPQ VAAVYCVFDS GFDEDALYRI
451  AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
501  VKAGKAEFAE LALPKFLDGV WDIASIVAVS VDNKPIGAFA LADALKADTA
551  EAIGRLKKHN IDVYIMSGDN QGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
601  KLKAAGKTVA MVGDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651  VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701  AASSVSVLSN ALRLKRVKID *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

              10      20      30      40      50      60
m589.pep      MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANKI
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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921

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g589      MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADIAKI
           10          20          30          40          50          60

           70          80          90         100         110
m589.pep  IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLTINIPFLIGMVGMMLKGLNWTRHDWMI
           70          80          90         100         110         120

           120         130         140         150         160         170
m589.pep  PPLWQFALASVVQLWLAI PFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      PPVWQFVLASIVQLWLAI PFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
           130         140         150         160         170         180

           180         190         200         210         220         230
m589.pep  AYGMAHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           190         200         210         220         230         240

           240         250         260         270         280         290
m589.pep  IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           250         260         270         280         290         300

           300         310         320         330         340         350
m589.pep  SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLT FIVTWL
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVGIALLT FIVAWL
           310         320         330         340         350         360
```


922

m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLVIAACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVALMHAVAVLVIAACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
m589.pep	420	430	440	450	460	470
	VVLDKGTGLTEGSPQVAAYVCVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKGTGLTEGRPQVAAYVYPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
m589.pep	480	490	500	510	520	530
	DIPAAQNAQTVVGAGITAEEVGVLVKAGKAFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEEVGVLVKSGKAFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTAEAIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSDALKADTAEAIGRLKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
m589.pep	660	670	680	690	700	710
	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLSNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLGNALRLK					
	670	680	690	700	710	720
m589.pep	720					
	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

```

a589.seq
1  ATGCAACAAA AAGTCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCATG
51  TGCTTCGCGC ATTGAAAAAG TGTGTAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCTC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GAGGTTGTGG CTTTGTGCTG CCATCAATAT CCCGTTTCCTT
301 ATCGGTATGG TAGGGATGAT GCTAAAAGGG CTGAATTGGA CACGGCATGA
351 TTGGATGTTG TCGCCCTTGT TGCAGTTTGC ATTGGCGAGT GTGGTGCAGC
401 TTTGGCTGGC GGTGCCATTT TACAAAAGCG CGTGGGCGAG CATTAAAGGC
451 GGGCTGGCGA ATATGGACGT ACTCGTTACC ATCGGCACGG TCTCGATTTA
501 CCTGTATTCC GTCTATATGC TGTTTTTCAG CCCGCACGCG GCGTACGGTA
551 TGGCGCATGT GTATTTTGAA GTAGGCATAA TGGTGATTGG TTTTGTGTCA
601 CTGGGTAAAT TTTTGAACA CCGCACCAA AAATCCAGCC TGAACAGCTT
651 GGGCTTGCTG CTCAACTCA CGCCAACCA AGTCAACGTG CAACGCGATG
701 GCGAATGGCG GCAGTACCC ATCGACCAAG TGCAAATCGG CGACCTAATC
751 CGCGCCAATC ACGGCGAAG CATTGCCGCC GACGGCATCA TAGAAAGCGG
801 CAGCGGCTGG GCGGACGAAA GCCATCTTAC CGGCGAATCC AATCCCGAAG
851 AGAAAAAGGC AGGCGGCAAA GTATTGGCGG GCGCGTGAT GACTGAAGGC
901 AGCGTGGTGT ACCGCGCCGC GCAGCTCGGC AGCCAAACCC TGCTCGGCGA
951 CATGATGAAC GCGCTCTCCG AAGCGCAAGG CAGTAAAGCA CCGATTGCGC
1001 GTGTGGCGGA CAAGGCGGCG GCGGTATTCG TGCCTGCCGT TGTGGGCATC
1051 GCACTTTTGA CTTTATATCG TACTTGCTG ATTAAGGCG ATTGGACGCT
1101 CGCATTGATG CACGCCGTCG CCGTTTGGT GATTGCCTGC CCGTGTGCAC

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1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCCAGGC GCGCGGTTTG GAGATTCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTTGGTAAA AGCAGGCAAA GCCGAATTG CCGAAGTGAC
1551 CTGCGCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAA CGGCAAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCCGCGGAAG TGCAGAACT CAAAGCCGCC GGCAAAACCG TGGCGATGGT
1851 CGGCGACGGC ATCAACGACG CGCCCGCGCT CGCCCGCGCC AACGTCAGCT
1901 TCGCCATGAA AGGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCCGG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCGCTC GCGCGCTCG GCTTTTAAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGGTAAAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

a589.pep

```

1  MQQKVRFAQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIANK IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMLKG LNWTRHDWML SPLLOFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSGW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIA PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGLT EGKPOVAAVY CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVVG DG INDAPALAAA NVSFAMKGGG DVAEHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*

```

m589/a589 94.9% identity in 725 aa overlap

```

          10      20      30      40      50      60
m589.pep  MQQKIRFAQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
          ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      MQQKVRFAQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
          10      20      30      40      50      60

          70      80      90      100     1      110
m589.pep  IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVFPFLIGMAGMMIG-----RHDWMI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLAINIPFLIGMVGMMMLKGLNWTRHDWML
          70      80      90      100     110     120

          120     130     140     150     160     170
m589.pep  PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      SPLLOFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          130     140     150     160     170     180

          180     190     200     210     220     230
m589.pep  AYGMHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWRQLP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      AYGMHVYFEVGIMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
          190     200     210     220     230     240

```

924

m589.pep	240	250	260	270	280	290
	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
a589	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
	250	260	270	280	290	300
m589.pep	300	310	320	330	340	350
	SVVYRATQLGSQTLGDMMNALSEAQSGKAPIARVADKAAAVFVPAVVGIALLTFIIVTWL					
a589	SVVYRAAQLGSQTLGDMMNALSEAQSGKAPIARVADKAAAVFVPAVVGIALLTFIATWL					
	310	320	330	340	350	360
m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
a589	IKGDWTLALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
m589.pep	420	430	440	450	460	470
	VVLDKTGTLTGEGSPQVAAYVCVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
a589	VVLDKTGTLTGEGKPQVAAYVCVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
m589.pep	480	490	500	510	520	530
	DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAFAELALPKFLDGVWDIASIVAVSVDNKP					
a589	EIPTAQNQITVVGAGITAEVKGAGLVKAGKAFAELTLPKFSDGVWEIASVAVSVNGKP					
	490	500	510	520	530	540
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTAEAIIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
a589	IGAFALADALKADTAEAIIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
	550	560	570	580	590	600
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
a589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
m589.pep	660	670	680	690	700	710
	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
a589	DALSVSRATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
	670	680	690	700	710	720
m589.pep	720					
	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:

g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcggca gtattgctcg gcgttgcttt
51  ggggtacacct tattatttgg gtgtcaaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctggtttac ctctacggaa acgacgggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtgttgga acagcgggtt acgctggtaa accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgctgaa acggaaaaag ttttggaacg ctttttggg aaacaagttc
401 cggtttcctt tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtggtc ccgctttcga ttatgaagaa ctgtcgggca tcaggctgca

```

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501 ctgggaaggc ctgacggggg aaacggttta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttgttca aaatcaagct ggcagacaaa
601 ggcgatgccg cgtttgaaaa agcgcatttc gattcggaaa cttcagacgg
651 catcaatccg cttgcttttg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggt gtcgattaca acgtcaaatt gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccgggga atcgggcgcg tttatcgaca gcgaaggcg gttccgtttc
901 gatacgttg tgtacggcga tgaaaaatac ggcccgctgg acatccatat
951 cgctgccgaa cacctcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgceg cagtcaaagg cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag ggaaaaattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tcctcaaaaa atgttggaag atttgccggt aagtcaggct ggaaatattt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgcct gatggtggac agtacggctc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgcccctg aagttaaacg ggaaaacgct gcaaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttcgggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

```

g590.pep..
1  M KKPLISVAA VLLGVALGTP YYLGVKAEES LTQQQKILQK TGFLTVESHQ
51  YDRGWFTSTE TTVIRLKP EL LHNAQKYL PD NLKIVLEQPV TLVNHITHGP
101 FAGGFGTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVVGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKG MKKEDLN
401 QLGLMLKKT E ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEARASIAD
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

```

m590.seq (partial) ..
1  ..TGGTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51  GAATAATGCC CGAAATACC TGCCGGATAA CCTGAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCCGGACGC AGCGGTACAT TGAAACCGAG TTCAAATACG CGCCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAA GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG .CTGCACT GGGAAKGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTTGTTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCATTTCGA TTCGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGGA AAAATCTCTC CTAGAATGGA
551 AAGAGGTTGT CGATTACAAC GTCAAGTTAA ACGAATCGT CAATCTTGTT
601 ACCGATTTCG AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGCGAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTTACC AACAAATCCG TATTGGACAT
951 TAAAGCTTTC CGATTACGC TGCCATCGGG AAAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGCGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTTCT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGTT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590.pep.. (partial)

```

1  WFTSMETTVI RLKPELLNNA RYLPDNLKT VLEQPVTLVN HITHGPFAGG
51  FGTQAYIETE FKYAPETEKV LERFFGKQVP ASLANTVYFN GSGKMEVSVP
101 AFDYEELSGI XLHWEXLTGE TVYQKGFKSY RNYDAPLKF IKLADKGDAA
151 FEKVHFDSET SDGINPLALG SSNLTLEKFS LEWKEGVDYN VKLNELVNLV
201 TDLQIGAFIN PNGSIAPSKI EVGKLAFSTK TGESGAFINS EGQFRFDTLV
251 YGDEKYGPLD IHIAAEHLDA SALTVLKRKF AQISAKKMTE EQIRNDLIAA
301 VKGEASGLFT NNPVLDIKTF RFTLPSGKID VGGKIMFKDM KKEDLNQLGL
351 MLKKTEADIR MSIPQKMLED LAVSQAGNIF SVNAEDEAEG RASLDDINET
401 LRLMVDSTVQ SMAREKYLT NGDQIDTAIS LKNNQLKLNG KTLQNEPEPD
451 FDEGGMVSEP QQ*

```

m590 / g590 93.1% identity in 462 aa overlap

```

                                10      20      30
m590.pep                      WFTSMETTIVIRLKPELLNNARKYLPDNLKT
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      VKAESLTQQQKILQKTGFLTVESHQYDRGWFTSTETTIVIRLKPELLHNAQKYLDPNLKI
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m590.pep      VLEQPVTLNVNITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      VLEQPVTLNVNITHGPFAGGFGTQAHIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m590.pep      GSGKMEVSVPAPFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      GSGKMEVSVPAPFDYEELSGIRLHWEGLTGETVYQKGFKSYRNSYDAPLFKIKLADKGDAA
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m590.pep      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      FEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
                                210     220     230     240     250     260

                                220     230     240     250     260     270
m590.pep      PNGSIAPSKIEVGKLAFSTKTGESGAFINSEGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      PNGSIAPSKIEVGKLAFSTKTGESGAFIDSEGRFRFDTLVYGDEKYGPLDIHIAAEHLDA
                                270     280     290     300     310     320

                                280     290     300     310     320     330
m590.pep      SALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSGKID
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      SALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGDASGLFTHDPVLNLIKIFRFTLPQGKID
                                330     340     350     360     370     380

                                340     350     360     370     380     390
m590.pep      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      VGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEA
                                390     400     410     420     430     440

                                400     410     420     430     440     450
m590.pep      RASLDDINETLRLMVDSTVQSMAREKYLTNGDQIDTAISLKNQLKLNGKTLQNEPEPD
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      RASLADINETLRLMVDSTVQSMAREKYLTLDGNQIDTVISLKNALKLNGKTLQNEPDPD
                                450     460     470     480     490     500

                                460
m590.pep      FDEGGMVS-EPQQX
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      FDEGDMVSGQPHX
                                510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1   ATGAAAAAAC CTTTGATTTT GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTTGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
301 TTTGCCGGCG GATTGCGGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451 GTCAGTGTTT CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCCG CGTTTGAAAA AGTGCATTTC GATTTCGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGT
751 GTCAATCTTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGACG ATTAATACTT TCCGATTACG GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGCGCGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1   MKKPLISVAA ALLGVALGTP YYLGVKAEEES LTQQQKILQE AGFLTVESHQ
51  YERGWFSTTE TTVIRLKPTEL LHNAQKYLDP NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLT L EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDEKY GPLDIHIAAE HLDASALTVL KKKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTLNGDQID TAISLKNQNL KLNGKTLQNE
501 PEPDFDEGGM VSEPPQ*
```

m590/a590 97.8% identity in 462 aa overlap

```
m590.pep
10 20 30
WFTSMETTIVIRLKPPELLNNARKYLPDNLKT
|||||
a590 VKAEEESLTQQQKILQEAGFLTVESHQYERGWFSTETTIVIRLKPPELLHNAQKYLDPNLKT
30 40 50 60 70 80

40 50 60 70 80 90
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
|||||
a590 VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
90 100 110 120 130 140

100 110 120 130 140 150
m590.pep GSGKMEVSVPAFDYEEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
```

928

```

|||||
a590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKLNELVNLVTDLQIGAFIN
          |||||
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKLNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLA FSTKTGESGAFINSEGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLA FSTKTGESGAFIDSEGQFRFCTLVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKMTEE QIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLP SGKID
          |||||
a590      SALTVLKRKFARISAKMTEE QIRNDLIAAVKGEASGLFTHNPVLDIKTFRFTLP SGKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLT LNGDQIDTAISLKNQKLKNGKTLQNEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLT LNGDQIDTAISLKNQKLKNGKTLQNEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEFPQQX
          |||||
a590      FDEGGMVSEFPQQX
          510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTTGATTTC GGTTCGCGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101  AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151  TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGTCTGAA
201  ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251  CAGTGTGGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301  TTCGCCGGCG GATTCCGGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351  CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401  CGGCTTCCTT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451  GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501  CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551  ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601  GGCAGATGCC CGTTTGAAAA AGTGCATTTC GATTTCGAAA CTTCAGACGG
651  CATCAATCCG CTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701  CCCTAGAAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAC TG
751  GTCAATCTTG TTACCGATT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801  CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851  AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901  GATACACTGG TGTACGGCGA TGAAAAATAC GGCCCGCTGG ACATCCATAT
951  CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTCA CCAACAATCC
1101 CGTATTGGAG ATTAAACTT TCCGATTCAC GCTGCCATCG GAAAAATCG
1151 ATGTGGGCGG AAAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAT
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT

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1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
 1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
 1351 ATCAACGAGA CCTTGGCCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
 1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
 1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAAAGTT GCAAAACGAA
 1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
 1551 A

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

1 MKKPLISVAA ALLGVALGTP YYLGVKAEEES LTQQQKILQE TGFLTVESHQ
 51 YERGWFSTME TTIVRLKPEL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
 101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
 151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
 201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
 251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
 301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
 351 LIAAVKGEAS GLFTNNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
 401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
 451 INETLRMLVD STVQSMAREK YLTNGDQID TAISLKNQNL KLNKTLQNE
 501 PEPDFDEGGM VSEPPQ*

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAA	ALLGVALGTP	YYLGVKAEEES	LTQQQKILQE	TGFLTVESHQ	YERGWFSTME
g590	MKKPLISVAA	VLLGVALGTP	YYLGVKAEEES	LTQQQKILQKT	TGFLTVESHQ	YDRGWFTSTE
	10	20	30	40	50	60
	70	80	90	100	110	120
m590-1.pep	TTIVRLKPEL	LNNARKYLPD	NLKTVLEQPV	TLVNHITHGP	FAGGFGTQAY	IETEFKYAPE
g590	TTIVRLKPEL	LHNAQKYL	PDNLKIVLEQ	PVTLVNHITHGP	FAGGFGTQAH	IETEFKYAPE
	70	80	90	100	110	120
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFG	KQVPASLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
g590	TEKVLERFFG	KQVPVSLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
	130	140	150	160	170	180
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDA	PLFKIKLADK	GDAAFEKVHF	DSETSDGINP	LALGSSNLTL	EKFSLEWKEG
g590	FKSYRNSYDA	PLFKIKLADK	GDAAFEKAH	FDSETSDGINP	LALGSSNLTL	EKFSLEWKEG
	190	200	210	220	230	240
	250	260	270	280	290	300
m590-1.pep	VDYNVKLNEL	VNLVTDLQIG	AFINPNGSIA	PSKIEVGKLA	FSTKTGESGA	FINSEGQFRF
g590	VDYNVKLNEL	VNLVTDLQIG	AFINPNGSIA	PSKIEVGKLA	FSTKTGESGA	FIDSEGRFRF
	250	260	270	280	290	300
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KRKFAQISAK	KMTEEQIRND	LIAAVKGEAS
g590	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KRKFAQISAK	KMTEEQIRND	LIAAVKGDAS
	310	320	330	340	350	360
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVLD	IKTFRFTLPS	GKIDVGGKIM	FKDMKKEDLN	QLGLMLKKTE	ADIRMSIPQK
g590	GLFTHDPVLI	NIKIFRFTLP	QKIDVGGKIM	FKGMKKEDLN	QLGLMLKKTE	ANIRMSIPQK
	370	380	390	400	410	420
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQA	GNIFSVNAED	EAEGRASLDD	INETLRMLVD	STVQSMAREK	YLTNGDQID
g590	MLEDLAVSQA	GNIFSVNAED	EAERASIADI	NETLRMLVD	STVQSMAREK	YLTLDGNQID
	430	440	450	460	470	480
	490	500	510			
m590-1.pep	TAISLKNQNL	KLNKTLQNE	PEPDFDEGGM	VSEPPQX		

930

```

g590      |:||||| |:||||| |:||||| |:||||| |:|:|
          TVISLKNNAKLNKKTQNEPDPDFDEGDMVSGQPHX
          490      500      510

a590/m590-1 98.3% identity in 516 aa overlap

a590.pep      10      20      30      40      50      60
MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQEAGFLTVESHQYERGWFTSTE
m590-1      10      20      30      40      50      60
MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQETGFLTVESHQYERGWFTSME

a590.pep      70      80      90      100     110     120
TTVIRLKPELLHNAQKYLDPNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
m590-1      70      80      90      100     110     120
TTVIRLKPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE

a590.pep     130     140     150     160     170     180
TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
m590-1     130     140     150     160     170     180
TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG

a590.pep     190     200     210     220     230     240
FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
m590-1     190     200     210     220     230     240
FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG

a590.pep     250     260     270     280     290     300
VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTSTKTGESGAFIDSEGQFRF
m590-1     250     260     270     280     290     300
VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTSTKTGESGAFINSEGQFRF

a590.pep     310     320     330     340     350     360
GTLVYGDEKYGPLDIHIAAEHLASALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEAS
m590-1     310     320     330     340     350     360
DTLVYGDEKYGPLDIHIAAEHLASALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEAS

a590.pep     370     380     390     400     410     420
GLFTHNPVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK
m590-1     370     380     390     400     410     420
GLFTNPNVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK

a590.pep     430     440     450     460     470     480
MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTLNGDQID
m590-1     430     440     450     460     470     480
MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTLNGDQID

a590.pep     490     500     510
TAISLKNQKLKLNKKTQNEPEPDPDFDEGGMVSEPQQX
m590-1     490     500     510
TAISLKNQKLKLNKKTQNEPEPDPDFDEGGMVSEPQQX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1841>:

```

g591.seq
1   TTGCAAACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG GTTGTGCGGC GTC AAGGTTG
101 TGCGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGCT ACGTCAA AAT
201 GGTGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGTCCG
301 CTGACCAACC TCGCAActggc ggTTTTGCTG TACGGACTGa gctTttcctt
351 cggcgtaaCC GAACTGCGGC CCTatgtcgg cacagtcgaA cccgacaccg

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931

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401 ttgccgCCCC CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGA AAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC ctcaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCCg ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAaCagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGA
1001 CAACCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTCAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CAAAACATC GGTTCGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCGCCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1  LQTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKR
51  DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVLNLL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFLGLALMM LMMAAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCG TGGGGCGGTT ACGTCAAAAT
201 GGTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGA AAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAA TCACCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGA
1001 CAACCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTGAG
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CAAAACATC GGTTCGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..